ANTI-CLEC2D ANTIBODIES AND METHODS OF USE THEREOF

RELATED APPLICATION

[001] This application claims priority to and the benefit of Indian Provisional Patent Application No. 201941005395, filed on February 11, 2019, the entire contents of which are incorporated herein by reference.

TECHNICAL FIELD

[002] The present disclosure relates to immunology, especially immune-oncology. Particularly, this disclosure relates to novel antibody molecules against CLEC2D antigen. This disclosure also relates to multiple formats and amino acid compositions of the disclosed antibody molecules, variable regions of the heavy and light chains of the antibody molecules, and CDR composition and length distribution against CLEC2D antigen. The compositions of this disclosure can be used either as monotherapies or in combination with other antibody molecules or any other therapeutic agents that are relevant for the treatment or prevention of diseases, such as cancer.

BACKGROUND

[003] Modulation of immune cell checkpoint receptors via antibody-based/directed therapeutic approaches has been gaining constant interest over the last decade. Many of these receptors are involved in T cell checkpoint modulation. However, B cell, natural killer (NK) cell, and myeloid cell checkpoint modulation is attracting attention.

[004] NK cells are part of the innate immunity which recognize and induce cytotoxicity against a wide range of target cells, such as tumor cells or virus infected cells. In addition, NK cells participate in the initiation and progress of the adaptive immune response through the production of various cytokines. Usually, these responses are regulated by the interaction of a wide array of activating and inhibitory receptors with ligands on the surface of the target cells and immune cells.

[005] The NK cell receptors are divided into two main structural classes: the immunoglobulin and C-type lectin-like (CTL) superfamilies. The NKR-P1 receptors (e.g., CD161) are a family of C-type lectin-like transmembrane molecules that are important immuno-regulatory genes and are expressed on various cell types, including spleen dendritic cells, subsets of T cells and

granulocytes. The Lectin-Like Transcript 1 (LLT1) or C-Type Lectin Domain Family 2 Member D (CLEC2D) or osteoclast inhibitory lectin (OCIL) molecule is a ligand for the CD161 receptor and this interaction differentially regulates the NK cell and T cell function. There are six splice variants of CLEC2D, isoform 1 being the canonical sequence which is expressed on NK cells, T cells, monocytes/macrophages, activated B cells and dendritic cells, and functions as a human NK cell activating receptor. The polypeptide chain of CLEC2D can be divided into the N-terminal cytoplasmic part, trans-membrane and stalk regions and C-terminal CTL ectodomain with two predicted N-glycosylation sites.

[006] CLEC2D and CD161 interaction leads to escape from the host defense in several disease scenarios, including various cancers. Such immune escape has been reported in human glioblastoma and other diseases. Moreover, CLEC2D expression on B cells is thought to regulate cross-talk between NK cells and antigen presenting cells (APC). Blocking CLEC2D-CD161 interaction therefore provides a new therapeutic option for the treatment of various cancers.

[007] The downstream signaling of CLEC2D-CD161 interactions is poorly understood. The interaction of CLEC2D / CD161 inhibits NK cell functions and stimulates T cell proliferation and secretion of cytokines. Hence, the effects of CLEC2D / CD161 interaction could be reversed by using monoclonal antibodies specifically binding to CLEC2D, and disrupting the interaction between CLEC2D and its known receptor CD161 or other unknown cellular mechanisms.

SUMMARY

[008] The disclosure provides an isolated antibody or antigen-binding fragment thereof comprising a heavy chain and a light chain, wherein the heavy chain comprises a sequence selected from the group consisting of: (a) a sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 46, SEQ ID NO: 65, SEQ ID NO: 59, and SEQ ID NO: 99; (b) a sequence that is at least 80%, at least 81%, at least 82%, at least 83% , at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 57, SEQ ID NO: 91, SEQ ID NO: 98, SEQ ID NO: 84, SEQ ID NO: 58, SEQ ID NO: 88, SEQ ID NO: 96, SEQ ID NO: 47, SEQ ID

NO: 17, and SEQ ID NO: 8; (c) a sequence that is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 93, SEQ ID NO: 53, SEQ ID NO: 95, SEQ ID NO: 23, SEQ ID NO: 103, and SEQ ID NO: 7; (d) a sequence that is at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 45, SEQ ID NO: 15, SEQ ID NO: 51, SEQ ID NO: 44, SEQ ID NO: 73, SEQ ID NO: 36, SEQ ID NO: 77, SEQ ID NO: 50, and SEQ ID NO: 6; (e) a sequence that is at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5% or at least 99.9% identical or 100% identical to a sequence selected from SEQ ID NO: 97, SEQ ID NO: 16, SEQ ID NO: 76, SEQ ID NO: 9, SEQ ID NO: 89, SEQ ID NO: 107, SEQ ID NO: 68, SEQ ID NO: 29, SEQ ID NO: 67, SEQ ID NO: 74, SEQ ID NO: 32, SEQ ID NO: 81, SEQ ID NO: 106, SEQ ID NO: 31, SEQ ID NO: 62, SEQ ID NO: 48, SEQ ID NO: 75, SEQ ID NO: 12, SEQ ID NO: 102, SEQ ID NO: 54, SEQ ID NO: 80, SEQ ID NO: 26, SEQ ID NO: 30, SEQ ID NO: 92, SEQ ID NO: 108, and SEQ ID NO: 79; (f) a sequence that is at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5% or at least 99.9% identical or 100% identical to a sequence selected from SEQ ID NO: 105, SEQ ID NO: 101, SEQ ID NO: 4, SEQ ID NO: 72, SEQ ID NO: 28, SEQ ID NO: 64, SEQ ID NO: 25, SEQ ID NO: 60, SEQ ID NO: 55, SEQ ID NO: 52, SEQ ID NO: 27, SEQ ID NO: 43, SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 14, SEQ ID NO: 85, SEQ ID NO: 13, SEQ ID NO: 61, SEQ ID NO: 42, SEQ ID NO: 39, SEQ ID NO: 10, SEQ ID NO: 49, SEQ ID NO: 24, SEQ ID NO: 40, SEQ ID NO: 63, SEQ ID NO: 78, SEQ ID NO: 2, SEQ ID NO: 94, and SEQ ID NO: 5; (g) a sequence that is at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5% or at least 99.9%

identical or 100% identical to a sequence selected from SEQ ID NO: 11, SEQ ID NO: 35, SEQ ID NO: 86, SEQ ID NO: 22, SEQ ID NO: 69, SEQ ID NO: 41, SEQ ID NO: 3, SEQ ID NO: 66, SEQ ID NO: 37, SEQ ID NO: 56, SEQ ID NO: 21, SEQ ID NO: 38, SEQ ID NO: 90, SEQ ID NO: 100, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 83, SEQ ID NO: 1, and SEQ ID NO: 19; and (h) a sequence that is at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5% or at least 99.9% identical or 100% identical to a sequence selected from SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 87, SEQ ID NO: 82, and SEQ ID NO: 104, wherein the antibody or antigen-binding fragment thereof binds to C-Type Lectin Domain Family 2 Member D (CLEC2D).

[009] The disclosure provides isolated antibodies or antigen-binding fragments thereof comprising a heavy chain and a light chain, wherein the light chain comprises a sequence selected from the group consisting of: (a) sequence that is at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 218, SEQ ID NO: 249, SEQ ID NO: 230, SEQ ID NO: 279, SEQ ID NO: 316, SEQ ID NO: 237, SEQ ID NO: 322, SEQ ID NO: 225, SEQ ID NO: 318, SEQ ID NO: 233, SEQ ID NO: 305, SEQ ID NO: 280, SEQ ID NO: 283, SEQ ID NO: 242, SEQ ID NO: 286, SEQ ID NO: 297, SEQ ID NO: 309, and SEQ ID NO: 246; (b) a sequence that is at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 222, SEQ ID NO: 258, SEQ ID NO: 219, SEQ ID NO: 313, SEQ ID NO: 294, SEQ ID NO: 303, SEQ ID NO: 317, SEQ ID NO: 273, SEQ ID NO: 266, SEQ ID NO: 315, SEQ ID NO: 257, SEQ ID NO: 288, SEQ ID NO: 301, SEQ ID NO: 221, SEQ ID NO: 240, SEQ ID NO: 299, SEQ ID NO: 247, SEQ ID NO: 263, and SEQ ID NO: 274; (c) a sequence that is at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 231, SEQ ID NO: 250, SEQ ID NO: 260, SEQ ID NO: 226, SEQ ID NO: 271, SEQ ID NO: 256, SEQ ID NO: 272, SEQ ID NO: 278, SEQ ID NO: 302, SEQ ID NO: 320, SEQ ID NO: 295, SEQ ID

NO: 292, SEQ ID NO: 229, SEQ ID NO: 264, SEQ ID NO: 252, SEQ ID NO: 267, SEQ ID NO: 304, SEQ ID NO: 300, SEQ ID NO: 311, and SEQ ID NO: 324; (d) a sequence that is at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 259, SEQ ID NO: 239, SEQ ID NO: 281, SEQ ID NO: 228, SEQ ID NO: 217, SEQ ID NO: 227, and SEQ ID NO: 251; (e) a sequence that is at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100%identical to a sequence selected from SEQ ID NO: 307, SEQ ID NO: 262, SEQ ID NO: 253, SEQ ID NO: 276, SEQ ID NO: 323, SEQ ID NO: 234, SEQ ID NO: 261, SEQ ID NO: 312, and SEQ ID NO: 290; (f) a sequence that is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 254, SEQ ID NO: 289, SEQ ID NO: 238, SEQ ID NO: 268, SEQ ID NO: 248, SEQ ID NO: 284, SEQ ID NO: 244, SEQ ID NO: 310, SEQ ID NO: 243, SEQ ID NO: 285, SEQ ID NO: 220, SEQ ID NO: 255, SEQ ID NO: 293, SEQ ID NO: 298, SEQ ID NO: 235, SEQ ID NO: 319, SEQ ID NO: 245, SEQ ID NO: 224, SEQ ID NO: 291, SEQ ID NO: 277, and SEQ ID NO: 232; and (g) a sequence that is at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 282, SEQ ID NO: 308, SEQ ID NO: 287, SEQ ID NO: 321, SEQ ID NO: 236, SEQ ID NO: 265, SEQ ID NO: 270, SEQ ID NO: 275, SEQ ID NO: 306, SEQ ID NO: 296, SEQ ID NO: 241, SEQ ID NO: 314, and SEQ ID NO: 223; wherein the antibody or antigen-binding fragment thereof binds to CLEC2D.

[010] The disclosure provides isolated antibodies or antigen-binding fragments thereof, comprising: (a) a heavy chain comprising a sequence selected from: (i) a sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 46, SEQ ID NO: 65, SEQ ID NO: 59, and SEQ ID NO: 99; (ii) a

sequence that is at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 57, SEQ ID NO: 91, SEQ ID NO: 98, SEQ ID NO: 84, SEQ ID NO: 58, SEQ ID NO: 88, SEQ ID NO: 96, SEQ ID NO: 47, SEQ ID NO: 17, and SEQ ID NO: 8; (iii) a sequence that is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 93, SEQ ID NO: 53, SEQ ID NO: 95, SEQ ID NO: 23, SEQ ID NO: 103, and SEQ ID NO: 7; (iv) a sequence that is at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 45, SEQ ID NO: 15, SEQ ID NO: 51, SEQ ID NO: 44, SEQ ID NO: 73, SEQ ID NO: 36, SEQ ID NO: 77, SEQ ID NO: 50, and SEQ ID NO: 6; (v) a sequence that is at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 97, SEQ ID NO: 16, SEQ ID NO: 76, SEQ ID NO: 9, SEQ ID NO: 89, SEQ ID NO: 107, SEQ ID NO: 68, SEQ ID NO: 29, SEQ ID NO: 67, SEQ ID NO: 74, SEQ ID NO: 32, SEQ ID NO: 81, SEQ ID NO: 106, SEQ ID NO: 31, SEQ ID NO: 62, SEQ ID NO: 48, SEQ ID NO: 75, SEQ ID NO: 12, SEQ ID NO: 102, SEQ ID NO: 54, SEQ ID NO: 80, SEQ ID NO: 26, SEQ ID NO: 30, SEQ ID NO: 92, SEQ ID NO: 108, and SEQ ID NO: 79; (vi) a sequence that is at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 105, SEQ ID NO: 101, SEQ ID NO: 4, SEQ ID NO: 72, SEQ ID NO: 28, SEQ ID NO: 64, SEQ ID NO: 25, SEQ ID NO: 60, SEQ ID NO: 55, SEQ ID NO: 52, SEQ ID NO: 27, SEQ ID NO: 43, SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 14, SEQ ID NO: 85, SEQ ID NO: 13, SEQ ID NO: 61, SEQ ID NO: 42, SEQ ID NO: 39, SEQ ID NO: 10, SEQ ID NO: 49, SEQ ID NO: 24, SEQ ID NO: 40, SEQ ID NO: 63, SEQ ID NO: 78, SEQ ID NO: 2,

SEQ ID NO: 94, and SEQ ID NO: 5; (vii) a sequence that is at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 11, SEQ ID NO: 35, SEQ ID NO: 86, SEQ ID NO: 22, SEQ ID NO: 69, SEQ ID NO: 41, SEQ ID NO: 3, SEQ ID NO: 66, SEQ ID NO: 37, SEQ ID NO: 56, SEQ ID NO: 21, SEQ ID NO: 38, SEQ ID NO: 90, SEQ ID NO: 100, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 83, SEQ ID NO: 1, and SEQ ID NO: 19; and (viii) a sequence that is at least 35%, at least 40%,a t least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 87, SEQ ID NO: 82, and SEQ ID NO: 104; and (b) a light chain comprising a sequence selected from: (i) a sequence that is at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 218, SEQ ID NO: 249, SEQ ID NO: 230, SEQ ID NO: 279, SEQ ID NO: 316, SEQ ID NO: 237, SEQ ID NO: 322, SEQ ID NO: 225, SEQ ID NO: 318, SEQ ID NO: 233, SEQ ID NO: 305, SEQ ID NO: 280, SEQ ID NO: 283, SEQ ID NO: 242, SEQ ID NO: 286, SEQ ID NO: 297, SEQ ID NO: 309, and SEQ ID NO: 246; (ii) a sequence that is at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 222, SEQ ID NO: 258, SEQ ID NO: 219, SEQ ID NO: 313, SEQ ID NO: 294, SEQ ID NO: 303, SEQ ID NO: 317, SEQ ID NO: 273, SEQ ID NO: 266, SEQ ID NO: 315, SEQ ID NO: 257, SEQ ID NO: 288, SEQ ID NO: 301, SEQ ID NO: 221, SEQ ID NO: 240, SEQ ID NO: 299, SEQ ID NO: 247, SEQ ID NO: 263, and SEQ ID NO: 274; (iii) a sequence that is at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 231, SEQ ID NO: 250, SEQ ID NO: 260, SEQ ID NO: 226, SEQ ID NO: 271, SEQ ID NO: 256, SEQ ID NO: 272, SEQ ID NO: 278, SEQ ID NO: 302, SEQ ID NO: 320, SEQ ID NO: 295, SEQ ID

NO: 292, SEQ ID NO: 229, SEQ ID NO: 264, SEQ ID NO: 252, SEQ ID NO: 267, SEQ ID NO: 304, SEQ ID NO: 300, SEQ ID NO: 311, and SEQ ID NO: 324; (iv) a sequence that is at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 259, SEQ ID NO: 239, SEQ ID NO: 281, SEQ ID NO: 228, SEQ ID NO: 217, SEQ ID NO: 227, and SEQ ID NO: 251; (v) a sequence that is at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 307, SEQ ID NO: 262, SEQ ID NO: 253, SEQ ID NO: 276, SEQ ID NO: 323, SEQ ID NO: 234, SEQ ID NO: 261, SEQ ID NO: 312, and SEQ ID NO: 290; (vi.) a sequence that is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 254, SEQ ID NO: 289, SEQ ID NO: 238, SEQ ID NO: 268, SEQ ID NO: 248, SEQ ID NO: 284, SEQ ID NO: 244, SEQ ID NO: 310, SEQ ID NO: 243, SEQ ID NO: 285, SEQ ID NO: 220, SEQ ID NO: 255, SEQ ID NO: 293, SEQ ID NO: 298, SEQ ID NO: 235, SEQ ID NO: 319, SEQ ID NO: 245, SEQ ID NO: 224, SEQ ID NO: 291, SEQ ID NO: 277, and SEQ ID NO: 232; and (vii) a sequence that is at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 282, SEQ ID NO: 308, SEQ ID NO: 287, SEQ ID NO: 321, SEQ ID NO: 236, SEQ ID NO: 265, SEQ ID NO: 270, SEQ ID NO: 275, SEQ ID NO: 306, SEQ ID NO: 296, SEQ ID NO: 241, SEQ ID NO: 314, and SEQ ID NO: 223; wherein the antibody or antigen-binding fragment thereof binds to CLEC2D.

[011] The disclosure provides isolated antibodies or antigen-binding fragments thereof comprising a heavy chain and a light chain, wherein the heavy chain comprises a sequence selected from any one of SEQ ID NOs: 1-108.

[012] The disclosure provides isolated antibodies or antigen-binding fragments thereof comprising a heavy chain and a light chain, wherein the light chain comprises a sequence selected from any one of SEQ ID NOs: 217-324.

[013] The disclosure provides isolated antibodies or antigen-binding fragments thereof comprising a heavy chain and a light chain, wherein the heavy chain comprises a sequence selected from any one of SEQ ID NOs: 1-108, and the light chain comprises a sequence selected from any one of SEQ ID NOs: 217-324.

[014] The disclosure provides isolated antibodies or antigen-binding fragments thereof comprising a heavy chain and a light chain, wherein the heavy chain comprises: (i) a heavy chain (HC) CDR1 comprising a sequence selected from SEQ ID NOs: 433-485; (ii) an HC CDR2 comprising a sequence selected from SEQ ID NOs: 486-546; and (iii) an HC CDR3 comprising a sequence selected from SEQ ID NOs: 547-653, wherein the antibody or antigen-binding fragment thereof binds to CLEC2D.

[015] The disclosure provides isolated antibodies or antigen-binding fragments thereof comprising a heavy chain and a light chain, wherein the light chain comprises: (i) a light chain (LC) CDR1 comprising a sequence selected from SEQ ID NOs: 654-726; (ii) an LC CDR2 comprising a sequence selected from SEQ ID NOs: 727-783; and (iii) an LC CDR3 comprising a sequence selected from SEQ ID NOs: 784-885; wherein the antibody or antigen-binding fragment thereof binds to CLEC2D.

[016] The disclosure provides isolated antibodies or antigen-binding fragments thereof, comprising: a heavy chain comprising an HC CDR1 sequence selected from SEQ ID NOs: 433-485, an HC CDR2 sequence selected from SEQ ID NOs: 486-546, and an HC CDR3 sequence selected from SEQ ID NOs: 547-653; a light chain comprising a LC CDR1 sequence selected from SEQ ID NOs: 654-726, a LC CDR2 sequence selected from SEQ ID NOs: 727-783, and a LC CDR3 sequence selected from SEQ ID NOs: 784-885; or a combination thereof.

[017] In some embodiments of the antibodies or antigen binding fragments thereof of the disclosure, the antibody or antigen-binding fragment thereof binds to: a human CLEC2D polypeptide comprising a sequence selected from SEQ ID NOs: 886-909; a human CLEC2D polypeptide comprising a sequence selected from SEQ ID NOs: 930-1003; a cynomolgus CLEC2D polypeptide comprising a sequence selected from SEQ ID NOs: 918-920; a mouse CLEC2D polypeptide comprising a sequence selected from SEQ ID NOs: 911-915; a rat

CLEC2D polypeptide comprising a sequence of SEQ ID NO: 910; and/or a dog CLEC2D polypeptide comprising a sequence selected from SEQ ID NOs: 916-917.

[018] The disclosure provides an isolated antibody or antigen-binding fragment thereof, comprising a heavy chain and a light chain, wherein the heavy chain comprises a heavy chain complementarity determining region (CDRH) 1, CDRH2 and CDRH3 amino acid sequence of an anti-CLEC2D antibody selected from the group consisting of: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, as disclosed in Table 9A, and wherein the light chain comprises a light chain complementarity determining region (CDRL)1, CDRL2 and CDRL3 amino acid sequence of an anti-CLEC2D antibody selected from the group consisting of: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, as disclosed in Table 9A.

[019] The disclosure provides an isolated antibody or antigen-binding fragment thereof, comprising a heavy chain and a light chain, wherein the heavy chain comprises a variable heavy chain amino acid sequence of an anti-CLEC2D antibody selected from the group consisting of: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, as disclosed in Table 9A, and wherein the light chain comprises a variable light chain amino acid sequence of an anti-CLEC2D antibody selected from the group consisting of: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, as disclosed in Table 9A.

[020] The disclosure provides an isolated antibody or antigen-binding fragment thereof, comprising a heavy chain and a light chain, wherein the heavy chain comprises a heavy chain frame work region sequence of a Germline family of an anti-CLEC2D antibody selected from the group consisting of: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, of Table 9B, as disclosed herein, and wherein the light chain comprises a frame work region sequence of a light chain Germline family of an anti-CLEC2D antibody selected from the group consisting of: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, of Table 9B, as disclosed herein.

[021] In some embodiments of the antibodies or antigen binding fragments thereof of the disclosure, the antibody or antigen-binding fragment thereof is a monoclonal antibody.

[022] In some embodiments of the antibodies or antigen binding fragments thereof of the disclosure, the antibody or antigen-binding fragment thereof blocks binding of CLEC2D to a receptor. In some embodiments, the receptor comprises a CD161 receptor, and the CD161 receptor comprises a sequence selected from SEQ ID NOs: 921-929.

[023] In some embodiments of the antibodies or antigen binding fragments thereof of the disclosure, the antibody or antigen-binding fragment thereof is human, murine or chimeric. In

some embodiments, the antigen-binding fragment is selected from the group consisting of Fv, Fav, F(ab')2, Fab', dsFv, scFv, sc(Fv)2, scFv-CH3, scFv-Fc, and diabody fragments. In some embodiments, the antibody or antigen-binding fragment thereof binds to human CLEC2D with an affinity (KD) of less than 100 nM.

[024] The disclosure provides pharmaceutical compositions comprising peptides (e.g., antibodies or antigen-binding fragments thereof) or nucleic acids described in the disclosure.

[025] The disclosure provides pharmaceutical compositions comprising antibodies or antigen-binding fragments thereof of the disclosure.

[026] The disclosure provides pharmaceutical compositions comprising nucleic acids encoding the antibodies or antigen-binding fragments thereof of the disclosure.

[027] In some embodiments of the pharmaceutical compositions of the disclosure, the pharamaceutical composition further comprises at least one of a buffer, a pharmaceutically acceptable diluent, a carrier, a solubilizer, an emulsifier, and a preservative.

[028] The disclosure provides isolated nucleic acids comprising a polynucleotide sequence that encodes an amino acid heavy chain sequence selected from SEQ ID NOs: 109-216.

[029] The disclosure provides isolated nucleic acids comprising a polynucleotide sequence that encodes an amino acid light chain sequence selected from SEQ ID NOs: 325-432.

[030] The disclosure provides an isolated nucleic acid, comprising a polynucleotide sequence that encodes a heavy chain comprising a CDRH1, CDRH2 and CDRH3 amino acid sequence according to the CDRH1, CDRH2 and CDRH3 amino acid sequence respectively, of an anti-CLEC2D antibody selected from the group consisting of: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, of Table 9A, as disclosed herein.

[031] The disclosure provides an isolated nucleic acid, comprising a polynucleotide sequence that encodes a light chain comprising a CDRL1, CDRL2 and CDRL3 amino acid sequence according to the CDRL1, CDRL2 and CDRL3 amino acid sequence respectively, of an anti-CLEC2D antibody selected from the group consisting of: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, of Table 9A, as disclosed herein.

[032] The disclosure provides an isolated nucleic acid, comprising a polynucleotide sequence that encodes a heavy chain amino acid sequence according to variable heavy chain amino acid sequence of an anti-CLEC2D antibody antibody selected from the group consisting of: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, of Table 9A, as disclosed herein.

[033] The disclosure provides an isolated nucleic acid, comprising a polynucleotide sequence that encodes a light chain amino acid sequence according to variable light chain amino acid sequence of an anti-CLEC2D antibody selected from the group consisting of: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, of Table 9A, as disclosed herein.

[034] The disclosure provides an isolated nucleic acid, comprising a polynucleotide sequence that encodes a heavy chain comprising a framework region amino acid sequence according to heavy chain framework region amino acid sequence of an anti-CLEC2D antibody selected from the group consisting of: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, of Table 9B, as disclosed herein.

[035] The disclosure provides an isolated nucleic acid comprising a polynucleotide sequence that encodes a light chain comprising a framework region amino acid sequence according to light chain framework region amino acid sequence of an anti-CLEC2D antibody selected from the group consisting of: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, of Table 9B, as disclosed herein.

[036] The disclosure provides isolated nucleic acids comprising a polynucleotide sequence that encodes a heavy chain amino acid sequence of an antibody or antigen binding fragment thereof of the disclosure.

[037] The disclosure provides isolated nucleic acids comprising a polynucleotide sequence that encodes a light chain amino acid sequence of an antibody or antigen binding fragment thereof of the disclosure.

[038] The disclosure provides compositions comprising a first nucleic acid that encodes a polypeptide selected from SEQ ID NOs: 109-216 and a second nucleic acid that encodes a polypeptide selected from SEQ ID NOs: 325-432.

[039] The disclosure provides vectors comprising the nucleic acids of the disclosure.

[040] The disclosure provides cells comprising the nucleic acids, nucleic acid compositions or vectors of the disclosure. In some embodiments, the cell is a eukaryotic cell. In some embodiments, the eukaryotic cell is a mammalian cell. In some embodiments, the mammalian cell is selected from the group consisting of a CHO cell, a 293 cell, an NSO cell, a PER.C6 cell, and a B cell. In some embodiments, the mammalian cell is a 293-6E cell or a DG44 cell. In some embodiments, the cells express the antibodies or antigen binding fragments thereof of the disclosure. In some embodiments, the cell is a germline cell.

[041] The disclosure provides cells producing the antibodies or antigen-binding fragments thereof of the disclosure

[042] The disclosure provides a method of treating a disease in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of the antibodies or antigen-binding fragments thereof of the disclosure.

[043] The disclosure provides a composition for use in treating a disease in a subject in need thereof, comprising a therapeutically effective amount of the antibodies or antigen-binding fragments thereof of the disclosure or the nucleic acids encoding the antibodies or antigen-binding fragments thereof of the disclosure.

[044] The disclosure provides a composition for use in the manufacture of a medicament for the prevention or treatment of a disease in a subject in need thereof, comprising a therapeutically effective amount of the antibodies or antigen-binding fragments thereof of the disclosure or the nucleic acids encoding the antibodies or antigen-binding fragments thereof of the disclosure.

[045] In some embodiments of the methods or compositions for use of the disclosure, the disease is rheumatoid arthritis. In some embodiments, the subject exhibits bone loss as a result of having rheumatoid arthritis. In some embodiments, administration of a therapeutically effective amount of the antibody or antigen-binding fragment thereof slows or reverses the bone loss in the subject.

[046] In some embodiments of the methods or compositions for use of the disclosure, the disease is a cancer. In some embodiments, the cancer is selected from the group consisting of breast cancer, prostate cancer, endometrial cancer, uterine cancer, bladder cancer, kidney cancer, esophageal cancer, squamous cell carcinoma, uveal melanoma, glioma, glioblastoma, myeloma, pheochromocytoma, paraganglioma, follicular lymphoma, renal cell carcinoma, cendcal cancer, ovarian cancer, cervical cancer, lung cancer, colorectal cancer, brain cancer, pancreatic cancer, gastric cancer, intestinal cancer, testicular cancer, skin cancer, thyroid cancer, thymoma, head and neck cancer, liver cancer, pharynx cancer, adrenocortical cancer, cholangiocarcinoma, mesothelioma, sarcoma, leukemia, lymphoma, Hodgkin's disease, multiple myeloma, melanoma, astrocytoma, stomach cancer, and pulmonary adenocarcinoma. In some embodiments, a cell of the cancer expresses CLEC2D on the cell surface. In some embodiments, administration of a therapeutically effective amount of the antibodies or antigen-binding fragments thereof results in an anti-tumor response in the subject.

[047] In some embodiments of the methods or compositions for use of the disclosure, the antibodies or antigen-binding fragments thereof are administered as a monotherapy. In some

embodiments, the antibodies or antigen-binding fragments thereof are administered in combination with at least one of a T cell targeted immunomodulatory agent, a second immunomodulatory agent, a cancer vaccine, an adoptive cell therapy, an oncolytic virus, a second antibody therapy, a radiotherapy, an antibody drug conjugate, a small interfering RNA, a chemotherapy, an immunotherapy, an immune checkpoint inhibitor, a mitotic inhibitor, or a combination thereof. In some embodiments, the adoptive cell therapy comprises a CAR-T therapy. In some embodiments, administration of a therapeutically effective amount of the antibody or antigen-binding fragment thereof alleviates a sign or a symptom of the disease.

[048] The disclosure provides an antibody library comprising at least about 108 unique monoclonal antibody clones, wherein at least about 80% of the antibody clones detectably and specifically bind a CLEC2D antigen.

[049] In some embodiments of the antibody library of the disclosure, the CLEC2D antigen comprises an amino acid sequence selected from SEQ ID NOs: 886-920 and SEQ ID NOs: 930-1003. In some embodiments of the antibody library of the disclosure, the CLEC2D antigen comprises an amino acid sequence selected from SEQ ID NOs: 886-909 and SEQ ID NOs: 930-1003. In some embodiments, the CLEC2D antigen comprises a CLEC2D antigen expressed on a tumor cell surface, a variant of the CLEC2D antigen, or a homolog of the CLEC2D antigen. In some embodiments, the variant of the CLEC2D antigen comprises a fragment of the CLEC2D protein. In some embodiments, the homolog of the CLEC2D antigen comprises a human, a mouse, a dog, a rat or a cynomolgus CLEC2D.

[050] The disclosure provides a method of modulating immunity in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of the antibodies or antigen-binding fragments of the disclosure or the nucleic acids encoding the antibodies or antigen-binding fragments thereof of the disclosure.

[051] The disclosure provides a method of modulating (e.g., increasing) innate immunity in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of the antibodies or antigen-binding fragments of the disclosure or the nucleic acids encoding the antibodies or antigen-binding fragments thereof of the disclosure.

[052] The disclosure provides a method of increasing the cytotoxicity of a natural killer cell in a subject in need thereof, comprising administering to the subject a therapeutically effective

amount of the antibodies or antigen-binding fragments thereof of the disclosure or the nucleic acids encoding the antibodies or antigen-binding fragments thereof of the disclosure.

[053] The disclosure provides a method of modulating (e.g., increasing) adaptive immunity in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of the antibodies or antigen-binding fragments of the disclosure or the nucleic acids encoding the antibodies or antigen-binding fragments thereof of the disclosure.

[054] The disclosure provides methods of screening a high diversity antibody gene library for antibodies that to a CLEC2D antibody comprising: (a) inserting a library of antibody genes into a phage protein gene and transforming a plurality of phages to produce a phage library, wherein the phages in the phage library display the library of antibody genes on the surface of the phage; (b) panning the phage library with a CLEC2D antigen for individual phages that bind to the CLEC2D antigen, thereby producing an enriched phage library that is enriched for antibody genes that encode antibodies that bind to the CLEC2D antigen; (c) repeating step (b) at least once or at least twice; (d) transferring the antibody genes from the enriched phage library to a yeast surface display library; (e) isolating individual yeast cells that bind to the CLEC2D antigen from the yeast surface display library; (f) culturing the isolated individual yeast cells that bind to the CLEC2D antigen to produce yeast surface display library clones; and (g) sequencing the yeast surface display library clones; thereby isolating antibody genes that bind to the CLEC2D antigen.

[055] In some embodiments of the methods of screening of the disclosure, the panning step (b) comprises panning the phage library with CLEC2D coated magnetic beads. In some embodiments, the transferring step (d) comprises cloning the antibody genes into a yeast expression vector and transforming yeast cells. In some embodiments, the methods further comprise analyzing the surface expression of the antibody genes with a FLAG tag, a c-Myc tag, a polyhistidine tag or a V5 tag. In some embodiments, the testing step (e) comprises isolating yeast cells expressing antibody genes that bind to the CLEC2D antigen with flow cytometry. In some embodiments, the method further comprises repeating the flow cytometry isolation at least 1x, at least 2x, at least 3x, at least 4x or at least 5x. In some embodiments, the method further comprises cloning the antibody genes that bind to CLEC2D into a mammalian expression vector.

[056] The disclosure provides methods of making a composition comprising anti-CLEC2D antibodies or antigen binding fragments thereof, comprising (a) transforming mammalian cells

with a vector comprising a sequence encoding a promoter and a sequence encoding an anti-CLEC2D antibody or antibody fragment, wherein the sequence encoding the promoter and the anti-CLEC2D antibody or antibody fragment are operably linked; (b) culturing the mammalian cells under conditions suitable for the expression of the anti-CLEC2D antibody or antibody fragment; (c) centrifuging the cultured mammalian cells to produce a supernatant; (d) filtering the supernatant; and (e) purifiying the filtered supernatant using liquid chromatography.

[057] In some embodiments of the methods of the disclosure, the filration step (d) comprises a 3 μm - 30 μm filter. In some embodiments, the filtration step (d) further comprises a 0.22 μm filter. In some embodiments, the purifying step (e) comprises a Protein A column. In some embodiments, the protein A column is treated with a high salt wash buffer to remove host cell proteins. In some embodiments, the ani-CLEC2D antibody of fragment thereof is eluted using 30 mM Phosphate buffer at pH.3.0-4.0. In some embodiments, the purifying step (e) further comprises an anion exchange chromatography (AEX) step. In some embodiments, the AEX step comprises a Q Sepharose column. In some embodiments, the Q Sepharose is pre-equilibrated in a pre-equilibration buffer comprising 10-100 mM Histidine. In some embodiments, the pre-equilibration buffer further comprises citrate, phosphate 2-(N-morpholino)ethanesulfonic acid (MES), acetate or a combination thereof. In some embodiments, the pre-equilibration buffer comprises a pH of 4.5-6.5. In some embodiments, the anti-CLEC2D antibody is eluted at step (e) with an elution buffer comprising 200-1000 mM NaCl, KCl or a combination thereof. In some embodiments, the elution buffer comprises a pH of 4.5-6.5.

[058] In one aspect, this disclosure relates to the isolation of novel monoclonal antibodies that bind specifically to a CLEC2D antigen. The novel antibodies modulate (e.g., inhibit) the interaction of CD161 and CLEC2D to modify NK cell/immune cell mediated cytotoxicity and/or cytokine production.

[059] In another aspect, this disclosure relates to cancer cells expressing CLEC2D are specifically recognized by these novel antibodies which may kill the tumor cells via ADCC (antibody dependent cellular cytotoxicity) and/or CDC (complement dependent cytotoxicity) and/or ADCP (antibody dependent cellular phagocytosis).

[060] In a related aspect, this disclosure relates to methods of making an anti-CLEC2D antibody, comprising selecting from a high diversity antibody gene library an anti-CLEC2D antibody. In one embodiment, the high diversity antibody gene library is displayed through

phage and/or yeast surface display. In one embodiment, the phage- and/or yeast-displayed high diversity antibody gene library is selected using purified CLEC2D antigen as a target. In one embodiment, the selected anti-CLEC2D antibody genes are expressed in a mammalian cell (e.g., Chinese hamster ovary (CHO) cell). In one embodiment, a single cell clone expressing an anti-CLEC2D antibody is expanded into a cell line and verified for anti-CLEC2D antibody expression. In one embodiment, overexpression of selected antibody clones is achieved through defined culture media, supplements, and specific bioreactor processes cumulatively described herein as upstream process development. In one embodiment, the anti-CLEC2D antibodies expressed from the cell line are purified to homogeneity, for example, through various filtration and chromatography, referred to herein as downstream purification processes.

[061] The disclosure provides a method of treating a disease in a subject in need thereof, comprising: determining a level of CLEC2D protein in the subject; and administering a therapeutically effective amount of an anti-CLEC2D antibody to the subject.

[062] In some embodiments of the methods of the disclosure, the disease is a cancer. In some embodiments, the cancer comprises breast cancer, prostate cancer, endometrial cancer, uterine cancer, bladder cancer, kidney cancer, esophageal cancer, squamous cell carcinoma, uveal melanoma, glioma, glioblastoma, myeloma, pheochromocytoma, paraganglioma, follicular lymphoma, renal cell carcinoma, cendcal cancer, ovarian cancer, cervical cancer, lung cancer, colorectal cancer, brain cancer, pancreatic cancer, gastric cancer, intestinal cancer, testicular cancer, skin cancer, thyroid cancer, thymoma, head and neck cancer, liver cancer, pharynx cancer, adrenocortical cancer, cholangiocarcinoma, mesothelioma, sarcoma, leukemia, lymphoma, Hodgkin's disease, multiple myeloma, melanoma, astrocytoma, stomach cancer, pulmonary adenocarcinoma, adenocarcinoma, acinic cell adenocarcinoma, adrenal cortical carcinomas, alveoli cell carcinoma, anaplastic carcinoma, basaloid carcinoma, basal cell carcinoma, bronchiolar carcinoma, bronchogenic carcinoma, renaladinol carcinoma, embryonal carcinoma, anometroid carcinoma, fibrolamolar liver cell carcinoma, follicular carcinomas, giant cell carcinomas, hepatocellular carcinoma, intraepidermal carcinoma, intraepithelial carcinoma, leptomanigio carcinoma, medullary carcinoma, melanotic carcinoma, menigual carcinoma, mesometonephric carcinoma, oat cell carcinoma, squamal cell carcinoma, sweat gland carcinoma, transitional cell carcinoma, tubular cell carcinoma, ameloblastic sarcoma, angiolithic sarcoma, botryoid sarcoma, endometrial stroma sarcoma, ewing sarcoma, fascicular sarcoma,

giant cell sarcoma, granulositic sarcoma, immunoblastic sarcoma, juxaccordial osteogenic sarcoma, coppices sarcoma, leukocytic sarcoma (leukemia), lymphatic sarcoma (lympho sarcoma), medullary sarcoma, myeloid sarcoma (granulocitic sarcoma), austiogenci sarcoma, periosteal sarcoma, reticulum cell sarcoma (histiocytic lymphoma), round cell sarcoma, spindle cell sarcoma, synovial sarcoma, telangiectatic audiogenic sarcoma, Burkitt's lymphoma, NPDL, NML, NH, diffuse lymphomas, Hodgkin's lymphoma, non-Hodgkin's lymphoma, B-cell lymphoma, T-cell lymphoma, diffuse large B-cell lymphoma, acute myeloid lymphoma, chronic lymphocytic leukemia, chronic myeoloid leukemia, mantle cell lymphoma, and follicular lymphoma. In some embodiments, a cancer cell of the subject has an elevated level of CLEC2D protein when compared to a normal cell that does not have cancer. In some embodiments, an increased level of CLEC2D is associated with a poor prognostic outcome.

[063] In some embodiments of the methods of the disclosure, the disease is an autoimmune or inflammatory disorder. In some embodiments, the autoimmune or inflammatory disorder is type I diabetes, rheumatoid arthritis, lupus, inflammatory bowel diseases, celiac disease, Crohn disease, ulcerative Colitis, psoriasis, or multiple Sclerosis.

[064] In some embodiments of the methods of the disclosure, the disease is an autoimmune or inflammatory disorder. In some embodiments, the autoimmune disorder is type I diabetes, rheumatoid arthritis, lupus, inflammatory bowel diseases, celiac disease, Crohn disease, ulcerative Colitis, psoriasis, or multiple Sclerosis.

[065] In some embodiments of the methods of the disclosure, the disease is infectious disease. In some embodiments, the disease is HIV infection, human Cytomegalovirus infection, Hepatitis B infection, Hepatitis C infection, Ebola virus infection, Dengue, Yellow fever, Listeriosis, Tuberculosis, Cholera, Malaria, Leishmaniasis, or Trypanosoma infection.

[066] In another aspect, multiple *in vitro* and *in vivo* assays are used to characterize the novel antibodies produced from CHO cell lines which include, various biophysical parameters, antigen recognition, tumor cell surface binding, tumor cell death, production of cytokines, and analysis of downstream genes to define mode of action. These monoclonal antibodies are also tested for long term stability, various formulations relevant for therapeutic, prognostic and diagnostic uses in cancer, infectious diseases, autoimmune and chronic diseases. In another aspect, *in vivo* tumor suppression assays are carried out to establish anti-tumor activity of selected antibodies as monotherapy or in combination with other therapeutic products.

[067] In one aspect, this disclosure further relates to the isolation of novel and unique monoclonal antibodies that bind specifically to CLEC2D antigen. In some aspect, the novel antibodies influence the interaction of CD161 and CLEC2D to modify immune cell (e.g., NK cell, B-cell, or T-cell) mediated cytotoxicity and/or cytokine production. In some aspects, various cancer cells, expressing CLEC2D, are recognized by these novel antibodies and have revealed cytotoxic effects through various means including, ADCC (antibody dependent cellular cytotoxicity) and/or CDC (Complement dependent cytotoxicity and/or ADCP (Antibody dependent cellular phagocytosis). In one aspect, the disclosure provides emphasis and postulates on the role of CLEC2D in cross-talk between lymphocytes and immune tolerance. In another aspect, in the realm of approved therapeutics or those in pre-clinical or clinical testing, the methods for identifying novel antibody molecules and related compositions provided herein comprise pharmaceutical features amenable to manufacturability/ developability.

[068] In one aspect, this disclosure relates to a method of treating a disease or disorder in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of the antibody or antigen-binding fragment thereof of, wherein the antibody is an anti-CLEC2D antibody selected from the group consisting of: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, of Table 9A and B, as disclosed herein.

[069] In one aspect, this disclosure relates to a method of modulating immunity in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of the antibody or antigen-binding fragment, wherein the antibody is an anti-CLEC2D antibody selected from the group consisting of: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, of Table 9A and B, as disclosed herein.

[070] In one aspect, this disclosure relates to a method of modulating (e.g., increasing) innate immunity in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of the antibody or antigen-binding fragment, wherein the antibody is an anti-CLEC2D antibody selected from the group consisting of: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, of Table 9A and B, as disclosed herein.

[071] In one aspect, this disclosure relates to a method of modulating (e.g., increasing) adaptive immunity in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of the antibody or antigen-binding fragment, wherein the antibody is an anti-

CLEC2D antibody selected from the group consisting of: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, of Table 9A and B, as disclosed herein.

[072] In one aspect, this disclosure relates to a method of increasing the cytotoxicity of a natural killer cell in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of the antibody or antigen-binding fragment, wherein the antibody is an anti-CLEC2D antibody selected from the group consisting of: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, of Table 9A and B, as disclosed herein.

BRIEF DESCRIPTION OF THE FIGURES

[073] The features of the present disclosure will become fully apparent from the following description taken in conjunction with the accompanying figures. The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawings will be provided by the Office upon request and payment of the necessary fee. With the understanding that the figures depict only several embodiments in accordance with the disclosure and are not to be considered limiting its scope, the disclosure will be described further through use of the accompanying figures.

[074] FIGS. 1A-1C illustrate present disclosure in a schematic format in: FIG. 1A, scenario wherein CLEC2D and CD161 interacts resulting in tumor cells escaping immune cells; FIG. 1B, scenario wherein interaction between CLEC2D and CD161 is blocked using an anti CLEC2D antibody, resulting in lysis signal followed by killing of tumor cells; and FIG. 1C, scenario wherein ligation of CLEC2D antigen with anti CLEC2D antibody resulting in activation of NK cell and in elevation of cytokine expression followed by enhanced target cell clearance either by direct killing or by involving other immune cells

[075] FIGS. 2 A-2F illustrate expression and purification of CLEC2D antigen in mammalian cell in: FIG. 2A, generation of mammalian expression plasmids to express CLEC2D ecto-domain as soluble antigen. The construct was generated through gene synthesis followed by confirmation through restriction digestion and Sanger sequencing; FIG. 2B, IMAC chromatography profile displaying purification of a soluble CLEC2D (Q72-V191), with inset showing elution profile of the CLEC2D antigen; FIG. 2C, SDS–PAGE profile of load, wash and final eluted CLEC2D protein, demonstrating that the purified CLEC2D protein was homogenous and pure, and suitable for further downstream experimentation; FIG. 2D, western blot of the purified CLEC2D protein,

probed with a commercially available antibody against CLEC2D antigen; FIG. 2E, ELISA assay showing the binding specificity of a commercial antibody against different concentrations of the purified CLEC2D antigen; and FIG. 2F, SDS–PAGE analysis of the purified CLEC2D antigen incubated with PNGase enzyme under reducing conditions for 3 hrs or 6 hrs revealed deglycosylation of CLEC2D antigen.

[076] FIG.3 illustrates a schematic depiction of an antibody library screening strategy: the naïve antibody library screened against the target CLEC2D antigen using phage and yeast surface display systems.

[077] FIGS. 4A-4E illustrate phage panning of antibody library with CLEC2D antigen coated on magnetic beads in: FIG. 4A, estimation of magnetic bead conjugation efficiency by flow cytometry; FIG. 4B, restriction enzyme digestion of independent heavy chain clones after panning of Fab library; FIG. 4C, restriction enzyme digestion of independent kappa light chain clones after panning of Fab library; FIG. 4D, restriction enzyme digestion of independent heavy chain clones after panning of ScFv library; and FIG. 4E, restriction enzyme digestion of independent kappa light chain clones after panning of ScFv library.

[078] FIGS. 5A-5H illustrate screening of antibody against CLEC2D using yeast surface display in: FIG. 5A, plate images depicting yeast colony towards generation of ScFv antibody library through electroporation; FIG. 5B, plate images depicting generation of haploid heavy and light chain antibody libraries; FIG. 5C, plate images showing mating efficiency of haploid yeast strains containing heavy or light chain antibody libraries, wherein mating efficiency was estimated to be ~29% ; FIG. 5D, representative flow cytometric analysis of binding of antibody molecules expressed on the yeast cell surface with CLEC2D antigen, the ScFv libraries were sorted multiple times to enrich high affinity yeast clones; FIG. 5E, representative flow cytometric analysis of binding of antibody molecules expressed on the yeast cell surface with CLEC2D antigen, the Fab libraries were sorted multiple times to enrich high affinity yeast clones; FIG. 5F, representative data on enrichment of yeast clones after multiple rounds of sorting, both in terms of expression and antigen recognition; FIG. 5G, the individual yeast clones were separated and tested with CLEC2D antigen to identify yeast cell lines expressing high affinity antibody clones; and FIG. 5H, representative flow cytometry data to show the percentage binding of a soluble CLEC2D antigen with monoclonal antibody clones. At least about 80% of the clones detectably and specifically bound to the CLEC2D antigen.

[079] FIGS. 6A-6D illustrate the peer group sequence analysis of clones screened through yeast display platform in: FIG. 6A, bar graph showing the CDRH3 length distribution of selected molecules; FIG. 6B, bar graph displaying relative amino acid frequency distribution for heavy chain CDRH3 (Kabat nomenclature); FIG. 6C, pie chart exhibiting heavy chain consensus family distribution; and FIG. 6D, pie chart exhibiting light chain consensus family distribution.

[080] FIGS. 7A-7B illustrate the mammalian expression constructs used to generate full-length monoclonal antibody in: FIG. 7A, the vector designed to clone selected antibody variable heavy chain genes after screening through phage and yeast display platforms; and FIG. 7B, the vector designed to clone selected antibody variable light chain (kappa) genes after screening through phage and yeast display platforms. Constructs were generated through gene synthesis followed by confirmation through restriction digestion and Sanger sequencing.

[081] FIGS. 8A-8C illustrate mammalian expression system to express full-length CLEC2D on the cell surface, as shown in: FIG. 8A, CLEC2D gene expression construct was generated through gene synthesis followed by confirmation through restriction digestion and Sanger sequencing; and FIG. 8B, flow cytometry with commercially available anti-CLEC2D antibody (4C7) showing expression of CLEC2D on transfected CHO cell surface (C4548); and FIG. 8C, the surface expression of CLEC2D as monitored with anti-CLEC2D (4C7) antibody on fixed and non-permeabilized cells by confocal microscopy (60X). Binding of anti-CLEC2D antibody was observed on C4548 cells whereas no binding was observed in un-transfected CHO cells. The nucleus was counterstained with DAPI (blue). Scale bar is 10μm.

[082] FIGS. 9A-9C illustrate anti-CLEC2D monoclonal antibody clones purified from transiently transfected CHO cell. Antibody was purified using protein A column chromatography, as shown in: FIG. 9A, SDS –PAGE profile of representative Anti CLEC2D antibodies. The purified antibodies were subjected to SDS-PAGE analysis in both non-reducing and reducing conditions. Anti CLEC2D Antibody clone purified from C3566 was shown in lane 9, upper panel of reducing and non-reducing gels. All clones from lower panels, except clone in lane 4 revealed good profiles in reducing and non-reducing gels. Clones showing degraded products were not considered for further studies. Similar criteria was employed for other clones as described in example section; FIG. 9B, the interaction of purified anti-CLEC2D antibody with CLEC2D antigen expressed on CHO cell surface through flow cytometry; Representative antibody clones, as exemplified by, C4577, C2907, C3566, C5582, C5397, were evaluated for

CLEC2D binding on CHO cell lines either untransfected or transfected with full length CLEC2D construct. Shift in MFI towards right indicated binding of respective clones towards surface expressed CLEC2D antigen; and FIG. 9C, representative images of interaction of anti-CLEC2D antibodies with CLEC2D antigen expressed on PC3 tumor cells. As shown in Table 22 a qualitative rating of binding was carried out, "+" indicating low binding to "+++" indicating very high binding. As exemplified, surface binding was not detected with antibody C4252, whereas with antibody C0610, low binding was observed thereby rated as (+) while other clones have showed differential yet significant surface binding. The nucleus was counterstained with DAPI (violet). Scale bar is 10μm.

[083] FIGS. 10A-10E illustrate stable CHO cell line development expressing Anti CLEC2D antibody, as shown in: FIG. 10A, the binding studies carried out with surface expressed CLEC2D as monitored using supernatant obtained from CHO mini-pool samples transfected with Anti CLEC2D antibody expression plasmid, using flow cytometry. Histogram represents extent of binding against surface CLEC2D antigen expressed on C4548 cell, as observed for various clones. Fold change in MFI has been plotted against individual mini-pools binding. Higher fold change indicating higher binding of anti-CLEC2D antibody to CLEC2D antigen; FIG. 10B, single cell clone screening – Anti CLED2D antibody expressed from single cell clonal lines was purified and used for flow cytometry experiments. Higher fold change in fluorescence signal indicates stronger binding of anti CLEC2D antibody binding to CLEC2D antigen; FIG. 10C, flow cytometric analysis of monoclonal antibody producing stable CHO cell lines - anti-CLED2D antibody expressed from single cell clonal lines was purified and used for flow cytometry experiments. Multiple monoclonal cell lines expressing the Anti CLEC2D antibodies were (such as C4608, C5093, C5511, C6481, C6726, C7720, C9103, C5848 and C3452) were tested for binding to CHO cell surface expressed CLEC2D antigen by flow cytometry. Fold increase in median fluorescence intensity was estimated and was observed to be in the range of 3-10 fold for multiple stable clones; FIG. 10D, representative images of interaction of anti-CLED2D monoclonal antibodies produced from clonal CHO cell lines with the CLEC2D antigen expressed on PC3 tumor cell line. As depicted herein, various anti-CLEC2D antibodies showed differential yet significant surface binding to CLEC2D antigen on PC3 cell surface. The nucleus was counterstained with DAPI (violet). Scale bar is 10μm; and FIG. 10E, quantitative RT PCR performed on of anti CLEC2D antibody- stable cell clones C4608 and C5511 to confirm stable

integration of antibody heavy chain and light chain genes. GAPDH house-keeping gene was used as internal normalizer. The study was carried out for 60 generations of CHO monoclonal lines expressing the Anti CLEC2D antibodies.

[084] FIGS. 11A-11F illustrate functional characterization of monoclonal anti CLEC2D antibodies, as shown in: FIG. 11A, the binding of anti CLEC2D antibodies, C4608, C5511, C6481, C2438, C3452, C0949 on surface expressed CLEC2D on prostate cancer cell line, PC3. Shift in MFI towards right indicated binding of antibody to surface expressed CLEC2D antigen on PC3 cell line; and FIG. 11B, representative flow cytometric analysis of cytotoxicity assay performed on PC3 target cells using PBMC as effector cells, at a ratio of 1:5 at a fixed concentration of 100ug/mL of Anti CLEC2D antibodies. Clones assessed for functionality herein were C5511, C4608 and C6481 with PBMC from Donor 1, while antibodies purified from clones C5392 and C3452 were tested with PBMC from Donor 2. The percentage of PC3 live cells is indicated by APC (eFluor 670) positive cells and dead cells indicates Sytox green-positive cells. Respective single cell clones have been labelled against each plot; FIG. 11C, representative flow cytometry analysis of cytotoxicity assay performed on PC3 target cells using PBMC as effector cells (1:5), with increasing concentrations of anti-CLEC2D antibody (C5511) from 10 µg/mL to 200 ug/mL revealed increased dose dependent tumor cell cytotoxicity; FIG. 11D, representative flow cytometric analysis of cytotoxicity assay performed on PC3 target cells using PBMC as effector cells at fixed concentration of anti CLEC2D antibody C5511. The tumor to effector cell ratio (T:E) was increased from 1:5 to 1:10. The data revealed with increasing proportion of effector cells leads to higher levels of tumor cell cytotoxicity; and FIG. 11E, end point cytotoxicity assay revealed significant cytotoxicity of tumor cells at 10 µg/mL. The assay also determines optimum concentration of anti-CLEC2D antibody to kill target cells using confocal microscopy. Upper panel indicates all control treatments where no cytotoxicity was observed as expected, and lower panel indicates the enhanced PC3 tumour cell death when treated with increasing the concentration of anti CLEC2D antibody (C6726) in presence of PBMC (T:E = 1:5). The maximum cell death were observed at concentration of 50ug/ml of Anti CLEC2D antibody. PC3 tumor cells – Green; PBMC – red; Dead cells – Blue; and Fig. 11F, end point cytotoxicity assay using selected anti-CLEC2D antibody to kill target cells using confocal microscopy. No cytotoxicity observed in control treatments like PC3 tumor cell alone, PBMC alone, PBMC with isotype human IgG1 antibody. PC3 tumor cell cytotoxicity was observed

when Anti CLEC2D antibody (C6726, C5848, C4608, C5511 and C6481) clones were used. Size enhanced images revealed PC3 tumor cells were surrounded by effector cells inducing tumor cell death. PC3 tumor cells – Green; PBMC – red; Dead cells – Blue.

[085] FIGS. 12A-12D illustrate NK cell mediated cytotoxicity of tumor cells with anti-CLEC2D antibody, a shown in: FIG. 12A, cytotoxicity of PC3 tumor cells when treated with purified NK cells and anti-CLEC2D antibodies (C6481 & C5511) at 100ug/ml. The data revealed 86% NK cell mediated cytotoxicity of PC3 tumor cells at T:E of 1:1. The percentage of PC3 dead cells indicates Sytox green-positive cells; FIG. 12B, no target cell death was observed when incubated with either isotype control (human IgG1 antibody) or with only NK cells increasing T:E ratio starting from 1:0.5 to 1:10; Scale bar is 10µm and FIG. 12C, anti-CLEC2D antibody alone cannot induce cytotoxicity of PC3 tumor cell; Scale bar is 10µm and FIG. 12D anti-CLEC2D antibody C5511 (at 50ug/mL) revealed increasing PC3 tumor cell death with increasing T:E ratio starting from 1:0.5, 1:5 and 1:10 C5511. Scale bar is 10µm.

[086] FIG. 13 illustrates cytotoxicity of PC3 tumor cells treated with isolated T cells and anti CLEC2D antibodies (C5511 & C6481) at 100ug/ml. The percentage of dead PC3 tumor cells indicated by Sytox green-positive cells.

[087] FIGS. 14A-14B illustrate live cell imaging with Anti CLEC2D antibody dependent cytotoxicity of PC3 tumor cells, a shown in: FIG. 14A, live cell imaging revealed cytotoxicity of PC3 tumor cells over a period of incubation with human PBMC cells and Anti CLEC2D antibody at 200µg/ml. The assay was carried out for 20hrs in a humidifier maintained at 37°C and 5% CO2 during the image acquisition. On the contrary, incubation with Control human IgG1 antibody (200µg/ml) did not cause tumor cell cytotoxicity. Live PC3 tumor cells – Green; PBMC – Red; Dead cells – Blue; Scale bar is 20µm and FIG. 14B, live cell imaging revealed cytotoxicity of PC3 tumor cells over a period of incubation with human NK cells and Anti CLEC2D antibody at 200µg/ml. The assay was carried out for 20hrs in a humidifier maintained at 37°C and 5% CO2 during the image acquisition. On the contrary, incubation with Control human IgG1 antibody (200µg/ml) did not cause tumor cell cytotoxicity. Live PC3 tumor cells – Green; NK cells – Red; Dead cells – Blue. Scale bar is 20µm

[088] FIGS. 15A-15G illustrate predictive models of anti-CLEC2D antibodies, as shown in: FIG. 15A, cartoon representation of epitope recognition (Chain A - Dark Blue, Chain B - Cyan) & CD161 (Chain C – Orange red, Chain D - Purple) complex PDB ID 5MGT; FIG. 15B, the red

selections denote residues within 6Å of NKR-P1's chains; FIG. 15C, ribbon representation of refined anti-CLEC2D antibody structures; respective clones for specific anti CLEC2D monoclonal antibodies have been labelled appropriately. Variable light chain is depicted in darker shade while heavy chain variable region is shown in white; FIG. 15D, represents selected conformations following PIZSA scoring and conformation clustering principle, belonging to C4608, contributed to one of the clusters interacting against CLEC2D (darker shade); FIG. 15E, a visualization of the residues selected for mutation to determine if the G00001-G00004-G00007-G00010-G00015 cluster combination from C4608 contains the binding site towards CLEC2D antigen; FIG. 15F, represents selected conformations following PIZSA scoring and conformation clustering principle, belonging to C5511, contributed to one of the clusters interacting against CLEC2D (darker shade); and FIG. 15G, a visualization of the residues selected for mutation to determine if the G00001-G00005-G00011-G00019-G00020 cluster combination from C5511 contains the binding site towards CLEC2D antigen.

[089] FIGS. 16A-16G illustrate on identified epitope patch on CLEC2D antigen against anti CLEC2D antibody clones C4608 and C5511; FIG. 16A, surface representation of anti CLEC2D antibody C4608 contact points on CLEC2D antigen; FIG. 16B, anti CLEC2D antibody C4608 contact points on CLEC2D antigen that are overlapping with CD161 binding regions on CLEC2D; FIG. 16C, surface representation of anti CLEC2D antibody C5511 contact points on CLEC2D antigen; FIG. 16D, anti CLEC2D antibody C5511 contact points with CLEC2D antigen that are overlapping with CD161 binding regions on CLEC2D; In all depictions darker shade indicates the interacting residue locations on CLEC2D antigen; FIG. 16E, anti CLEC2D antibody mediated disruption of CLEC2D and CD161 interaction- monitoring of CLEC2D antigen bead conjugation efficiency check; FIG. 16F, binding of CD161-FC to CLEC2D antigen was observed on magnetic beads in concentration depend manner; FIG. 16G, flow cytometric monitoring of CD161 binding in the absence and presence of Anti-CLEC2D antibody as compared with control, as a measure of disruption of CD161 and CLEC2D binding, as indicated by the solid black arrow.

[090] FIGS. 17A-17B illustrate NK cell activation with anti-CLEC2D antibody, as shown in: FIG. 17A, anti-CLE2D antibody C5511 induces CD69 expression indicating NK cell activation towards becoming cytotoxic. Respective experimental conditions have been mentioned against each plot. IL2 treatment was carried out as positive control of CD69 overexpression; and FIG.

17B, anti-CLEC2D antibody mediated CD69 expression is higher compared to PC3 cell primed CD69 expression level on NK cells.

[091] FIGS. 18A-18D illustrate effects of anti CLEC2D antibody C5511 on cytokine expression by effector cells, as shown in: FIG. 18A, anti CLEC2D antibody C5511 was used at concentrations of 10μg/mL and 100μg/mL to monitor elevation in IFNγ expression level; FIG. 18B, anti-CLEC2D antibody C5511 was used at concentration of 100ug/mL in the presence or absence of PC3 cells (E:T = 10:1). IFNγ expression was monitored in the CD3+ve gated population; FIG. 18C, anti-CLEC2D antibody C5511 was used at concentration of 100ug/mL in the presence or absence of PC3 cells (E:T = 10:1). IFNγ expression was monitored in the CD3-ve gated population; and FIG. 18D, anti-CLEC2D antibody C5511 was used as at concentrations of 100μg/mL in the presence or absence of isolated NK cell. IFNγ overexpression was observed with anti CLEC2D antibody C5511.

[092] FIGS. 19A-19G illustrate mammalian expression constructs used to generate full-length monoclonal antibody. Constructs were generated through gene synthesis followed by confirmation through restriction digestion and Sanger sequencing, as shown in: FIG. 19A, vector designed to clone selected antibody variable heavy chain genes in IgG4 backbone; FIG. 19B, vector designed to clone selected antibody variable heavy chain genes in IgG1 N to A backbone; FIG. 19C, flow cytometric analysis of binding of Anti CLEC2D antibody with IgG4 isotype backbone (C3256 and C3276) to CLEC2D antigen expressed on surface of CHO cells. Binding was compared with un-transfected CHO cells, as estimated from peak shift towards right; FIG. 19D, cytotoxicity of Anti CLEC2D antibody using various antibody isotypes. IgG1 isotype (C3452 & C4608) and IgG4 isotype (C3256 & C3276) Anti CLEC2D antibodies exhibited significant cytotoxicity when incubated with freshly isolated PBMC and PC3 tumor cells; FIG. 19E, anti-CLEC2D antibody produced as afucosylated monoclonal antibodies C0613, C1301, C6268, C1699, C2437, C9832, C8900 and C7749 revealed binding to CHO cell surface expressed CLEC2D antigen by flow cytometry; FIG. 19F, NK cell-mediated cytotoxicity of PC3 tumor cells with the afucosylated anti-CLEC2D antibody (C7749, C8800,C9832) used at 5X lesser concentration than C5511. The data revealed afucosylated Anti CLEC2D antibodies achieved nearly equal cell death at 5 times less concentration, indicating afucosylated Anti CLEC2D antibodies are more cytotoxic; and FIG. 19G, CDC mediated cytotoxicity was

measured for anti-CLEC2D antibody C5511 using Ramos and PC3 tumor cell lines. Rituximab was used as positive control.

[093] FIGS. 20A-20K illustrate anti-tumor effects in cancer xenograft mouse model. HuNOG-EXL mice were used for PC3 xenograft and the tumor bearing animals were randomized and used for injecting Anti CLEC2D antibody product, as shown in: FIG. 20A, tumor volume vs. time plot demonstrating significant anti tumor effects observed with Anti-CLEC2D antibody alone or in combination with anti-PDL1 antibody; FIG. 20B, images displaying immune cell infiltration through staining of CD3+ T cells in the tumor micro environment; FIG. 20C, images of mice with the xenograft showing Alexa 647 labelled anti-CLEC2D antibody injected into the tumor over a 96-hour period; FIG. 20D, effect of test compounds on tumor volume in humanized (huNOG-EXL) mice bearing subcutaneous PC-3 tumor xenografts (up to day 36). Each treatment group consisted of 5 animals and named as C5511 mAb group, Vehicle control IgG1 group and C6481 mAb group. Values are expressed as mean of 2 - 5 animals in each group. Statistical analysis was carried out by Two-way ANOVA followed by Bonferroni post-tests using Graph Pad Prism (Version 8.3.0). ** $p<0.01$ statistically significant (Day 36) when C5511 mAb group was compared with Vehicle control IgG1 group; FIG. 20E, effect of test compounds on tumor volume in humanized (huNOG-EXL) mice bearing subcutaneous PC-3 tumor xenografts (up to day 24). Each treatment group consisted of 5 animals and named as C5511 mAb group, Vehicle control IgG1 group and C6481 mAb group. Values are expressed as mean of 2-5 animals in each group. Statistical analysis was carried out by Two-way ANOVA followed by Bonferroni post-tests using Graph Pad Prism (Version 8.3.0).*** $p<0.001$ and * $p<0.05$ statistically significant (Day 24) when C5511 mAb group and C6481 mAb group, respectively were compared to Vehicle control IgG1 group; FIG. 20F, effect of test compounds on delta tumor volume in humanized (huNOG-EXL) mice bearing subcutaneous PC-3 tumor xenografts (up to day 36). Each treatment group consisted of 5 animals and named as C5511 mAb group, Vehicle control IgG1 group and C6481 mAb group. Values are expressed as mean of 2-5 animals in each group. Statistical analysis was carried out by Two-way ANOVA followed by Bonferroni post-tests using Graph Pad Prism (Version 8.3.0). ** $p<0.01$ statistically significant (Day 36) when C5511 mAb group was compared to Vehicle control IgG1 group; FIG. 20G, effect of test compounds on delta tumor volume in humanized (huNOG-EXL) mice bearing subcutaneous PC-3 tumor xenografts (up to day 24). Each treatment group consisted of 5 animals and named as

C5511 mAb group, Vehicle control IgG1 group and C6481 mAb group. Values are expressed as mean of 2-5 animals in each group. Statistical analysis was carried out by Two-way ANOVA followed by Bonferroni post-tests using Graph Pad Prism (Version.8.3.0). *** $p<0.001$ and * $p<0.05$ statistically significant (Day 24) when C5511 mAb group and C6481 mAb group, respectively were compared to Vehicle control IgG1 group; FIG. 20H, effect of test compounds on relative tumor volume in humanized (huNOG-EXL) mice bearing subcutaneous PC-3 tumor xenografts (up to day 36). Each treatment group consisted of 5 animals and named as C5511 mAb group, Vehicle control IgG1 group and C6481 mAb group. Values are expressed as mean of 2-5 animals in each group. Statistical analysis was carried out by Two-way ANOVA followed by Bonferroni post-tests using Graph Pad Prism (Version 8.3.0). * $p<0.05$ statistically significant (Day 36) when C5511 mAb group was compared to Vehicle control IgG1 group; FIG. 20I, effect of test compounds on relative tumor volume in humanized (huNOG-EXL) mice bearing subcutaneous PC-3 tumor xenografts (up to day 24) . Each treatment group consisted of 5 animals and named as C5511 mAb group, Vehicle control IgG1 group and C6481 mAb group. Values are expressed as mean of 2-5 animals in each group. Statistical analysis was carried out by Two-way ANOVA followed by Bonferroni post-tests using Graph Pad Prism (Version.8.3.0). *** $p<0.001$ and * $p<0.05$ statistically significant (Day 24) when C5511 mAb group and C6481 mAb group, respectively were compared to Vehicle control IgG1 group; FIG. 20J, effect of test compounds on delta relative tumor volume in humanized (huNOG-EXL) mice bearing subcutaneous PC-3 tumor xenografts (up to day 36). Each treatment group consisted of 5 animals and named as C5511 mAb group, Vehicle control IgG1 group and C6481 mAb group. Values are expressed as mean of 2-5 animals in each group. Statistical analysis was carried out by Two-way ANOVA followed by Bonferroni post-tests using Graph Pad Prism (Version.8.3.0). * $p<0.05$; and statistically significant (Day 36) when C5511 mAb group was compared to Vehicle control IgG1 group; and FIG. 20K, effect of test compounds on delta relative tumor volume in humanized (huNOG-EXL) mice bearing subcutaneous PC-3 tumor xenografts (up to day 24). Each treatment group consisted of 5 animals and named as C5511 mAb group, Vehicle control IgG1 group and C6481 mAb group. Values are expressed as mean of 2-5 animals in each group. Statistical analysis was carried out by Two-way ANOVA followed by Bonferroni post-tests using Graph Pad Prism (Version.8.3.0). *** $p<0.001$ and * $p<0.05$ statistically significant (Day

24) when C5511 mAb group and C6481 mAb group, respectively were compared to Vehicle control IgG1 group.

[094] FIGS. 21A-21I illustrate characterization of purified Anti CLEC2D antibody product, as shown in: FIG. 21A, SDS-PAGE analysis of purified C5511 antibody in non reducing and reducing conditions; FIG. 21B, TIC chromatogram from Intact Mass spectrometry analysis of Anti CLEC2D antibody (3 replicates); FIG. 21C, WCX chromatogram analysis of Anti CLEC2D antibody; FIG. 21D, Size Exclusion chromatogram of Anti CLEC2D antibody; FIG. 21E, ELISA assay development of Anti CLEC2D antibody against CLEC2D purified biotinylated antigen. The data was fit to one site binding model to calculate Kd of Anti CLEC2D antibody; FIGS. 21E and 21F, CLEC2D antigen affinity based binding studies of representative Anti CLEC2D antibody. FIG. 21G, Purified CLEC2D antigen ecto-domain was used as source of antigen in BIACORE studies; Response monitored has been plotted against time; FIG. 21H, affinity based binding studies of representative Anti CLEC2D antibody molecules with FcRn at pH 5.9; and FIG. 21I, affinity based binding studies of representative Anti CLEC2D antibody molecules with FcRn at at pH 7.4.

[095] FIGS. 22A-22C illustrate that anti-CLEC2D antibody for plausible diagnostic and prognostic applications, as shown in: FIG. 22A, selection of Anti CLEC2D antibody (C0949) based on binding characteristics. Four Anti CLEC2D antibodies were evaluated (C2779, C2438, C0949 and C2543) for CLEC2D binding on PC3 target cells. C0949 showed excellent binding and peak median shift; FIG. 22B, anti-CLEC2D antibody C0949 recognizes CLEC2D antigen on multiple prostate cancer cell lines; and FIG. 22C, anti-CLEC2D antibody C0949 recognizes CLEC2D antigen on multiple tumor cell lines. Specific binding and fold change in mean fluorescence was calculated by ratio of mean FITC fluorescence between test and control.

[096] FIGS. 23A-23D illustrate that anti-CLEC2D antibody recognize CLEC2D antigen on prostate cancer tumor cells, as shown in: FIG. 23A, expression level of CLEC2D antigen on prostate cancer disease stage after TCGA data analysis; FIG. 23B, expression level of CLEC2D antigen on prostate cancer cell lines PC3, DU145, 22RV1 and LnCap; FIG. 23C, expression level of CLEC2D antigen on prostate cancer cell lines PC3, LnCap, 22RV1, and DU145 with induction using LPS, Poly I:C, IFN-γ, PBMC supernatant, PBMC cells, NK cells and T cells. Upper panel with anti-CLEC2D antibody, lower panel representing the merged image; and FIG.

23D, human tissue microarray slides stained with anti-CLEC2D antibody C2685 showing staining of tumor cells in malignant prostate cancer tissue.

[097] FIGS. 24A-24D illustrate that anti-CLEC2D antibody recognize CLEC2D antigen on various other tumor cells, as shown in: FIG. 24A, TCGA data analysis for CLEC2D antigen expression in various cancers; FIG. 24B, expression level of CLEC2D antigen on various tumor cell lines HepG2 (liver cancer), LN229 (Glioblastoma), SKOV3 (Ovary cancer), BT474 (Breast cancer), NCI-H929 (Myeloma), and Ramos (Lymphoma); FIG. 24C, expression level of CLEC2D antigen on BT474 (Breast cancer), SKOV3 (Ovary cancer), LN229 (Glioblastoma), Ramos (Lymphoma), NCI-H929 (Myeloma) and HepG2 (liver cancer), upon induction with LPS, Poly I:C, IFNγ; and FIG. 24D, anti CLEC2D antibody C5511 mediated cytotoxicity observed on SKOV3 (ovary cancer) at 100μg/ml; and anti-CLEC2D antibodies C5511 and C6481 mediated cytotoxicity observed on HepG2 (liver cancer) cell lines at 100μg/ml. The percentage of dead cells indicated by Sytox green-positive cells.

[098] FIGS. 25A-25E illustrate lymphocyte proliferation assay with anti-CLEC2D antibody using flow cytometry analysis, as shown in: FIG. 25A, Antibody wet-coating protocol; FIG. 25B, Air dried antibody coating protocol; FIG. 25C, High density pre-culture protocol; FIG. 25D, measurement of IFNγ cytokine secretion from effector cells when PBMC are incubated with Anti CLEC2D antibodies (C5511, C4608, C6481) for extended period. Treatment with OKT3 antibody was used as a positive control; and FIG. 25E, measurement of IL2 cytokine secretion from effector cells when PBMC are incubated with Anti CLEC2D antibodies (C5511, C4608, C6481) for extended period. Treatment with OKT3 antibody was used as a positive control. PBMCs were treated with anti CD3 antibody OKT3 (1μg/ml), Anti CLEC2D antibody C4608, C5511 and C6481 (1μg/ml, 10μg/ml, 50μg/ml & 100μg/ml) and incubated for four days. The fluorescent proliferation dye status was monitored using flow cytometer. Untreated PBMC was used as a control.

[099] FIG. 26 illustrates histogram overlay showing binding of anti-CLEC2D antibodies (C3566 and C5511) against CLEC2D antigen homologs from Rat, Mouse and cynomolgus monkey, expressed on CHO cell surface, using flow cytometric analysis.

DETAILED DESCRIPTION

[100] Modulation of immune cell checkpoint receptors via antibody-based/directed therapeutic approaches has been gaining constant interests over the past few years. The largest efforts have been centered on T cell checkpoint modulation. However, there is an increasing attention in B cell, NK cell, and myeloid cell checkpoint modulation as well. The innate immune system includes natural killer (NK) cells, which possess the ability to recognize and induce the cytotoxicity of a wide range of target cells, such as, tumor cells or virus infected cells. NK cells do not need any prior antigen sensitization. Apart from direct cytotoxicity, NK cells also participate in the initiation and progress of the adaptive immune response through the production and secretion of cytokines. Usually, these responses are regulated by adequate balance of signals induced by the interaction of a wide array of surface-activating and surface-inhibitory receptors with ligands on the surface of target cells. Modulation of NK cell numbers and/or its relevant function through a variety of agents such as monoclonal antibodies, cytokines may result in enhanced anti-tumor activity. These agents can be offered either alone or in combination as potential therapeutics. Therefore, anti-cancer activity of NK cell can be unleashed through harnessing surface receptors, both activating and/or inhibitory kinds.

[101] Blocking these interactions may be a new therapeutic option for treatment of several cancers. However, the finding, understanding and designs need to be tuned and therapeutic treatment needs to be further tailored for specific receptor as targets against various cancers, which is still unmet.

[102] Unless otherwise defined herein, scientific and technical terms used in connection with the present disclosure shall have the meanings that are commonly understood by those of ordinary skill in the art. Further, unless otherwise required by context, singular terms shall include the plural and plural terms shall include the singular as is considered appropriate to the context and/or application. The various singular/plural permutations may be expressly set forth herein for the sake of clarity. Generally, nomenclatures used in connection with, and techniques of biotechnology, immunology, molecular and cellular biology, recombinant DNA technology described herein are those well known and commonly used in the art. Certain references and other documents cited herein are expressly incorporated herein by reference. In case of conflict, the present specification, including definitions, will control. The materials, methods, figures and examples are illustrative only and not intended to be limiting.

[103] Furthermore, the methods, preparation and use of the antibody naïve library disclosed employ, unless otherwise indicated, conventional techniques in molecular biology, biochemistry, computational chemistry, cell culture, recombinant DNA technology, Polymerase Chain Reaction (PCR) and related fields. These techniques, their principles, and requirements are explained in the literature and known to a person skilled in the art.

[104] Before the method of generating the antibody naïve library and the nucleic acids which encode the antibody naïve library and other embodiments of the present disclosure are disclosed and described, it is to be understood that the terminologies used herein are for the purpose of describing particular embodiments only and are not intended to be limiting. It must be noted that, as used in the specification and the appended claims, the singular forms "a," "an" and "the" include plural referents unless the context clearly dictates otherwise.

[105] In one embodiment, the terms "library" and "libraries" are used interchangeably within this disclosure, which relate to the product of the disclosure. In one embodiment, it refers to a collection or pool of nucleic acid sequences. In one embodiment, it refers to a collection or pool of amino acid sequences. In some embodiments, it refers to a collection or pool of organisms that comprise a collection or pool of amino acid sequences or nucleic acid sequences. In some embodiments, the organisms are bacteriophages (phages) or yeast (e.g., Saccharomyces cerevisiae).

[106] In one embodiment, the terms 'pooling', 'pooled', 'pool', and 'pools' in the context of the instant disclosure means combining the samples/nucleic acid sequences/nucleic acid fragments/gene clones/amplified product/antibodies obtained by employing the method of the instant disclosure from multiple donors i.e., more than one donor.

[107] In one embodiment, the term "PBMC" refers to any peripheral blood cell having a round nucleus consisting of lymphocytes (T cells, B cells, NK cells) and monocytes, erythrocytes, platelet, and granulocytes (neutrophils, basophils, and eosinophils).

[108] *Antigens*

[109] As used herein, the terms "antigen" or "immunogen" refer to any foreign substance which induces an immune response in the body. In one embodiment, an antigen is a cellular protein. In one embodiment, an antigen is a cell surface protein.

[110] The antigen may be isolated or derived from any species. Representative species include, but are not limited to Homo sapiens, Mus musculus, Rattus norvegicus, Canis lupis familiaris

and Cynomolgus macaca fascicularis. In some embodiments, the antigen is a fragment of a wild type protein isolated or derived from Homo sapiens, Mus musculus, Rattus norvegicus, Canis lupis familiaris or Cynomolgus macaca fascicularis. In some embodiments, the antigen is a mutant variant of a protein from Homo sapiens, Mus musculus, Rattus norvegicus, Canis lupis familiaris or Cynomolgus macaca fascicularis. In some embodiments, antigens can be mutated to increase the solubility and/or stability of the antigen. For example, a CLEC2D antigens can include a mutation at H176C to introduce an additional disulphide bridge with the Cys163 amino acid to increase the stability and homogeneity of the expressed protein.

[111] In some embodiments, the antigen includes an epitope tag at either the N or C terminus of the polypeptide. Exemplary tags include, but are not limited to polyHistidine tags and FLAG tags. Any epitope tag known in the art is envisaged as within the scope of the disclosure.

[112] C-type lectin domain family 2 member D (CLEC2D), also referred to as CLAX, Lectin Like Transcript-1 (LLT1) and OCIL, is a member of the natural killer cell receptor C-type lectin family. CLEC2D binds to Killer Cell Lectin Like Receptor B1 (KLRB1). KLRB1 is also known as CD161, CLEC5B, NKR, NKR-P1, NKR-P1A, NKRP1A and hNKR-P1A. All orthologs and isoforms of CLEC2D and CD161 are considered to be within the scope of the present disclosure.

[113] In some embodiments, a C-type lectin domain family 2 member D (CLEC2D) protein or any of its aliases or homologs, known in the art, whether from humans or other species, represents a target antigen of an antibody produced by the methods described herein.

[114] In some embodiments, the antigen is a CLEC2D antigen that has at least 85%, at least 90%, at least 95%, at least 96%, at least 97% at least 98%, at least 99% or 100% identity to a CLEC2D sequence isolated or derived from Homo sapiens, Mus musculus, Rattus norvegicus, Canis lupis familiaris and Cynomolgus macaca fascicularis.

[115] In some embodiments, a CD161 protein or any of its aliases or homologs, known in the art, whether from humans or other species, represents a target antigen of an antibody produced by the methods described herein.

[116] In some embodiments, the CD161 antigen has at least 85%, at least 90%, at least 95%, at least 96%, at least 97% at least 98%, at least 99% or 100% identity to a CD161 sequence isolated or derived from Homo sapiens, Mus musculus, Rattus norvegicus, Canis lupis familiaris and Cynomolgus macaca fascicularis.

[117] Exemplary antigens are shown in Table 1 below.

Table 1. Representative CLEC2D and CD161 Polypeptide Sequences

SEQ ID	Description	Amino Acid Sequence
SEQ ID 886	Human (*Homo sapiens*) CLEC2D construct 1	MHDSNNVEKDITPSELPANPGCLHSKEHSIKATLIWRLFFLIMFLTIIVCGMVAALSAIRANCHQ EPSVCLQAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVESFQELNFLLRYKGP SDHWIGLSREQGQPWKWINGTEWTRQFPILGAGECAYLNDKGASSARHYTERKWICSKSDI HV
SEQ ID 887	Human (*Homo sapiens*) CLEC2D construct 2	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVESFQELNFLLRYKGPSDHWI GLSREQGQPWKWINGTEWTRQFPILGAGECAYLNDKGASSARHYTERKWICSKSDIHVHHH HHHHH
SEQ ID 888	Human (*Homo sapiens*) CLEC2D construct 3	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVESFQELNFLLRYKGPSDHWI GLSREQGQPWKWINGTEWTRQFPILGAGECAYLNDKGASSARCYTERKWICSKSDIHVHHH HHHHHG
SEQ ID 889	Human (*Homo sapiens*) CLEC2D construct 4	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVES FQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPILGAGECAYLNDKGASSARH YTERKWICSKSDIHVHHHHHHHH
SEQ ID 890	Human (*Homo sapiens*) CLEC2D construct 5	MMSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQV ESFQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPILGAGECAYLNDKGASSAR CYTERKWICSKSDIHVHHHHHHHHG
SEQ ID 891	Human (*Homo sapiens*) CLEC2D construct 6	MMSFVSLLLVGILFHATQAHHHHHHHHDDDDKQAACPESWIGFQRKCFYFSDDTKNWTSS QRFCDSQDADLAQVESFQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPILGA GECAYLNDKGASSARCYTERKWICSKSDIHV
SEQ ID 892	Human (*Homo sapiens*) CLEC2D construct 7	HHHHHHHHDDDDKQAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVESFQE LNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPILGAGECAYLNDKGASSARCYTER KWICSKSDIHV
SEQ ID 893	Human (*Homo sapiens*) CLEC2D construct 8	MMSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQV ESFQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPILGAGECAYLNDKGASSAA CAAAAAWICSKSDIHVHHHHHHHH
SEQ ID 894	Human (*Homo sapiens*) CLEC2D construct 9	MQLLRCFSIFSVIASVLAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVESF QELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPILGAGECAYLNDKGASSAACA AAAAWICSKSDIHVEFEQKLISEEDLDYKDDDDKENLYFQGLQASGGGGSGGGGSGGGGSQE LTTICEQIPSPTLESTPYSLSTTTILANGKAMQGVFEYYKSVTFVSNCGSHPSTTSKGSPINTQYV F
SEQ ID 895	Human (*Homo sapiens*) CLEC2D construct 10	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVESFQELNFLLRYKGPSDHWI GLSREQGQPWKWINGTEWTRQFPILGAGECAYLNDKGASSAACAAAAAWICSKSDIHVEFE QKLISEEDLDYKDDDDKENLYFQGLQASGGGGSGGGGSGGGGSQELTTICEQIPSPTLESTPYS LSTTTILANGKAMQGVFEYYKSVTFVSNCGSHPSTTSKGSPINTQYVF
SEQ ID 896	Human (*Homo sapiens*) CLEC2D construct 11	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVESFQELNFLLRYKGPSDHWI GLSREQGQPWKWINGTEWTRQFPILGAGECAYLNDKGASSAACAAAAAWICSKSDIHVHHH HHHHH

SEQ ID 897	Human (*Homo sapiens*) CLEC2D construct 12	MMSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQV ESFQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPILGAGECAALADKGASSAR CYTERKWICSKSDIHVHHHHHHHH
SEQ ID 898	Human (*Homo sapiens*) CLEC2D construct 13	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVESFQELNFLLRYKGPSDHWI GLSREQGQPWKWINGTEWTRQFPILGAGECAALADKGASSARCYTERKWICSKSDIHVHHH HHHHH
SEQ ID 899	Human (*Homo sapiens*) CLEC2D construct 14	MQLLRCFSIFSVIASVLAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVESF QELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPILGAGECAALADKGASSARCY TERKWICSKSDIHVEFEQKLISEEDLDYKDDDDKENLYFQGLQASGGGGSGGGGSGGGGSQE LTTICEQIPSPTLESTPYSLSTTTILANGKAMQGVFEYYKSVTFVSNCGSHPSTTSKGSPINTQYV F
SEQ ID 900	Human (*Homo sapiens*) CLEC2D construct 15	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVESFQELNFLLRYKGPSDHWI GLSREQGQPWKWINGTEWTRQFPILGAGECAALADKGASSARCYTERKWICSKSDIHVEFEQ KLISEEDLDYKDDDDKENLYFQGLQASGGGGSGGGGSGGGGSQELTTICEQIPSPTLESTPYSL STTTILANGKAMQGVFEYYKSVTFVSNCGSHPSTTSKGSPINTQYVF
SEQ ID 901	Human (*Homo sapiens*) CLEC2D construct 16	MMSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQV ESFQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPILGAGECAYLNDAGAASA RCYTERKWICSKSDIHVHHHHHHHH
SEQ ID 902	Human (*Homo sapiens*) CLEC2D construct 17	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVESFQELNFLLRYKGPSDHWI GLSREQGQPWKWINGTEWTRQFPILGAGECAYLNDAGAASARCYTERKWICSKSDIHVHHH HHHHH
SEQ ID 903	Human (*Homo sapiens*) CLEC2D construct 18	MQLLRCFSIFSVIASVLAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVESF QELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPILGAGECAYLNDAGAASARCY TERKWICSKSDIHVEFEQKLISEEDLDYKDDDDKENLYFQGLQASGGGGSGGGGSGGGGSQE LTTICEQIPSPTLESTPYSLSTTTILANGKAMQGVFEYYKSVTFVSNCGSHPSTTSKGSPINTQYV F
SEQ ID 904	Human (*Homo sapiens*) CLEC2D construct 19	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVESFQELNFLLRYKGPSDHWI GLSREQGQPWKWINGTEWTRQFPILGAGECAYLNDAGAASARCYTERKWICSKSDIHVEFEQ KLISEEDLDYKDDDDKENLYFQGLQASGGGGSGGGGSGGGGSQELTTICEQIPSPTLESTPYSL STTTILANGKAMQGVFEYYKSVTFVSNCGSHPSTTSKGSPINTQYVF
SEQ ID 905	Human (*Homo sapiens*) CLEC2D construct 20	MHDSNNVEKDITPSELPANPGCLHSKEHSIKATLIWRLFFLIMFLTIIVCGMVAALSAIRANCHQ EPSVCLQAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVESFQELNFLLRYKGP SDHWIGLSREQGQPWKWINGTEWTRQLVMKEDGANLYVAKVSQVPRMNPRPVMVSYPG SRRVCLFE
SEQ ID 906	Human (*Homo sapiens*) CLEC2D construct 21	MHDSNNVEKDITPSELPANPGCLHSKEHSIKATLIWRLFFLIMFLTIIVCGMVAALSAIRANCHQ EPSVCLQAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVESFQELNFLLRYKGP SDHWIGLSREQGQPWKWINGTEWTRQ
SEQ ID 907	Human (*Homo sapiens*) CLEC2D construct 22	MHDSNNVEKDITPSELPANPGCLHSKEHSIKATLIWRLFFLIMFLTIIVCGMVAALSAIRANCHQ EPSVCLQAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVESFQELVSYPGSRR VCLFE
SEQ ID 908	Human (*Homo sapiens*) CLEC2D construct 23	MHDSNNVEKDITPSELPANPAIRANCHQEPSVCLQAACPESWIGFQRKCFYFSDDTKNWTSS QRFCDSQDADLAQVESFQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPILGA GECAYLNDKGASSARHYTERKWICSKSDIHV

SEQ ID 909	Human (*Homo sapiens*) CLEC2D construct 24	MHDSNNVEKDITPSELPANPAIRANCHQEPSVCLQAACPESWIGFQRKCFYFSDDTKNWTSS QRFCDSQDADLAQVESFQELVSYPGSRRVCLFE
SEQ ID 910	Rat (*Rattus norvegicus*) CLEC2D construct 1	MPSSAHLQDPPPLLSRTLTQNEGQTSLRQSSSCGPSAASASESLSGSTESRIPHSKMLQGKLPR NIPLEYPAGLYCCYVVIIVLSVAVVALSVALSVKKTAQISTINTYAACPRNWIGVGNKCFYFNEIP SNWTLSQTLCKEQGAELARFDTEEELNFLRRYKGSSGYWFGLHRESSAHPWKWTDNTEYNN SVSIGGDEKHGFLSDNGFSSGRGYIVRKSICRKPNSYTSQCL
SEQ ID 911	Mouse (Mus Musculus) CLEC2D construct 1	MCVTKASLPMLSPTGSPQEVEVGKILQGKRHGTISPESCAKLYCYYGVIMVLTVAVIALSVALS ATKTEQIPVNKTYAACPQNWIGVENKCFYFSEYPSNWTFAQAFCMAQEAQLARFDNQDELN FLMRYKANFDSWIGLHRESSEHPWKWTDNTEYNNTIPIRGEERFAYLNNNGISSTRIYSLRM WICSKLNSYSLHCQTPFFPS
SEQ ID 912	Mouse (Mus Musculus) CLEC2D construct 2	MSFVSLLLVGILFHATQAYAACPQNWIGVENKCFYFSEYPSNWTFAQAFCMAQEAQLARFD NQDELNFLMRYKANFDSWIGLHRESSEHPWKWTDNTEYNNTIPIRGEERFAYLNNNGISSTRI YSLRMWICSKLNSYSLHCQTPFFPSHHHHHHHH
SEQ ID 913	Mouse (Mus Musculus) CLEC2D construct 3	YAACPQNWIGVENKCFYFSEYPSNWTFAQAFCMAQEAQLARFDNQDELNFLMRYKANFDS WIGLHRESSEHPWKWTDNTEYNNTIPIRGEERFAYLNNNGISSTRIYSLRMWICSKLNSYSLHC QTPFFPSHHHHHHHH
SEQ ID 914	Mouse (Mus Musculus) CLEC2D construct 4	MSFVSLLLVGILFHATQAYAACPQNWIGVENKCFYFSEYPSNWTFAQAFCMAQEAQLARFD NQDELNFLMRYKANFDSWIGLHRESSEHPWKWTDNTEYNNTIPIRGEERFAYLNNNGISSTR CYSLRMWICSKLNSYSLHCQTPFFPSHHHHHHHH
SEQ ID 915	Mouse (Mus Musculus) CLEC2D construct 5	YAACPQNWIGVENKCFYFSEYPSNWTFAQAFCMAQEAQLARFDNQDELNFLMRYKANFDS WIGLHRESSEHPWKWTDNTEYNNTIPIRGEERFAYLNNNGISSTRCYSLRMWICSKLNSYSLH CQTPFFPSHHHHHHHH
SEQ ID 916	Dog (*Canis lupus familiaris*) CLEC2D construct 1	MSFVSLLLVGILFHATQAEAACPESWIGFQRKCFYFSDDIKNWTFSQRFCDSYGADLVQIETLL ELNFLLRYKGPYDHWIGLSRDLGQPWKWVNGTEWTNCFPIRGGGECAYLNDKGASSARRYT ERKWICSKPDIYAQIKRQNSIHHHHHHHH
SEQ ID 917	Dog (*Canis lupus familiaris*) CLEC2D construct 2	EAACPESWIGFQRKCFYFSDDIKNWTFSQRFCDSYGADLVQIETLLELNFLLRYKGPYDHWIGL SRDLGQPWKWVNGTEWTNCFPIRGGGECAYLNDKGASSARRYTERKWICSKPDIYAQIKRQ NSIHHHHHHHH
SEQ ID 918	Cynomolgus (Macaca fascicularis) CLEC2D construct 1	MVTGSKMHDSNNVEKDIAPSELPANPGYRHSKQHSGKATLIWPLFFLIMFLTIIVCGMVVALS AIRANCHQKPSVCLQAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDAALAQVESFQEL NFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPILGAGEYAYLNDKGASSARYYTERK WICSKPDTYVQMVQQSPN
SEQ ID 919	Cynomolgus (Macaca fascicularis) CLEC2D construct 2	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDAALAQVES FQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPILGAGEYAYLNDKGASSARYY TERKWICSKPDTYVQMVQQSPNHHHHHHHH

SEQ ID 920	Cynomolgus (Macaca fascicularis) CLEC2D construct 3	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDAALAQVESFQELNFLLRYKGPSDHWI GLSREQGQPWKWINGTEWTRQFPILGAGEYAYLNDKGASSARYYTERKWICSKPDTYVQMV QQSPNHHHHHHHH
SEQ ID 921	Human *(Homo sapiens)* CD161 construct 1	MDQQAIYAELNLPTDSGPESSSPSSLPRDVCQGSPWHQFALKLSCAGIILLVLVVTGLSVSVTSL IQKSSIEKCSVDIQQSRNKTTERPGLLNCPIYWQQLREKCLLFSHTVNPWNNSLADCSTKESSLL LIRDKDELIHTQNLIRDKAILFWIGLNFSLSEKNWKWINGSFLNSNDLEIRGDAKENSCISISQTS VYSEYCSTEIRWICQKELTPVRNKVYPDS
SEQ ID 922	Human *(Homo sapiens)* CD161 construct 2	MSFVSLLLVGILFHATQAQKSSIEKCSVDIQQSRNKTTERPGLLNCPIYWQQLREKCLLFSHTVN PWNNSLADCSTKESSLLLIRDKDELIHTQNLIRDKAILFWIGLNFSLSEKNWKWINGSFLNSNDL EIRGDAKENSCISISQTSVYSEYCSTEIRWICQKELTPVRNKVYPDSHHHHHHHH
SEQ ID 923	Human *(Homo sapiens)* CD161 construct 3	QKSSIEKCSVDIQQSRNKTTERPGLLNCPIYWQQLREKCLLFSHTVNPWNNSLADCSTKESSLLL IRDKDELIHTQNLIRDKAILFWIGLNFSLSEKNW KWINGSFLNSNDLEIRGDAKENSCISISQTSVYSEYCSTEIRWICQKELTPVRNKVYPDSHHHHH HHH
SEQ ID 924	Dog(Canis lupus familiaris) CD161 construct 1	MSFVSLLLVGILFHATQAQNSSIEECRVDVQVNGNETTEKPNLLQCPVHWHLLQEKCLFFSHA SNTWKDSLTDCSAKESSLLLIQDQEELRLIRGLIYKKEILFWIGLNLTLSEKKWKWINGSFLNSNIL QIAGYNKESSCVYISLTGIVSENCDAENQWICQKELKPDRNKICSKFHHHHHHHH
SEQ ID 925	Dog(Canis lupus familiaris) CD161 construct 2	QNSSIEECRVDVQVNGNETTEKPNLLQCPVHWHLLQEKCLFFSHASNTWKDSLTDCSAKESSL LLIQDQEELRLIRGLIYKKEILFWIGLNLTLSEKKWKWINGSFLNSNILQIAGYNKESSCVYISLTGI VSENCDAENQWICQKELKPDRNKICSKFHHHHHHHH
SEQ ID 926	Cynomolgus *(Macaca fascicularis)* CD161 construct 1	MSFVSLLLVGILFHATQAQKPSIGKCSVDIQQNRTKTTERPDLLNCPIYWQQVQEKCLLFSHTV NPWNNSLADCSTKESSLLLIQDKDELTRTQNLIHDKAISFWIGLNFSLSEKNWKWINGSFLSSN DLKITGDAKENSCVYISQTSVYSEYCSTEMKWICQKELTLVRNKVSPDSWLHHHHHHHH
SEQ ID 927	Cynomolgus *(Macaca fascicularis)* CD161 construct 2	QKPSIGKCSVDIQQNRTKTTERPDLLNCPIYWQQVQEKCLLFSHTVNPWNNSLADCSTKESSL LLIQDKDELTRTQNLIHDKAISFWIGLNFSLSEKNWKWINGSFLSSNDLKITGDAKENSCVYISQ TSVYSEYCSTEMKWICQKELTLVRNKVSPDSWLHHHHHHHH
SEQ ID 928	Mouse (*Mus Musculus)* CD161 construct 1	MSFVSLLLVGILFHATQAQKPSREKCCVFIQENLNKTTDCSVNLECPQDWLLHRDKCFHVSQV SNTWEEGQADCGRKGATLLLIQDQEELRFLLDSIKEKYNSFWIGLRFTLPDMNWKWINGTTF NSDVLKITGVTENGSCASILGDKVTPESCASDNRWICQKELNHETPSNDSHHHHHHHH
SEQ ID 929	Mouse (*Mus Musculus)* CD161 construct 2	QKPSREKCCVFIQENLNKTTDCSVNLECPQDWLLHRDKCFHVSQVSNTWEEGQADCGRKGA TLLLIQDQEELRFLLDSIKEKYNSFWIGLRFTLPDMNWKWINGTTFNSDVLKITGVTENGSCASI LGDKVTPESCASDNRWICQKELNHETPSNDSHHHHHHHH
SEQ ID 930	Human (*Homo sapiens*) CLEC2D construct 25	MSFVSLLLVGILFHATQAQ A A C P E S W I G F Q R K C F Y F S D D T K N W T S S Q R F C D S Q D A D L A Q V E S F Q E L N F L L R Y K G a S D H W I G L S R E Q G Q P W K W I N G T E W T R Q F P I L G A G E C A Y L N D K G A S S A R C Y T E R K W I C S K S D I H V H H H H H H H H

SEQ ID 931	Human (*Homo sapiens*) CLEC2D construct 26	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVE SFQELNFLLRYKGaSDHWIGLSREQGQPWKWINGTEWTRQFPIL GAGECAYLNDKGASSARCYTERKWICSKSDIHVHHHHHHHHH
SEQ ID 932	Human (*Homo sapiens*) CLEC2D construct 27	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFC DSQDADLAQVESFQELNFLLRYKGPaDHWIGLSREQGQPWKWI NGTEWTRQFPILGAGECAYLNDKGASSARCYTERKWICSKSDIH VHHHHHHHH
SEQ ID 933	Human (*Homo sapiens*) CLEC2D construct 28	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVE SFQELNFLLRYKGPaDHWIGLSREQGQPWKWINGTEWTRQFPIL GAGECAYLNDKGASSARCYTERKWICSKSDIHVHHHHHHHH
SEQ ID 934	Human (*Homo sapiens*) CLEC2D construct 29	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFC DSQDADLAQVESFQELNFLLRYKGPSaHWIGLSREQGQPWKWI NGTEWTRQFPILGAGECAYLNDKGASSARCYTERKWICSKSDIH VHHHHHHHH
SEQ ID 935	Human (*Homo sapiens*) CLEC2D construct 30	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVE SFQELNFLLRYKGPSaHWIGLSREQGQPWKWINGTEWTRQFPIL GAGECAYLNDKGASSARCYTERKWICSKSDIHVHHHHHHHH
SEQ ID 936	Human (*Homo sapiens*) CLEC2D construct 31	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFC DSQDADLAQVESFQELNFLLRYKGPSDHWIGLSREaGQPWKWI NGTEWTRQFPILGAGECAYLNDKGASSARCYTERKWICSKSDIH VHHHHHHHH
SEQ ID 937	Human (*Homo sapiens*) CLEC2D construct 32	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVE SFQELNFLLRYKGPSDHWIGLSREaGQPWKWINGTEWTRQFPIL GAGECAYLNDKGASSARCYTERKWICSKSDIHVHHHHHHHH
SEQ ID 938	Human (*Homo sapiens*) CLEC2D construct 33	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFC DSQDADLAQVESFQELNFLLRYKGPSDHWIGLSREQGQPWKWI NGTEWTRQFPILGAGaCAYLNDKGASSARCYTERKWICSKSDIH VHHHHHHHH
SEQ ID 939	Human (*Homo sapiens*) CLEC2D construct 34	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVE SFQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPIL GAGaCAYLNDKGASSARCYTERKWICSKSDIHVHHHHHHHH
SEQ ID 940	Human (*Homo sapiens*) CLEC2D construct 35	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFC DSQDADLAQVESFQELNFLLRYKGPSDHWIGLSREQGQPWKWI NGTEWTRQFPILGAGECAaLNDKGASSARCYTERKWICSKSDIH VHHHHHHHH
SEQ ID 941	Human (*Homo sapiens*) CLEC2D construct 36	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVE SFQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPIL GAGECAaLNDKGASSARCYTERKWICSKSDIHVHHHHHHHH
SEQ ID 942	Human (*Homo sapiens*) CLEC2D construct 37	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFC DSQDADLAQVESFQELNFLLRYKGPSDHWIGLSREQGQPWKWI NGTEWTRQFPILGAGECAYLNDaGASSARCYTERKWICSKSDIHV HHHHHHHH

SEQ ID 943	Human (*Homo sapiens*) CLEC2D construct 38	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVE SFQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPIL GAGECAYLNDaGASSARCYTERKWICSKSDIHVHHHHHHHHH
SEQ ID 944	Human (*Homo sapiens*) CLEC2D construct 39	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFC DSQDADLAQVESFQELNFLLRYKGPSDHWIGLSREQGQPWKWI NGTEWTRQFPILGAGECAYLNDKGASaARCYTERKWICSKSDIH VHHHHHHHHH
SEQ ID 945	Human (*Homo sapiens*) CLEC2D construct 40	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVE SFQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPIL GAGECAYLNDKGASaARCYTERKWICSKSDIHVHHHHHHHHH
SEQ ID 946	Human (*Homo sapiens*) CLEC2D construct 41	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFC DSQDADLAQVESFQELNFLLRYKGPSDHWIGLSREQGQPWKWI NGTEWTRQFPILGAGECAYLNDKGASSAaCYTERKWICSKSDIHV HHHHHHHH
SEQ ID 947	Human (*Homo sapiens*) CLEC2D construct 42	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVE SFQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPIL GAGECAYLNDKGASSAaCYTERKWICSKSDIHVHHHHHHHH
SEQ ID 948	Human (*Homo sapiens*) CLEC2D construct 43	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFC DSQDADLAQVESFQELNFLLRYKGPSDHWIGLSREQGQPWKWI NGTEWTRQFPILGAGECAYLNDKGASSARCaTERKWICSKSDIH VHHHHHHHH
SEQ ID 949	Human (*Homo sapiens*) CLEC2D construct 44	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVE SFQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPIL GAGECAYLNDKGASSARCaTERKWICSKSDIHVHHHHHHHH
SEQ ID 950	Human (*Homo sapiens*) CLEC2D construct 45	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFC DSQDADLAQVESFQELNFLLRYKGPSDHWIGLSREQGQPWKWI NGTEWTRQFPILGAGECAYLNDKGASSARCYaERKWICSKSDIH VHHHHHHHH
SEQ ID 951	Human (*Homo sapiens*) CLEC2D construct 46	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVE SFQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPIL GAGECAYLNDKGASSARCYaERKWICSKSDIHVHHHHHHHH
SEQ ID 952	Human (*Homo sapiens*) CLEC2D construct 47	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFC DSQDADLAQVESFQELNFLLRYKGPSDHWIGLSREQGQPWKWI NGTEWTRQFPILGAGECAYLNDKGASSARCYTaRKWICSKSDIH VHHHHHHHH
SEQ ID 953	Human (*Homo sapiens*) CLEC2D construct 48	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVE SFQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPIL GAGECAYLNDKGASSARCYTaRKWICSKSDIHVHHHHHHHH
SEQ ID 954	Human (*Homo sapiens*) CLEC2D construct 49	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFC DSQDADLAQVESFQELNFLLRYKGPSDHWIGLSREQGQPWKWI NGTEWTRQFPILGAGECAYLNDKGASSARCYTEaKWICSKSDIHV HHHHHHHH

SEQ ID 955	Human (*Homo sapiens*) CLEC2D construct 50	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVE SFQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPIL GAGECAYLNDKGASSARCYTEaKWICSKSDIHVHHHHHHHH
SEQ ID 956	Human (*Homo sapiens*) CLEC2D construct 51	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFC DSQDADLAQVESFQELNFLLRYKGPSDHWIGLSREQGQPWKWI NGTEWTRQFPILGAGECAYLNDKGASSARCYTERaWICSKSDIHV HHHHHHHH
SEQ ID 957	Human (*Homo sapiens*) CLEC2D construct 52	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVE SFQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPIL GAGECAYLNDKGASSARCYTERaWICSKSDIHVHHHHHHHH
SEQ ID 958	Human (*Homo sapiens*) CLEC2D construct 53	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFC DSQDADLAQVESFQELNFLLRYKGPSDHWIGLSREQGQPWKWI NGTEWTRQFPILGAGECAALADaGAaSARCYTERKWICSKSDIH VHHHHHHH
SEQ ID 959	Human (*Homo sapiens*) CLEC2D construct 54	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVE SFQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPIL GAGECAALADaGAaSARCYTERKWICSKSDIHVHHHHHHH
SEQ ID 960	Human (*Homo sapiens*) CLEC2D construct 55	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFC DSQDADLAQVESFQELNFLLRYKGPSDHWIGLSREQGQPWKWI NGTEWTRQFPILGAGECAaLaDAGAASARCYTERKWICSKSDIH VHHHHHHH
SEQ ID 961	Human (*Homo sapiens*) CLEC2D construct 56	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVE SFQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPIL GAGECAaLaDAGAASARCYTERKWICSKSDIHVHHHHHHH
SEQ ID 962	Human (*Homo sapiens*) CLEC2D construct 57	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQaFC DSQDADLAQVESFQELNFLLRYKGPSDHWIGLSREQGQPWKWI NGTEWTRQFPILGAGECAYLNDKGASSARCYTERKWICSKSDIH VHHHHHHHH
SEQ ID 963	Human (*Homo sapiens*) CLEC2D construct 58	QAACPESWIGFQRKCFYFSDDTKNWTSSQaFCDSQDADLAQVES FQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPILG AGECAYLNDKGASSARCYTERKWICSKSDIHVHHHHHHHH
SEQ ID 964	Human (*Homo sapiens*) CLEC2D construct 59	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFC DSQDADLAQVESFQELNFLLRYKGPSDHWIGLSREQGaPWKWI NGTEWTRQFPILGAGECAYLNDKGASSARCYTERKWICSKSDIH VHHHHHHHH
SEQ ID 965	Human (*Homo sapiens*) CLEC2D construct 60	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVE SFQELNFLLRYKGPSDHWIGLSREQGaPWKWINGTEWTRQFPIL GAGECAYLNDKGASSARCYTERKWICSKSDIHVHHHHHHHH
SEQ ID 966	Human (*Homo sapiens*) CLEC2D construct 61	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFC DSQDADLAQVESFQELNFLLRYKGPSDHWIGLSREQGQPWKWI NGTEWTaQFPILGAGECAYLNDKGASSARCYTERKWICSKSDIHV HHHHHHHH

SEQ ID 967	Human (*Homo sapiens*) CLEC2D construct 62	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVE SFQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTaQFPIL GAGECAYLNDKGASSARCYTERKWICSKSDIHVHHHHHHHHH
SEQ ID 968	Human (*Homo sapiens*) CLEC2D construct 63	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFC DSQDADLAQVESFQELNFLLRYKGPSDHWIGLSREQGQPWKWI NGTEWTRQFPILGAGECAYLNDKGASSARCYTERKWICSKaDIH VHHHHHHHH
SEQ ID 969	Human (*Homo sapiens*) CLEC2D construct 64	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVE SFQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPIL GAGECAYLNDKGASSARCYTERKWICSKaDIHVHHHHHHHH
SEQ ID 970	Human (*Homo sapiens*) CLEC2D construct 65	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFC DSQDADLAQVESFQELNFLLRYKGPSDHWIGLSREQGQPWKWI NGTEWTRQFPILGAGECAYLNDKGASSARCYTERKWICSKSDIaV HHHHHHHH
SEQ ID 971	Human (*Homo sapiens*) CLEC2D construct 66	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVE SFQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPIL GAGECAYLNDKGASSARCYTERKWICSKSDIaVHHHHHHHH
SEQ ID 972	Human (*Homo sapiens*) CLEC2D construct 67	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFC DSQDADLAQVESFQELNFLLRYKGPSDHWIGLSREQGQPWKWI NGTEWTRQFPILGAGECAYLNDKGASSAaCaTaRKWICSKSDIHV HHHHHHHH
SEQ ID 973	Human (*Homo sapiens*) CLEC2D construct 68	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVE SFQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPIL GAGECAYLNDKGASSAaCaTaRKWICSKSDIHVHHHHHHHH
SEQ ID 974	Human (*Homo sapiens*) CLEC2D construct 69	MSFVSLLLVGILFHATQAQAACPESWIGFQaKCFYFSDDTKNWTSSQRFC DSQDADLAQVESFQELNFLLRYKGPSDHWIGLSREQGQPWKWI NGTEWTRQFPILGAGECAYLNDKGASSARCYTERKWICSKSDIaV HHHHHHHH
SEQ ID 975	Human (*Homo sapiens*) CLEC2D construct 70	QAACPESWIGFQaKCFYFSDDTKNWTSSQRFCDSQDADLAQVES FQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPILG AGECAYLNDKGASSARCYTERKWICSKSDIaVHHHHHHHH
SEQ ID 976	Human (*Homo sapiens*) CLEC2D construct 71	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFC DSQDADLAQVESFQELNFLLRYKGPSDHWIGLSREQGQPWKWI NGTaWaaaFPILGAGECAYLNDKGASSARCYTERKWICSKSDIHV HHHHHHHH
SEQ ID 977	Human (*Homo sapiens*) CLEC2D construct 72	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVE SFQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTaWaaaFPIL GAGECAYLNDKGASSARCYTERKWICSKSDIHVHHHHHHHH
SEQ ID 978	Human (*Homo sapiens*) CLEC2D construct 73	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQaFC DaQDADLAQVESFQELNFLLRYKGPSDHWIGLSREQGQPWKWI NGTEWTRQFPILGAGECAYLNDKGASSARCYTERKWICSKSDIH VHHHHHHHH

SEQ ID 979	Human (*Homo sapiens*) CLEC2D construct 74	QAACPESWIGFQRKCFYFSDDTKNWTSSQaFCDaQDADLAQVES FQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPILG AGECAYLNDKGASSARCYTERKWICSKSDIHVHHHHHHHH
SEQ ID 980	Human (*Homo sapiens*) CLEC2D construct 75	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFC DSQaADLAQVESFQELNFLLRYKGPSDHWIGLSREQGQPWKWI NGTEWTRQFPILGAGECAYLNDKGASSARCYTERKWICSKSDIaV HHHHHHHH
SEQ ID 981	Human (*Homo sapiens*) CLEC2D construct 76	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQaADLAQVES FQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPILG AGECAYLNDKGASSARCYTERKWICSKSDIaVHHHHHHHH
SEQ ID 982	Human (*Homo sapiens*) CLEC2D construct 77	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFC DSQDADLAQVESFQELNFLLRYKGPSDHWIGLSREQGaPWKWI NGTEWTaQFPILGAGECAYLNDKGASSARCYTERKWICSKSDIHV HHHHHHHH
SEQ ID 983	Human (*Homo sapiens*) CLEC2D construct 78	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVE SFQELNFLLRYKGPSDHWIGLSREQGaPWKWINGTEWTaQFPIL GAGECAYLNDKGASSARCYTERKWICSKSDIHVHHHHHHHH
SEQ ID 984	Human (*Homo sapiens*) CLEC2D construct 79	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDaaaNWTSSQRFC DSQDADLAQVESFQELNFLLRYKGPSDHWIGLSREQGQPWKWI NGTEWTRQFPILGAGECAYLNDKGASSARCYTERKWICSKSDIH VHHHHHHHH
SEQ ID 985	Human (*Homo sapiens*) CLEC2D construct 80	QAACPESWIGFQRKCFYFSDaaaNWTSSQRFCDSQDADLAQVES FQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPILG AGECAYLNDKGASSARCYTERKWICSKSDIHVHHHHHHHH
SEQ ID 986	Human (*Homo sapiens*) CLEC2D construct 81	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFC DSQDADLAQVESFQELNFLLRYKGPSDHWIGLSREQGaPWaWIN GTEWTRQFPILGAGECAYLNDKGASSARCYTERKWICSKSDIHV HHHHHHHH
SEQ ID 987	Human (*Homo sapiens*) CLEC2D construct 82	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVE SFQELNFLLRYKGPSDHWIGLSREQGaPWaWINGTEWTRQFPIL GAGECAYLNDKGASSARCYTERKWICSKSDIHVHHHHHHHH
SEQ ID 988	Human (*Homo sapiens*) CLEC2D construct 83	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFC DSQDADLAQVESFQELNFLLRYKGPSDHWIGLSRaQGQPWKWI NGTEWTRQFPILGAGECAYLNDKGASSARaYTERKWICSKSDIHV HHHHHHHH
SEQ ID 989	Human (*Homo sapiens*) CLEC2D construct 84	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVE SFQELNFLLRYKGPSDHWIGLSRaQGQPWKWINGTEWTRQFPIL GAGECAYLNDKGASSARaYTERKWICSKSDIHVHHHHHHHH
SEQ ID 990	Human (*Homo sapiens*) CLEC2D construct 85	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFC DSQDADLAQVESFQELNFLLRYKGPSDHWIGLSRaaGaPWKWIN GTEWTRQFPILGAGECAYLNDKGASSAaCYTERKWICSKSDIHVH HHHHHHH

SEQ ID 991	Human (*Homo sapiens*) CLEC2D construct 86	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVE SFQELNFLLRYKGPSDHWIGLSRaaGaPWKWINGTEWTRQFPIL GAGECAYLNDKGASSAaCYTERKWICSKSDIHVHHHHHHHH
SEQ ID 992	Human (*Homo sapiens*) CLEC2D construct 87	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDaTKNWTSSQRFC DSQDADLAQVESFQELNFLLRYKGPSDHWIGLSREQGQPWKWI NGTEWTRQFPILGAGECAYLNDKGASSARCaTERaWICSKSDIHV HHHHHHHH
SEQ ID 993	Human (*Homo sapiens*) CLEC2D construct 88	QAACPESWIGFQRKCFYFSDaTKNWTSSQRFCDSQDADLAQVES FQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPILG AGECAYLNDKGASSARCaTERaWICSKSDIHVHHHHHHHH
SEQ ID 994	Human (*Homo sapiens*) CLEC2D construct 89	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFC DSQDADLAQVESaQELNFLLRYKGPSDHWIGLSREQGQPWKWI NGTEWTaQFPILGAGECAYLNDKGASSARCYTERKWICSKSDIHV HHHHHHHH
SEQ ID 995	Human (*Homo sapiens*) CLEC2D construct 90	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVE SaQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTaQFPIL GAGECAYLNDKGASSARCYTERKWICSKSDIHVHHHHHHHH
SEQ ID 996	Human (*Homo sapiens*) CLEC2D construct 91	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDaKaWTSSQRFC DSQDADLAQVESFQELNFLLRYKGPSDHWIGLSREQGQPWKWI NGTEWTRQFPILGAGECAYLNDKGASSARCYTERKWICSKSDIH VHHHHHHHH
SEQ ID 997	Human (*Homo sapiens*) CLEC2D construct 92	QAACPESWIGFQRKCFYFSDDaKaWTSSQRFCDSQDADLAQVES FQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPILG AGECAYLNDKGASSARCYTERKWICSKSDIHVHHHHHHHH
SEQ ID 998	Human (*Homo sapiens*) CLEC2D construct 93	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDaKNWTSSQRFC DSQDADLAQVESFQELNFLLRYKGPSDHWIGLSREQGQPWKWI NGTEWTRQFPILGAGECAYLNDKGASSARCaTaRKWICSKSDIH VHHHHHHHH
SEQ ID 999	Human (*Homo sapiens*) CLEC2D construct 94	QAACPESWIGFQRKCFYFSDDaKNWTSSQRFCDSQDADLAQVE SFQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPIL GAGECAYLNDKGASSARCaTaRKWICSKSDIHVHHHHHHHH
SEQ ID 1000	Human (*Homo sapiens*) CLEC2D construct 95	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTaNWTSSQaFC DSQDADLAQVESFQELNFLLRYKGPSDHWIGLSREQGQPWKWI NGTEWTRQFPILGAGECAYLNDKGASSARCYTaRKWICSKSDIH VHHHHHHHH
SEQ ID 1001	Human (*Homo sapiens*) CLEC2D construct 96	QAACPESWIGFQRKCFYFSDDTaNWTSSQaFCDSQDADLAQVES FQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPILG AGECAYLNDKGASSARCYTaRKWICSKSDIHVHHHHHHHH
SEQ ID 1002	Human (*Homo sapiens*) CLEC2D construct 97	MSFVSLLLVGILFHATQAQAACPESWIGFQRKCFYFSDDTKNWTSSQRFC DSQDADLAQVESFQELNFLLRYKGPSDHWIGLSREQGQPWKWI NGTEWTRQFPILGAGECAYLNDKGASSAaCaTEaKWICSKSDIHV HHHHHHHH

SEQ ID 1003	Human (*Homo sapiens*) CLEC2D construct 98	QAACPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVE SFQELNFLLRYKGPSDHWIGLSREQGQPWKWINGTEWTRQFPIL GAGECAYLNDKGASSAaCaTEaKWICSKSDIHVHHHHHHHHH

[118] *Antibodies*

[119] In one embodiment, the term "antibody" refers to an immunoglobulin, which may be derived from natural sources or synthetically produced, in whole or in part. The terms "antibody" and "immunoglobulin" are used synonymously throughout the specification unless otherwise stated.

[120] In one embodiment, the term “antibody” includes both polyclonal and monoclonal antibody preparations and also includes the following: chimeric antibody molecules, F(ab’)2 and F(ab) fragments, Fv molecules, single chain Fv molecules (ScFv), dimeric and trimeric antibody fragments, bispecific antibody, minibodies, humanized monoclonal antibody molecules, human antibodies, fusion proteins comprising Fc region of antibody and any functional fragments arising out of these molecules, where derivative molecules retain immunological functionality of the parent antibody molecule. The antibody according to this disclosure is a human antibody, humanized antibody, chimeric antibody, or further genetically engineered antibody as long as the characteristic properties according to this disclosure are retained.

[121] "Native antibodies and immunoglobulins" are usually heterotetrameric glycoproteins of about 150,000 daltons, composed of two identical light (L) chains and two identical heavy (H) chains. Each light chain is linked to a heavy chain by one covalent disulfide bond, while the number of disulfide linkages varies between the heavy chains of different immunoglobulin isotypes. Each heavy and light chain also has regularly spaced intrachain disulfide bridges. Each heavy chain has at one end a variable domain (VH) followed by a number of constant domains. Each light chain has a variable domain at one end (VL) and a constant domain at its other end; the constant domain of the light chain is aligned with the first constant domain of the heavy chain, and the light chain variable domain is aligned with the variable domain of the heavy chain. Particular amino acid residues are believed to form an interface between the light- and heavy-chain variable domains (Clothia et al., J. Mol. Biol. 186:651 (1985); Novotny and Haber, Proc. Natl. Acad. Sci. U.S.A. 82:4592 (1985)).

[122] The term "antigen-binding site," or "binding portion" refers to the part of the immunoglobulin molecule that participates in antigen binding. The antigen binding site is formed

by amino acid residues of the N-terminal variable ("V") regions of the heavy ("H") and light ("L") chains. Three highly divergent stretches within the V regions of the heavy and light chains, referred to as "hypervariable regions," are interposed between more conserved flanking stretches known as "framework regions," or "FRs". Thus, the term "FR" refers to amino acid sequences which are naturally found between, and adjacent to, hypervariable regions in immunoglobulins. In an antibody molecule, the three hypervariable regions of a light chain and the three hypervariable regions of a heavy chain are disposed relative to each other in three dimensional space to form an antigen-binding surface. The antigen-binding surface is complementary to the three-dimensional surface of a bound antigen, and the three hypervariable regions of each of the heavy and light chains are referred to as "complementarity-determining regions," or "CDRs."

[123] The term "variable" refers to the fact that certain portions of the variable domains differ extensively in sequence among antibodies and are used in the binding and specificity of each particular antibody for its particular antigen. However, the variability is not evenly distributed throughout the variable domains of antibodies. It is concentrated in three segments called complementarity-determining regions (CDRs) or hypervariable regions both in the light-chain and the heavy-chain variable domains. The more highly conserved portions of variable domains are called the framework (FR). The variable domains of native heavy and light chains each comprise four FR regions, largely adopting a β-sheet configuration, connected by three CDRs, which form loops connecting, and in some cases forming part of, the β-sheet structure. The CDRs in each chain are held together in close proximity by the FR regions and, with the CDRs from the other chain, contribute to the formation of the antigen-binding site of antibodies (see Kabat et al., Sequences of Proteins of Immunological Interest, Fifth Edition, National Institute of Health, Bethesda, Md. (1991)). The constant domains are not involved directly in binding an antibody to an antigen, but exhibit various effector functions, such as participation of the antibody in antibody-dependent cellular toxicity.

[124] "Antibody fragments" comprise a portion of a full length antibody, preferably the variable domain thereof, or at least the antigen binding site thereof. scFv antibodies are, e.g., described in Huston, J.S., Methods in Enzymol. 203 (1991) 46-88. In one embodiment, “antibody fragment" is a portion of a whole antibody which retains the ability to exhibit antigen binding activity. In addition, antibody fragments comprise single chain polypeptides having the characteristics of a VH domain, namely being able to assemble together with a VL domain, or of

a VL domain binding to the respective antigen being able to assemble together with a VH domain to a functional antigen binding site and thereby providing the properties of an antibody according to this disclosure.

[125] Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, whose name reflects its ability to crystallize readily. Pepsin treatment yields an F(ab')2 fragment that has two antigen-combining sites and is still capable of cross-linking antigen.

[126] "Fv" is the minimum antibody fragment which contains a complete antigen-recognition and binding site. This region consists of a dimer of one heavy- and one light-chain variable domain in tight, non-covalent association. It is in this configuration that the three CDRs of each variable domain interact to define an antigen-binding site on the surface of the VH -VL dimer. Collectively, the six CDRs confer antigen-binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

[127] A single chain Fv ("scFv") polypeptide molecule is a covalently linked VH:VL heterodimer, which can be expressed from a gene fusion including VH- and VL-encoding genes linked by a peptide-encoding linker. A number of methods have been described to discern chemical structures for converting the naturally aggregated, but chemically separated, light and heavy polypeptide chains from an antibody V region into an scFv molecule, which will fold into a three dimensional structure substantially similar to the structure of an antigen-binding site. See, e.g., U.S. Patent Nos. 5,091,513; 5,132,405; and 4,946,778.

[128] The Fab fragment also contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab' fragments differ from Fab fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group.

F(ab')2 antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

[129] The "light chains" of antibodies (immunoglobulins) from any vertebrate species can be assigned to one of two clearly distinct types, called kappa (k) and lambda (l), based on the amino acid sequences of their constant domains.

[130] As used herein, the terms "immunological binding" and "immunological binding properties" refer to the non-covalent interactions of the type which occur between an immunoglobulin molecule and an antigen for which the immunoglobulin is specific. The strength, or affinity of immunological binding interactions can be expressed in terms of the dissociation constant (Kd) of the interaction, wherein a smaller Kd represents a greater affinity. Immunological binding properties of selected polypeptides can be quantified using methods well known in the art. One such method entails measuring the rates of antigen-binding site/antigen complex formation and dissociation, wherein those rates depend on the concentrations of the complex partners, the affinity of the interaction, and geometric parameters that equally influence the rate in both directions. Thus, both the "on rate constant" (Kon) and the "off rate constant" (Koff) can be determined by calculation of the concentrations and the actual rates of association and dissociation. The ratio of Koff /Kon enables the cancellation of all parameters not related to affinity, and is equal to the dissociation constant Kd. In some embodiments, an antibody of the present disclosure binds to CLEC2D at a Kd ≤ 10 μM, preferably ≤ 1 μM, more preferably ≤ 100 nM, for example, ≤ 90 nM, ≤ 80 nM, ≤ 70 nM, ≤ 60 nM, ≤ 50 nM, ≤ 40 nM, ≤ 30 nM, ≤ 20 nM, ≤ 10 nM, ≤ 5 nM, or ≤ 1 nM, as measured by assays such as radioligand binding assays or similar assays known to those skilled in the art. In some embodiment, the binding affinity of the antibody of this disclosure is within the range of 10^{-5}M to 10^{-12} M. For example, the binding affinity of the antibody of this disclosure is from 10^{-6} M to 10^{-12} M, from 10^{-7} M to 10^{-12} M, from 10^{-8} M to 10^{-12} M, from 10^{-9} M to 10^{-12} M, from 10^{-5} M to 10^{-11} M, from 10^{-6} M to 10^{-11} M, from 10^{-7} M to 10^{-11} M, from 10^{-8} M to 10^{-11} M, from 10^{-9} M to 10^{-11} M, from 10^{-10} M to 10^{-11} M, from 10^{-5} M to 10^{-10} M, from 10^{-6} M to 10^{-10}, from 10^{-7} M to 10^{-10} M, from 10^{-8} M to 10^{-10}, from 10^{-9} M to 10^{-10} M, from 10^{-5} M to 10^{-9} M, from 10^{-6} M to 10^{-9} M, from 10^{-7} M to 10^{-9} M, from 10^{-8} M to 10^{-9} M, from 10^{-5} M to 10^{-8} M, from 10^{-6} M to 10^{-8} M, from 10^{-7} M to 10^{-8} M, from 10^{-5} M to 10^{-7} M, from 10^{-6} M to 10^{-7} M or from 10-^{5} M to 10^{-6} M.

[131] The present disclosure also features antibodies that have a specified percentage identity or similarity to the amino acid or nucleotide sequences of the CLEC2D antibodies described herein. For example, the antibodies may have at least 30%, 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity when compared a specified region or the full length of any one of the CLEC2D antibodies described herein. Preferably, the antibodies may have at least 60%, 70%, 75%, 80%, 85%, 90%, 91%,

92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity when compared a specified region or the full length of any one of the CLEC2D antibodies described herein. More preferably, the antibodies may have at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity when compared a specified region or the full length of any one of the CLEC2D antibodies described herein. Even more preferably, the antibodies may have at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity when compared a specified region or the full length of any one of the CLEC2D antibodies described herein. Sequence identity or similarity to the nucleic acids and proteins of the present disclosure can be determined by sequence comparison and/or alignment by methods known in the art. For example, sequence comparison algorithms (i.e., BLAST or BLAST 2.0), manual alignment or visual inspection can be utilized to determine percent sequence identity or similarity for the nucleic acids and proteins of the present disclosure.

[132] As to amino acid sequences, one of skill in the art will readily recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds, deletes, or substitutes a single amino acid or a small percentage of amino acids in the encoded sequence is collectively referred to herein as a “conservatively modified variant”. In some embodiments, the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art.

[133] Depending on the amino acid sequence of the constant domain of their heavy chains, immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, and several of these can be further divided into subclasses (isotypes), e.g., IgG1, IgG2, IgG3, IgG4, IgA1, and IgA2. The heavy-chain constant domains that correspond to the different classes of immunoglobulins are called α, ∂, ε, γ, and μ, respectively. The subunit structures and three-dimensional configurations of different classes of immunoglobulins are well known.

[134] In one embodiment, a humanized antibody may be used in the compositions and methods provided herein. In some embodiments, the term "humanized antibody" or "humanized version of an antibody" refers to antibodies in which the framework or "complementarity determining regions" (CDR) have been modified to comprise the CDR of an immunoglobulin of different specificity as compared to that of the parent immunoglobulin. In other embodiments, the CDRs

of the VH and VL are grafted into the framework region of human antibody to prepare the "humanized antibody." See e.g., Riechmann, L., et al, Nature 332 (1988) 323-327; and Neuberger, M.S., et al, Nature 314 (1985) 268-270. The heavy and light chain variable framework regions can be derived from the same or different human antibody sequences. The human antibody sequences can be the sequences of naturally occurring human antibodies. Human heavy and light chain variable framework regions are listed e.g., in Lefranc, M.-P., Current Protocols in Immunology (2000) - Appendix IP A.1P.1-A.1P.37 and are accessible via IMGT, the international ImMunoGeneTics information system® (http://imgt.cines.fr) or via http://vbase.mrc-cpe.cam.ac.uk. Optionally the framework region can be modified by further mutations. Particularly preferred CDRs correspond to those representing sequences recognizing the antigens noted above for chimeric antibodies. The term "humanized antibody" as used herein also comprises such antibodies which are modified in the constant region to generate the properties according to this disclosure, especially in regard to Clq binding and/or FcR binding, e.g., by "class switching" i.e., change or mutation of Fc parts (e.g., from IgGl to IgG4 and/or IgGl/IgG4 mutation). The term "human antibody", as used herein, is intended to include antibodies having variable and constant regions derived from human germ line immunoglobulin sequences. Human antibodies are well-known in the state of the art (van Dijk, M.A., and van de Winkel, J.G., Curr. Opin. Chem. Biol. 5 (2001) 368-374). Human antibodies can also be produced in transgenic animals (e.g., mice) that are capable, upon immunization, of producing a full repertoire or a selection of human antibodies in the absence of endogenous immunoglobulin production. Transfer of the human germ-line immunoglobulin gene array in such germ-line mutant mice will result in the production of human antibodies upon antigen challenge (see, e.g., Jakobovits, A., et al, Proc. Natl. Acad. Sci. USA 90 (1993) 2551-2555; Jakobovits, A., et al, Nature 362 (1993) 255-258; Brueggemann, M.D., et al., Year Immunol. 7 (1993) 33-40). Human antibodies can also be produced in phage display libraries (Hoogenboom, H.R., and Winter, G., J. Mol. Biol. 227 (1992) 381-388; Marks, J.D., et al, J. Mol. Biol. 222 (1991) 581- 597). The techniques of Cole, A., et al. and Boerner, P., et al. are also available for the preparation of human monoclonal antibodies (Cole, A., et al., Monoclonal Antibodies and Cancer Therapy, Liss, A.L., p. 77 (1985); and Boerner, P., et al, J. Immunol. 147 (1991) 86-95). As already mentioned for humanized antibodies according to this disclosure the term "human antibody" as

used herein also comprises such antibodies which are modified in the constant region to generate the properties according to this disclosure.

[135] In one embodiment, the term "monoclonal antibody" refers to an antibody composition having a homogeneous antibody population. The antibody is not limited to the species or source of the antibody or by the manner in which it is made. In another embodiment, the term encompasses whole immunoglobulins as well as fragments such as Fab, F(ab')2, Fv, and other fragments, as well as chimeric and humanized homogeneous antibody populations that exhibit immunological binding properties of the parent monoclonal antibody molecule. In another embodiment, the terms "monoclonal antibody" or "monoclonal antibody composition" as used herein refer to a preparation of antibody molecules of a single amino acid composition. In another embodiment, the terms Fab or ScFv are used as antibody fragments with specific mention.

[136] In some embodiments, a chimeric antibody may be used in the compositions and methods provided herein. In one embodiment, the term "chimeric antibody" refers to a monoclonal antibody comprising a variable region, i.e., binding region, from one species (e.g., a mouse or rat) and at least a portion of a constant region derived from a different source or species (e.g., human), usually prepared by recombinant DNA techniques. Chimeric antibodies comprising a mouse variable region and a human constant region are especially preferred. Such chimeric antibodies are the product of expressed immunoglobulin genes comprising DNA segments encoding immunoglobulin variable regions from one species and DNA segments encoding immunoglobulin constant regions for a different species. Other forms of "chimeric antibodies" encompassed by the present disclosure are those in which the class or subclass has been modified or changed from that of the original antibody. Such "chimeric" antibodies are also referred to as "class-switched antibodies." Methods for producing chimeric antibodies involve conventional recombinant DNA and gene transfection techniques now well known in the art. See, e.g., Morrison, S.L., et al, Proc. Natl. Acad Sci. USA 81 (1984) 6851-6855; US 5,202,238 and US 5,204,244.

[137] In one embodiment, “antibody display library” refers to a platform(s) expressing antibodies on the surface of a cell or cell-free suited for a screening methodology against target antigens. Herein, phage display library and yeast display library are used with accurate specification unless indicated otherwise.

[138] In one embodiment, the term “naïve library” refers to a collection of nucleic acid sequences encoding a naturally occurring VH repertoire from a non-immunized source.

[139] In one embodiment, the term "VH" refers to the single heavy chain variable domain of antibody of the type that can be found in mammals which are naturally devoid of light chains or parts of the same; Naive VH can be understood accordingly.

[140] In one embodiment, the term “VL” refers to single light chain variable domain of the antibody; they are found in two types based on the constant domain sequence. Vk (with kappa constant region) and Vl (lambda constant region) are understood accordingly.

[141] In one embodiment, the term "CDR" refers to complementary determining region of the antibody structure.

[142] In one embodiment, the term "repertoire," means a collection, indicating genetic diversity.

[143] In one embodiment, the term "framework region" is used herein to refer to the nucleic acid sequence regions of an antibody molecule that encode the structural elements of the molecule.

[144] In another embodiment, the term "vector" refers to a DNA related to a cloning or expression system to accommodate antibody genes in specific designated restriction sites. Phagemid vectors (applicable to phage display systems) or yeast vectors (applicable to yeast display systems) are understood accordingly or mammalian expression vectors (applicable to mammalian expression systems).

[145] The disclosure provides antibodies and antibody fragments that bind to a CLEC2D antigen of the disclosure.

[146] The disclosure provides VH and VL domains of antibodies or antibody fragments that bind to a CLEC2D antigen or an epitope of CLEC2D as described in the disclosure.

[147] The disclosure provides sequences of CDR1, CDR2 and CDR3 of the VH domain and CDR1, CDR2 and CD3 of the VL domain of antibodies that bind to a CLEC2D antigen or an epitope of CLEC2D as described in the disclosure.

[148] Any combinations of VH and VL sequences of the disclosure are considered within the scope of this disclosure. Any combinations of the CDR1, CDR2 and CDR3 sequences of the VH domains, or the CDR1, CDR2 and CD3 sequences of the VL domains are considered within the scope of this disclosure.

[149] Those skilled in the art will recognize that it is possible to determine, without undue experimentation, if a monoclonal antibody has the same specificity as a monoclonal antibody of the disclosure by ascertaining whether the former prevents the latter from binding to CLEC2D. If the monoclonal antibody being tested competes with the monoclonal antibody of the disclosure, as shown by a decrease in binding by the monoclonal antibody of the disclosure, then it is likely that the two monoclonal antibodies bind to the same, or to a closely related, epitope.

[150] Another way to determine whether a monoclonal antibody has the specificity of a monoclonal antibody of the disclosure is to pre-incubate the monoclonal antibody of the disclosure with the CLEC2D protein, with which it is normally reactive, and then add the monoclonal antibody being tested to determine if the monoclonal antibody being tested is inhibited in its ability to bind CLEC2D. If the monoclonal antibody being tested is inhibited then, in all likelihood, it has the same, or functionally equivalent, epitopic specificity as the monoclonal antibody of the disclosure. Screening of monoclonal antibodies of the disclosure can be also carried out by utilizing CLEC2D and determining whether the test monoclonal antibody is able to neutralize CLEC2D.

[151] Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the disclosure, or against derivatives, fragments, analogs homologs or orthologs thereof. (See, for example, Antibodies: A Laboratory Manual, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference).

[152] Antibodies can be purified by well-known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

[153] Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to

elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

[154] The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

[155] Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies. (See Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63)).

[156] The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980). Moreover, in

therapeutic applications of monoclonal antibodies, it is important to identify antibodies having a high degree of specificity and a high binding affinity for the target antigen.

[157] After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. (See Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.

[158] The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

[159] Monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the disclosure can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). In some embodiments, the hybridoma cells of the disclosure serve as a source of such DNA. In some embodiments, antibody gene sequences are isolated and cloned using the methods of the disclosure (e.g., phage and yeast library display), and serve as the source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (see U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the disclosure, or can be substituted for the variable domains of one antigen-combining site of an antibody of the disclosure to create a chimeric bivalent antibody.

[160] All cell lines suitable for the expression and purification of antibodies or antibody fragments are considered to be within the scope of the disclosure. In some embodiments, the cell

line is a mammalian cell line. Cell lines can be isolated or derived from any source, including human, mouse and hamster. Suitable cell lines include, but are not limited to, Chinese Hamster Ovary (CHO) cells, HEK 293 cells, HEK293T cells, BHK21 cells, NSO cells, PER.C6 cells, B cells, HEK 293-6E cells, Sp2/0-Ag14 cells and DG44 cells. In some embodiments, the cell line is a hybridoma cell line.

[161] The antibody can be expressed by a vector containing a DNA segment encoding the single chain antibody described herein.

[162] These can include vectors, liposomes, naked DNA, adjuvant-assisted DNA, gene gun, catheters, etc. Vectors include chemical conjugates such as described in WO 93/64701, which has targeting moiety (e.g., a ligand to a cellular surface receptor), and a nucleic acid binding moiety (e.g., polylysine), viral vector (e.g., a DNA or RNA viral vector), fusion proteins such as described in PCT/US 95/02140 (WO 95/22618) which is a fusion protein containing a target moiety (e.g., an antibody specific for a target cell) and a nucleic acid binding moiety (e.g., a protamine), plasmids, phage, etc. The vectors can be chromosomal, non-chromosomal or synthetic.

[163] Preferred vectors include viral vectors, fusion proteins and chemical conjugates. Retroviral vectors include moloney murine leukemia viruses. DNA viral vectors are preferred. These vectors include pox vectors such as orthopox or avipox vectors, herpesvirus vectors such as a herpes simplex I virus (HSV) vector (see Geller, A. I. et al., J. Neurochem, 64:487 (1995); Lim, F., et al., in DNA Cloning: Mammalian Systems, D. Glover, Ed. (Oxford Univ. Press, Oxford England) (1995); Geller, A. I. et al., Proc Natl. Acad. Sci.: U.S.A. 90:7603 (1993); Geller, A. I., et al., Proc Natl. Acad. Sci USA 87:1149 (1990), Adenovirus Vectors (see LeGal LaSalle et al., Science, 259:988 (1993); Davidson, et al., Nat. Genet 3:219 (1993); Yang, et al., J. Virol. 69:2004 (1995) and Adeno-associated Virus Vectors (see Kaplitt, M. G.. et al., Nat. Genet. 8:148 (1994).

[164] Pox viral vectors introduce the gene into the cells cytoplasm. Avipox virus vectors result in only a short term expression of the nucleic acid. Adenovirus vectors, adeno-associated virus vectors and herpes simplex virus (HSV) vectors are preferred for introducing the nucleic acid into neural cells. The adenovirus vector results in a shorter term expression (about 2 months) than adeno-associated virus (about 4 months), which in turn is shorter than HSV vectors. The particular vector chosen will depend upon the target cell and the condition being treated. The

introduction can be by standard techniques, e.g., infection, transfection, transduction or transformation. Examples of modes of gene transfer include e.g., naked DNA, CaPO4 precipitation, DEAE dextran, electroporation, protoplast fusion, lipofection, cell microinjection, and viral vectors.

[165] Exemplary VH amino acid sequences of CLEC2D antibodies of the disclosure are shown in Table 2 below. VH amino acid sequences having at least 50% identity, at least 55% identity, at least 60% identity, at least 65% identity, at least 70% identity, at least 75% identity, at least 80% identity, at least 85% identity, at least 90% identity, at least 91% identity, at least 92% identity, at least 93% identity, at least 94% identity, at least 95% identity, at least 96% identity, at least 97% identity, at least 98% identity, at least 99% identity, at least 99.5% identity, at least 99.8% identity, at least 99.9% identity or 100 % identity to the sequences listed in Table 2 are considered within the scope of the disclosure.

Table 2. VH Amino Acid Sequences

SEQ ID	VH Amino Acid Sequence
SEQ ID 1	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQRLEWMGWINAGNGN TKYSQKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARGSLSRSGWYAGLFDYWGQ GTLVTVSS
SEQ ID 2	QITLKESGGGVVQPGRSLRLSCAASGFTFSSYSMNWVRQAPGKGLQWVAIISDDGSKSYY ADSVQGRFTISRDNSRNTVFLQMNSLRAEDTAMYYCARDRGTKWNQLNDVFDMWGQG TMVTVSS
SEQ ID 3	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGSTS YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGRGYSSSRLYYFDYWGQGTL VTVSS
SEQ ID 4	QVTLKESGGGLVRPGGSLRLSCEASGFTFSDPYMDWVRQAPGKGLEWVGRITNKRTGYA TTYAASVKDRFTISRDDSRKSVYLQMNSLKTEDTAVYYCATDVSGSFAAYGGQGTLVTV SS
SEQ ID 5	EVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGQRLEWMGWINAGNGNT KYSQKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCAGEGGAVAGTVYWGQGTLVTV SS
SEQ ID 6	QVQLVQSGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVGRIKSKTDGG TTDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTDEYFYWGQGTLVTVSS
SEQ ID 7	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYN PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARVNPGSYTREVSNFDYWGQGTLVT VSS
SEQ ID 8	QVQLQQSGPELVKPSQTLTLTCGISGDSVSSNSVTWNWVRQSPSRGLEWLGRTYYRSQW YYNYAVSVKSRITISPDTSKNQFSLQLNSVTPEDTAVYYCATRGHNYGVDYWGPGTTVTV SS
SEQ ID 9	QVQLVQSGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVCRIKSKTDGET TDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYHCTTGVGWSPFQYWGQGTLVTV SS
SEQ ID 10	EVQLVQSGGGLVQPGRSLRLSCTASGFTFGDYAMSWFRQAPGKGLEWVGFIRSKAYGGT TEYAASVKGRFTISRDDSKSIAYLQMNSLKTEDTAVYYCTRDDKIAAAGFTYWYFDLWG RGTLVTVSS

SEQ ID 11	QVQLVQSGAEVKKPGASVKVSCKASGYTFAAYYLHWVRQAPGQGLEWMGRISPGNGVT SYAQKFQGRVTMTGDTSINTVYMQLNNLISGDTAVYYCAREAADDPFDHWGQGALVTV SS
SEQ ID 12	EVQLVQSGGGVVQPGRSLTLSCAASGFTFSSHLMHWVRQAPGKGLEWVAVISYDGTSKY YGDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCAKADYKYDWGQGTLVTVSS
SEQ ID 13	EVQLVQSGGGLVKPGGSLRLSCTASGFTFGDYAMSWVRQAPGKGLEWVGFIRSKAYGGT TEYAASVKGRFTISRDDSKSIAYLQMNSLKTEDTAVYYCTTHRRPIYDILTGFDYWGQGTL VTVSS
SEQ ID 14	QLQLQESGGGLVQPGRSLRLSCTASGFTFGDYAMSWVRQAPGKGLEWVGFIRSKAYGGT TEYAASVKGRFTISRDDSKSIAYLQMNSLKTEDTAVYYCTREDTMVRGVIPWGQGTLVTV SS
SEQ ID 15	QLQLQESGSGLVKPSQTLSLTCAVSGGSISSGGYSWSWIRQPPGKGLEWIGYIYHSGSTYY NPSLKSRVTISVDRSKNQFSLKLSSVTAADTAVYYCARDRRYYDSSGYYPAYYFDYWGQ GTLVTVSS
SEQ ID 16	EVQLVQSGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYISSSGSYTNY ADSVKGRFTISRDNAKNSLYLQINSLRAEDTAIYYCARDGGYDSSGFHFDYWGQGTLVTV SS
SEQ ID 17	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSNNRAAWNWIRQSPSRGLEWLGRTYYRSKW YNEYAVSVKSRITINPDTSKNQFSLQLNSMTPEDSAVYYCAILPSSGYLQDHHYYGMDVW GQGTTVTVSS
SEQ ID 18	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNT NYAQKLQGRVTMTTDTSTSTAYMELSSLRSEDTAVYYCARAAVGDGYSYGRLDWGQGT LVTVSS
SEQ ID 19	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARLPSYYYDSSGYFTWYFDLWGRG TLVTVSS
SEQ ID 20	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWIIPIFGIANY AQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARELYNYGSKDYFDYWGQGTLVT VSS
SEQ ID 21	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRY SPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARGGTWDTAMVTGFDYWGQGTLV TVSS
SEQ ID 22	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIAWVRQMPGKGLEWMGVIYPGDSDTR YSPSFQGQVTISADKSINTAYLQWSSLKASDTAMYYCARPHYDILTGSRAPFDYWGQGTL VTVSS
SEQ ID 23	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYN PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARARVESKDGYFDYWGQGTLVTVSS
SEQ ID 24	EVQLVESGGGVVQPGRSLRLSCAASGFTFTDAWMNWVRQAPGKGLEWIGRVKNKADGE TTDYAAPVKGRITISRDDAKNTLYVQMNSLKTEDTAVYYCTADLRLSTWDAYDFWGQGT MVTVSS
SEQ ID 25	QITLKESGGGLVQPGGSLRLSCTVSGFTFSNNWMTWVRQTPGKGLEWVANIKQDGTEKH YVDSVKGRFTISRDNAENSLYLQMNSLRGEDTAVYYCARNSQRSFDYWGQGTLVTVSS
SEQ ID 26	QVTLKESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKY YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDLGDPRGGILNYWGQGTLVT VSS
SEQ ID 27	EVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKY YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSSPWGELSLYQGAFDIWGQG TMVTVSS
SEQ ID 28	QITLKESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSAISGSGGSTYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDNDFWSGKVFDYWGQGTLVT VSS
SEQ ID 29	EVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYISSTSSTIYY ADSVKGRFTISRDNSKNMLFLQMNSLRAEDTAVYYCAKEGGSGWRHYFDYWGQGTLVT VSS

SEQ ID 30	QVTLKESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKY YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDYCSSTSCQNWFDPWGQGTL VTVSS
SEQ ID 31	QVQLVQSGGGLVQPGGSLRLSCAASGFTFSNYVMSWVRQAPGKGLEWVSAISGIGDTTY YADSVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYCARGRVAGDAFDIWGQGTMVTV SS
SEQ ID 32	QLQLQESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDQGAAAGTLGYFDYWGQGTL VTVSS
SEQ ID 33	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGN TGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCTRGIYDSSGSSNPFDSWGQGT LVTVSS
SEQ ID 34	EVQLVQSGAEVKKPGASVKISCEASGYTFTDYAIHWVRQAPGQRLEWMGWINAGDGGT KSSREFQGRVTITRDTSATTAYMEVSSLRSEDTAVYYCARGYCSGGSCPGTDFDYWGQGT LVTVSS
SEQ ID 35	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGSTS YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARDGVGGRDGYNFDYWGQGTL VTVSS
SEQ ID 36	EVQLVQSGGGLVQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVIYSGGSTYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARAPLAADGYFDYWGQGTLVTVS S
SEQ ID 37	EVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARARGLQYLIWYFDLWGRGTLVT VSS
SEQ ID 38	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGSTS YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCASPGMVRGVITAPLDYWGQGTL VTVSS
SEQ ID 39	EVQLVQSGGGLVKPGGSLRLSCAASGFTFSSYAISWVRQAPGQGLEWMGGIIPMYGTANY AQKFQGRVTITADESTSTAYMELSSLRSEDTALYYCAREAKWGMYYFDYWGQGTLVTVS S
SEQ ID 40	EVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAIHWVRQAPGKGLEWVAIISDDGSKSYY ADSVQGRFTISRDNSRNTVYLQMNSLRAEDTAMYYCARDRGTKWNQLNDVFDMWGQG TMVTVSS
SEQ ID 41	QMQLVQSGAEVKKPGASVKVSCTASGYTFTSSDINWVRQATGQGLEWMGWMNPNSGN TGYAEKFQGRVTMTSDSSISTAYMELRSLTTEDTAVYYCARGGGASYTDSWGQGTLVTV SS
SEQ ID 42	QVQLVQSGGGLVQPGRSLRLSCTASGFTFGDYAMSWFRQAPGKGLEWVGFIRSKAYGGT TEYAASVKGRFTISRDDSKSIAYLQMNSLKTEDTAVYYCTAKGGYVGYSYGPFGGYWGQ GTLVTVSS
SEQ ID 43	QVQLVQSGGGLVQPGRSLRLSCTASGFTFGDYAMSWFRQAPGKGLEWVGFIRSKAYGGT TEYAASVKGRFTISRDDSKSIAYLQMNSLKTEDTAVYYCTRGGTMVRGFGFNYWGQGTL VTVSS
SEQ ID 44	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYN PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARARRAMIGPLPRLVGYFDLWGRGT LVTVSS
SEQ ID 45	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYN PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGRPAPSWVKTRNWFDPWGQGTL VTVSS
SEQ ID 46	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSNSAAWNWIRQSPSRGLEWLGRTYYRSKWY NDYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCAREASSGWNWGQGTLVTVSS
SEQ ID 47	QVQLQESGPGLVKPSQTLSLTCAISGDSVSSNNAAWNWIRQSPSRGLEWLGRTFYRSKWY NDYAVSVKSRLTVNPDTSKNQFSLRLNSVSPEDTAVYYCARGGRYTKGGYFDDWGQGTL VTVSS

SEQ ID 48	QVTLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWDDDKR YSPSLKSRLTITKDTSKNQVVLTMTNMDPVDTATYYCAHRLDSSGRGGYFDYWGQGTLV TVSS
SEQ ID 49	EVQLVESGGGVVQPGRSLRLSCTASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKY YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKELVGTSSPYYYYYYGMDVW GQGTMVTVSS
SEQ ID 50	QLQLQESGGGLVQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVIYSGGSTYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDYYYGSGSSPWGQGTLVTVSS
SEQ ID 51	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYN PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGRPYCSSTSCYPEWFDPWGQGTL VTVSS
SEQ ID 52	QVTLKESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKY YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLRGIDYYDSSGYQRGFDYWG QGTLVTVSS
SEQ ID 53	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTGSTNYNPS LKSRVTISVDTSKNQFSLKLSSVTTADTAVYYCARGGRGDGAAFDIWGQGTMVTVSS
SEQ ID 54	QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSSAMHWVRQAPGKGLEWVAMIWHDESKK YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARPPDGGNSGRWYFDLWGRG TLVTVSS
SEQ ID 55	QMQLVQSGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTY YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDKNVRKHDYGDHPYGGYFD YWGQGTLVTVSS
SEQ ID 56	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQRLEWMGWINAGNGN TKYSQKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARVAGATSLWYWGQGTLVTV SS
SEQ ID 57	QVQLQQSGPGLVKPSQSLSLTCAISGDSVSSNSAAWNWIRQSPSRGLEWLGRTYYRSKWY NDYAVSVKSRITIKPDTSKNQFSLQLNSVTPEDTAVYYCTRLANSDGVDVWGQGTMVTV SS
SEQ ID 58	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSDSAVWTWIRQSPSRGLEWLGRTYYKSKWY NDYAASVKSRITINPDTSKNQFSLHLNSVTPEDTAVYYCARGVTRTFDYWGQGTTVTVSS
SEQ ID 59	QLQLQESGPGLVKPSQTLSLTCAISGDSVSSNSAAWNWIRQSPSRGLEWLGRTYYRSKWY NDYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCAEGNGPFDPWGQGTLVTVSS
SEQ ID 60	QITLKESGGGVVQPGRSLRLSCVASGFTFSTYPMHWVRQAPGKGLEWVAVISYDGRNEY YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATRDTPLVGVSIYWGQGTLVTV SS
SEQ ID 61	QMQLVQSGGGLVKAGGSLRLSCSASGFTFSSYAMHWVRQAPGKGLEYVSAISSNGGSTY YADSVKGRFTISRDNSKNTLYLQMSSLRAEDTAVYYCVNRAGYGDYRHFQHWGQGTLV TVSS
SEQ ID 62	EVQLVQSGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFISYDGSNKY YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATTGDRFQEFDYWGQGTLVTVS S
SEQ ID 63	QMQLVQSGGVLLQPGRSLRLSCTASGFTFAAYNINWFRQGPGGGLEWVGFIRANADSGTT EYAASVKGRFFISRDDSRSTAYLQMTSLKTEDTAVYYCARDDRGRGDDFDYWGQGTLVT VSS
SEQ ID 64	QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYGMTWVRQAPGKGLEWVSTISGNGVGTY YPDSVKDRFTISRDSSKNTVYLQMNSLRAEDTAVYYCVKHGRAGINWYFDLWGRGTLVT VSS
SEQ ID 65	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSNSAAWNWIRQSPSRGLEWLGRTYYRSKWY NDYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCARGGGLWAFDIWGQGTTVTVS S
SEQ ID 66	EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGG TNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARDKIGSCPYWGQGTLVTVS S

SEQ ID 67	QVTLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALIYWDDDKR YSPSLKSRLTITKDTSKNQVVLTMTNMDPVDTATYYCAHRPDSSSQCFDYWGQGTLVTVS S
SEQ ID 68	QVTLKESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKY YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSSGWSLPEDYWGQGTLVTVS S
SEQ ID 69	QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEDGET IYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCATDVNPELLGAGFDYWGQGTL VTVSS
SEQ ID 70	QVTLKESGGGLVQPGGSLRLSCAASGFTFSDQYMDWVRQAPGKGLEWVGRVRNKANSY TTEYAASVKGRFTISRDDSKNSLYLQMNSLNTEDTAMYFCASSLNSGGYRCFHHWGQGT LVTVSS
SEQ ID 71	QVQLVQSGGGLVQPGGSLRLSCSASGFTFSSYAMHWVRQAPGKGLEYVSAISSNGGSTYY ADSVKGRFTISRDNSKNTLYLQMSSLRAEDTAVYYCVKAPRGVVPAAMRGGYWGQGTL VTVSS
SEQ ID 72	QVQLQESGGGLVQPGRSLRLSCTASGFTFGDYAMSWFRQAPGKGLEWVGFIRSKAYGGT TEYAASVKGRFTISRDDSKSIAYLQMNSLKTEDTAVYYCTRLVGNSGSYYPFGYWGQGTL VTVSS
SEQ ID 73	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYN PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGRSLPYRGLAPRSFGGYYFDYWG QGTLVTVSS
SEQ ID 74	QVQLQESGGGLVRPGGSLRLSCGDSGFNFSGYEMNWVRQAPGKGLEWVSYVSTSGSTRY YADSVKGRFTISRDNAKNTLYLQMNSLRVEDTAVYYCARGRTHWGPQDFDYWGQGTLV TVSS
SEQ ID 75	QVQLQESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTY YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKGGMYYYGSGSSYFDYWGQG TLVTVSS
SEQ ID 76	QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSGISGSGGSTY YADSVKGRFTISRDNSKNMLFLQMNSPRAEDTAVYYCAKKIAAAGKQPVDYWGQGTLV TVSS
SEQ ID 77	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYN PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARRKVYDYVWGSYRLPGSVSYYFDY WGQGTLVTVSS
SEQ ID 78	QVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTR YSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARLPGRAARPDYWGQGTLVTVSS
SEQ ID 79	QVTLKESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKY YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGPGAVAGTKPKYYFDYWGQ GTLVTVSS
SEQ ID 80	EVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKY YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARATYYYDSSGYRFDYWGQGTL VTVSS
SEQ ID 81	EVQLVQSGGGLVEPGGSLRLSCAASRFTFSDAWMSWVRQAPGKGLEWVGRIKSKISGGT TDYAAPVQGRFTISRDDSKNTLYLQMDSLKTEDTAVYYCANRNLGYWGQGTLVTVSS
SEQ ID 82	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQRLEWMGWINAGNGN TKYSQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARARYYDSSGYIAPSGYFDY WGQGTLVTVSS
SEQ ID 83	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQRLEWMGWINAGNGN TKYSQKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGPAVDGAEYFQHWGQGT LVTVSS
SEQ ID 84	QLQLQESGPGLVKPSQTLSLTCAISGDSVSSNSAAWNWIRQSPSRGLEWLGRTYYRSKWY NDYAVSLKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCASLASGSPPPGDYWGQGTLVTV SS
SEQ ID 85	QVTLKESGGGVVQPGRSLRLSCAASGFTFSTYGMHWVRQAPGKGLEWVALISYDGSKKY YANSVKGRFTISRDNSKNTLYLQMKSLRAEDTAMYYCAKGPIVGATMDYWGQGALVTV SS

SEQ ID 86	EVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGWISAYNGNTN YAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARWYGDYGLDYWGQGTLVTV SS
SEQ ID 87	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQRLAWMGWINAGNGN TKYSEKFEGRVTITRDTSASTAYMELSSLRSEDTAVYYCARVAKYYYESGGYRASNWFDP WGQGTLVTVSS
SEQ ID 88	QVQLQESGPGLVKPSQTLSLTCAISGDSVSSNSAAWNWIRQSPSRGLEWLGRTYYRSKWY NDYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCARAPPPTVGWYAPVFDYWGQG TLVTVSS
SEQ ID 89	QLQLQESGGGLVQPGGSLRLSCSASGISFRDYWMHWIRQTPGKGLVWVSRINPDGSSTSY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKVTGRRVGAHDYWGQGTLVTV SS
SEQ ID 90	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGG TNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCAFAQPGAETLNFDLWGRGTL VTVSS
SEQ ID 91	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSKSAAWNWIRQSPSRGLEWLGRTYYRSKWN NDYALSVKSRITINPDTSKNQFSLQLKSVTPEDTALYYCVRQVAGGMDVWGQGTTVTVSS
SEQ ID 92	QVQLVQSGGGLVQPGRSLRLSCTASGFTFGDYAMSWFRQAPGKGLEWVSAISGSGGSTY YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKGSVYSGSYYMLIDYWGQGTL VTVSS
SEQ ID 93	QVQLQQSGPGLVRPSQTLSLTCVISGDSVSSGSAAWNWIRQSPSRGLEWLGRTYYRAKWY NEYAGSVKSRITISPDTSKNQFSLQLNSVTPEDTAVYFCTRQDKDNTRYSGLGVWGQGTT VTVSS
SEQ ID 94	EVQLVETGGGLVQPGGSLRLSCAASEFTLRNYGVSWVRQAPGKGLEWVSGMSGSGYSTY YADSVKGRFTISRDSSKNTLFLQMDSLRAEDTAIYYCARGPRMWSSGIDAFDIWGHGTMV TVSS
SEQ ID 95	QVQLQQWGAGLLKPSETLSLTCAVYGGSVSGYYWSWIRQPPGKGLEWMGEIHHSGSTNY NPSLKSRVTISLDTPKNQFSLKLSSVTAADTAVYYCARRDWAGKRVWGQGTLVTVSS
SEQ ID 96	QVQLQQSGPGLLKPSQTLSLTCAISGDSVSSNTATWNWIRQSPSRGLEWLGRTYYRSKWY KDNALSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCAGGRAGIAAFDIWGQGTTVTVS S
SEQ ID 97	QVQLVQSGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSLIYSDGRTNY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKGALQGEWRRFDYWGQGTLVT VSS
SEQ ID 98	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSNSAAWNWIRQSPSRGLEWLGRTYYRSKWY NDYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCTRTNQGYGGNSGVFDYWGQGT LVTVSS
SEQ ID 99	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSGNSAAWNWIRQSPSRGLEWLGRTYYRSKW YNDYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCARIVGGAVDCWGQGTLVTVS S
SEQ ID 100	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQRLEWMGWINAGNGN TKYSQKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARVRVGATTVYDSWFDPWGQ GTLVTVSS
SEQ ID 101	QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTY YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDGGSSPYYDSSGLLPWYFDL WGRGTLVTVSS
SEQ ID 102	QVQLQESGGGLVQPGGSLRLSCAASGFTFSSYAMHWVRQAPGKGLEYVSAISSNGGSTYY ANSVKGRFTISRDNSKNTLYLQMGSLRAEDMAVYYCARAKFWTYYFDYWGQGTLVTVS S
SEQ ID 103	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYN PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGGSGSYYKRFFDYWGQGTLVTV SS
SEQ ID 104	EVQLVQSGAEVRKPGASVKVSCKASGYTFTSYAISWVRQAPGQGLEWMGWISAYDGNT NYAQKLQGRVTMTTDTSTSTAYMEVRSLRSDDTAVYYCARDGTVRRVVGATTPGNFDY RGQGTLVTVSS

SEQ ID 105	EVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNK YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLNRGYCSGGSCFGYWGQ GTLVTVSS
SEQ ID 106	QVQLQESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSYISSSGTTIYY ADSVKGRFTVSRDNAKNSLYLQMNSLRAEDTAVYYCARDYSSSGECFDYWGQGTLVTV SS
SEQ ID 107	EVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNK YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQAAMVGYFDYWGQGTLV TVSS
SEQ ID 108	QVTLKESGGGVVQPGRSLRLSCAASGFIFSNYAIHWVRQAPGKGLEWVAVISYDGSNKYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARTFAGYSSKLGYFDLWGRGTLV TVSS

[166] A VH amino acid sequence of the disclosure may be encoded by a polynucleotide shown in Table 3 below.

Table 3. VH DNA Sequences

SEQ ID	VH DNA Sequence
SEQ ID 109	GAAGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGG TTTCCTGCAAGGCTTCTGGATACACCTTCACTAGCTATGCTATGCATTGGGTGCGCCAGG CCCCCGGACAAAGGCTTGAGTGGATGGGATGGATCAACGCTGGCAATGGTAACACAAA ATATTCACAGAAGTTCCAGGGCAGAGTCACCATTACCAGGGACACATCCGCGAGCACAG CCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCTGTGTATTACTGTGCGAGA GGCTCCTTGTCCCGAAGTGGCTGGTACGCCGGACTCTTTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTCTCCTCA
SEQ ID 110	CAGATCACCTTGAAGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACT CTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGTTATAGCATGAACTGGGTCCGCCAGGC TCCAGGCAAGGGGCTGCAGTGGGTGGCAATTATATCAGATGATGGAAGTAAGAGTTACT ACGCAGACTCCGTGCAGGGCCGATTCACCATCTCCAGAGACAATTCGAGGAACACAGTA TTTCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATGTATTACTGTGCGAGAGA CAGGGGAACTAAATGGAACCAATTGAATGATGTTTTTGATATGTGGGGCCAAGGGACAA TGGTCACCGTCTCTTCA
SEQ ID 111	GAAGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGG TTTCCTGCAAGGCATCTGGATACACCTTCACCAGCTACTATATGCACTGGGTGCGACAGG CCCCTGGACAAGGGCTTGAGTGGATGGGAATAATCAACCCTAGTGGTGGTAGCACAAGC TACGCACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAG TCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA GGCCGAGGGTATAGCAGCAGTCGGCTCTACTACTTTGACTACTGGGGCCAGGGAACCCT GGTCACCGTCTCCTCA
SEQ ID 112	CAGGTCACCTTGAAGGAGTCTGGGGGAGGCTTGGTCCGGCCTGGAGGGTCCCTGAGACT CTCCTGTGAAGCCTCTGGATTCACCTTCAGTGACCCCTACATGGACTGGGTCCGCCAGGC TCCAGGCAAGGGGCTGGAGTGGGTTGGCCGAATTACAAATAAGCGTACCGGTTACGCCA CAACATATGCCGCGTCTGTGAAGGACAGATTCACCATCTCAAGAGATGATTCAAGGAAG TCAGTATATCTGCAAATGAACAGCCTGAAGACCGAGGACACGGCCGTATATTATTGTGC AACAGATGTCAGTGGGTCCTTCGCGGCCTACGGGGGCCAGGGCACCCTGGTCACCGTCT CCTCA
SEQ ID 113	GAGGTCCAGCTGGTACAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACT CTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGCTATGCATTGGGTGCGCCAGGC CCCCGGACAAAGGCTTGAGTGGATGGGATGGATCAACGCTGGCAATGGTAACACAAAA TATTCACAGAAGTTCCAGGGCAGAGTCACCATTACCAGGGACACATCCGCGAGCACAGC CTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCTGTGTATTACTGTGCGGGAG AGGGCGGAGCAGTGGCTGGTACTGTCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCC TCA

SEQ ID 114	CAGGTCCAGCTGGTGCAGTCTGGGGGAGGCTTGGTAAAGCCTGGGGGGTCCCTTAGACT CTCCTGTGCAGCCTCTGGATTCACTTTCAGTAACGCCTGGATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGGAGTGGGTTGGCCGTATTAAAAGCAAAACTGATGGTGGGACA ACAGACTACGCTGCACCCGTGAAAGGCAGATTCACCATCTCAAGAGATGATTCAAAAAA CACGCTGTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTACTGTA CCACAGACGAGTATTTCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
SEQ ID 115	CAGGTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCT CACCTGCGCTGTCTATGGTGGGTCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCC CCCAGGGAAGGGGCTGGAGTGGATTGGGGAAATCAATCATAGTGGAAGCACCAACTAC AACCCGTCCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTC CCTGAAGCTGAGCTCTGTGACCGCCGCGGACACGGCTGTGTATTACTGTGCGAGAGTAA ATCCGGGGAGTTATACGAGGGAGGTGAGCAACTTTGACTACTGGGGCCAGGGAACCCTG GTGACCGTCTCCTCA
SEQ ID 116	CAGGTACAGCTGCAGCAGTCAGGTCCAGAATTGGTGAAGCCCTCGCAGACCCTCACACT CACCTGTGGCATCTCCGGGGACAGTGTCTCTAGCAACAGTGTTACTTGGAACTGGGTCA GGCAGTCCCCATCGAGAGGCCTTGAGTGGCTGGGAAGGACTTACTACCGGTCCCAGTGG TATTATAATTATGCGGTGTCTGTGAAAAGTCGAATAACCATCAGCCCAGACACATCCAA GAACCAGTTCTCCCTGCAGTTGAATTCTGTGACTCCCGAGGACACGGCTGTCTATTACTG TGCAACCAGGGGACATAACTACGGTGTAGATTACTGGGGCCCGGGGACCACGGTCACCG TCTCCTCA
SEQ ID 117	CAGGTGCAGCTGGTGCAGTCTGGGGGAGGCTTGGTAAAGCCTGGGGGGTCCCTTAGACT CTCCTGTGCAGCCTCTGGATTCACTTTCAGTAACGCCTGGATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGGAGTGGGTTTGCCGTATTAAAAGCAAAACTGATGGTGAGACA ACAGACTACGCTGCACCCGTGAAAGGCAGATTCACCATCTCAAGAGATGATTCAAAAAA CACGCTGTATCTGCAAATGAACAGCCTGAAAACTGAGGACACAGCCGTGTATCACTGTA CCACAGGGGTGGGATGGTCGCCCTTCCAATACTGGGGCCAGGGCACCCTGGTCACCGTC TCCTCA
SEQ ID 118	GAGGTCCAGCTGGTACAGTCTGGGGGAGGCTTGGTACAGCCAGGGCGGTCCCTGAGACT CTCCTGTACAGCTTCTGGATTCACCTTTGGTGATTATGCTATGAGCTGGTTCCGCCAGGC TCCAGGGAAGGGGCTGGAGTGGGTAGGTTTCATTAGAAGCAAAGCTTATGGTGGGACAA CAGAATACGCCGCGTCTGTGAAAGGCAGATTCACCATCTCAAGAGATGATTCCAAAAGC ATCGCCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTACTGTAC TAGAGACGACAAAATAGCAGCAGCTGGATTCACATACTGGTACTTCGATCTCTGGGGCC GTGGCACCCTGGTCACCGTCTCCTCA
SEQ ID 119	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGT CTCCTGCAAGGCTTCTGGATACACCTTCGCCGCCTATTATTTACACTGGGTGCGACAGGC CCCTGGACAAGGCCTTGAGTGGATGGGGCGGATCAGCCCTGGTAACGGTGTCACAAGTT ATGCACAGAAATTTCAGGGCAGAGTCACCATGACCGGGGACACGTCCATTAACACAGTC TACATGCAACTGAACAATTTGATTTCTGGCGACACGGCCGTATATTACTGTGCGAGAGA GGCTGCCGACGACCCGTTTGACCATTGGGGCCAGGGAGCCCTGGTCACCGTCTCCTCA
SEQ ID 120	GAAGTGCAGCTGGTGCAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGACACT CTCCTGTGCAGCCTCTGGATTCACCTTCAGTTCCCATCTTATGCACTGGGTCCGCCAGGC TCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAACTAGTAAATATT ACGGAGACTCCGTGAAGGGCCGCTTCACCATCTCCAGAGACAATTCCAAGAACACGTTG TATCTGCAAATGAACAGCCTGCGAGCTGAAGACACGGCTATATATTACTGTGCGAAAGC AGATTATAAATATGACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
SEQ ID 121	GAGGTGCAGCTGGTGCAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACT CTCCTGTACAGCTTCTGGATTCACCTTTGGTGATTATGCTATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGGAGTGGGTAGGTTTCATTAGAAGCAAAGCTTATGGTGGGACAA CAGAATACGCCGCGTCTGTGAAAGGCAGATTCACCATCTCAAGAGATGATTCCAAAAGC ATCGCCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTACTGTAC TACTCATAGACGCCCAATTTACGATATTTTGACTGGTTTTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTCTCCTCA
SEQ ID 122	CAGCTGCAGCTGCAGGAGTCCGGGGGAGGCTTGGTACAGCCAGGGCGGTCCCTGAGACT CTCCTGTACAGCTTCTGGATTCACCTTTGGTGATTATGCTATGAGCTGGGTCCGCCAGGC

	TCCAGGGAAGGGGCTGGAGTGGGTAGGTTTCATTAGAAGCAAAGCTTATGGTGGGACAA CAGAATACGCCGCGTCTGTGAAAGGCAGATTCACCATCTCAAGAGATGATTCCAAAAGC ATCGCCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTACTGTAC TAGAGAGGATACTATGGTTCGGGGAGTTATTCCCTGGGGCCAGGGAACCCTGGTCACCG TCTCCTCA
SEQ ID 123	CAGCTGCAGCTGCAGGAGTCCGGCTCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCT CACCTGCGCTGTCTCTGGTGGCTCCATCAGCAGTGGTGGTTACTCCTGGAGCTGGATCCG GCAGCCACCAGGGAAGGGCCTGGAGTGGATTGGGTACATCTATCATAGTGGGAGCACCT ACTACAACCCGTCCCTCAAGAGTCGAGTCACCATATCAGTAGACAGGTCCAAGAACCAG TTCTCCCTGAAGCTGAGCTCTGTGACCGCCGCGGACACGGCTGTGTATTACTGTGCGAGA GATCGGCGTTACTATGATAGTAGTGGTTATTATCCCGCCTACTACTTTGACTACTGGGGC CAGGGAACCCTGGTCACCGTCTCCTCA
SEQ ID 124	GAAGTGCAGCTGGTGCAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACT CTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATAGCATGAACTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGGAGTGGGTTTCATACATTAGTAGTAGTGGTAGTTACACAAACT ACGCAGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTG TATCTGCAAATAAACAGCCTGAGAGCCGAGGACACGGCCATTTATTACTGTGCGAGAGA CGGGGGCTATGATAGTAGTGGTTTTCACTTTGACTACTGGGGCCAGGGAACCCTGGTCA CCGTCTCCTCA
SEQ ID 125	CAGGTACAGCTGCAGCAGTCAGGTCCAGGACTGGTGAAGCCCTCGCAGACCCTCTCACT CACCTGTGCCATCTCCGGGGACAGTGTCTCTAACAACAGGGCTGCTTGGAACTGGATCA GGCAGTCGCCATCGAGAGGCCTTGAGTGGCTGGGAAGGACATACTACAGGTCCAAGTGG TATAATGAATATGCAGTCTCTGTGAAAAGTCGAATAACCATCAACCCAGACACATCCAA GAACCAGTTCTCCCTGCAGCTGAACTCTATGACTCCCGAGGACTCGGCTGTGTATTACTG TGCAATTTTGCCTAGTAGTGGTTATCTACAGGACCACCACTACTACGGTATGGACGTCTG GGGCCAAGGGACCACGGTCACCGTCTCCTCA
SEQ ID 126	GAGGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGG TCTCCTGCAAGGCTTCTGGTTACACCTTTACCAGCTACGGTATCAGCTGGGTGCGACAGG CCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCAGCGCTTACAATGGTAACACAAAC TATGCACAGAAGCTCCAGGGCAGAGTCACCATGACCACAGACACATCCACGAGCACAG CCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA GCCGCGGTGGGGGATGGATACAGCTATGGTCGGCTCGATTGGGGCCAGGGAACCCTGGT CACCGTCTCCTCA
SEQ ID 127	GAGGTCCAGCTGGTACAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCTCTGAAGA TCTCCTGTAAGGGTTCTGGATACAGCTTTACCAGCTACTGGATCGGCTGGGTGCGCCAGA TGCCCGGGAAAGGCCTGGAGTGGATGGGGATCATCTATCCTGGTGACTCTGATACCAGA TACAGCCCGTCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCACCGC CTACCTGCAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATGTATTACTGTGCGAGAC TCCCCTCGTATTACTATGATAGTAGTGGTTACTTTACCTGGTACTTCGATCTCTGGGGCCG TGGCACCCTGGTGACCGTCTCTTCA
SEQ ID 128	GAGGTCCAGCTGGTACAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGT CTCCTGCAAGGCTTCTGGTTACACCTTTACCAGCTATGGTATCAGCTGGGTGCGACAGGC CCCTGGACAAGGGCTTGAGTGGATGGGATGGATCATCCCTATCTTTGGTATAGCAAACT ACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGC CTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAG AACTATACAACTATGGTTCAAAGGACTACTTTGACTACTGGGGCCAGGGAACCCTGGTC ACCGTCTCCTCA
SEQ ID 129	GAAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCTCTGAAGA TCTCCTGTAAGGGTTCTGGATACAGCTTTACCAGCTACTGGATCGGCTGGGTGCGCCAGA TGCCCGGGAAAGGCCTGGAGTGGATGGGGATCATCTATCCTGGTGACTCTGATACCAGA TACAGCCCGTCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCACCGC CTACCTGCAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATGTATTACTGTGCGAGGG GCGGTACTTGGGATACAGCTATGGTTACGGGCTTTGACTACTGGGGCCAGGGAACCCTG GTCACCGTCTCCTCA

SEQ ID 130	GAAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCTCTGAAGA TCTCCTGTAAGGGTTCTGGATACAGCTTTACCAGCTACTGGATCGCCTGGGTGCGCCAGA TGCCCGGGAAAGGCCTGGAGTGGATGGGGGTCATCTATCCTGGTGACTCTGATACCAGA TACAGCCCGTCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAATACCGC CTACCTGCAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATGTATTACTGTGCGAGAC CCCATTACGATATTTTGACTGGTTCCCGGGCGCCCTTTGACTACTGGGGCCAGGGAACCC TGGTCACCGTCTCCTCA
SEQ ID 131	CAGGTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCT CACCTGCGCTGTCTATGGTGGGTCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCC CCCAGGGAAGGGGCTGGAGTGGATTGGGGAAATCAATCATAGTGGAAGCACCAACTAC AACCCGTCCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTC CCTGAAGCTGAGCTCTGTGACCGCCGCGGACACGGCTGTGTATTACTGTGCGAGAGCCC GAGTGGAATCCAAGGATGGGTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTC TCCTCA
SEQ ID 132	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACT CTCCTGTGCAGCCTCTGGATTCACTTTCACTGATGCCTGGATGAACTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGGAGTGGATTGGCCGTGTTAAAAACAAAGCTGATGGTGAGACA ACGGACTACGCTGCACCCGTCAAAGGCAGAATCACCATCTCAAGAGATGATGCAAAGA ACACTCTGTATGTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTATTGT ACCGCTGACCTGCGACTTTCTACGTGGGATGCTTATGATTTCTGGGGCCAAGGGACAATG GTCACCGTCTCTTCA
SEQ ID 133	CAGATCACCTTGAAGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTAAGACT CTCTTGTACAGTCTCAGGATTCACCTTTAGTAACAATTGGATGACCTGGGTCCGCCAGAC TCCAGGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAACTGAGAAACAC TATGTGGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCGAGAACTCACT GTATCTGCAGATGAACAGCCTGAGAGGTGAGGACACGGCCGTGTATTATTGTGCGAGAA ACAGTCAACGTTCGTTTGACTACTGGGGCCAGGGCACCCTGGTGACCGTCTCCTCA
SEQ ID 134	CAGGTCACCTTGAAGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACT CTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGC TCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACT ATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTG TATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGA TTTAGGGGATCCCCGGGGTGGTATTTTGAACTACTGGGGCCAGGGCACCCTGGTCACCG TCTCCTCA
SEQ ID 135	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACT CTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGCTATGCACTGGGTCCGCCAGGC TCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACT ACGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTG TATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCCCGGTC GAGCCCCTGGGGGGAGTTATCGTTATACCAGGGGGCTTTTGATATCTGGGGCCAAGGGA CAATGGTCACCGTCTCTTCA
SEQ ID 136	CAGATCACCTTGAAGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAGGTCCCTGAGACT CTCCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGGCAAGC TCCAGGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACT ACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTG TATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAAAGA TAACGATTTTTGGAGTGGGAAAGTCTTTGACTACTGGGGCCAGGGCACCCTGGTCACCG TCTCCTCA
SEQ ID 137	GAAGTGCAGCTGGTGCAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACT CTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGTTATAGCATGAACTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGGAGTGGGTTTCATACATCAGTAGTACTAGTAGTACCATATACT ACGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAATATGCTG TTTCTACAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGA AGGGGGCAGTGGCTGGCGCCACTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCG TCTCCTCA

SEQ ID 138	CAGGTCACCTTGAAGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACT GTCCTGTGCAGCCTCTGGATTCACCTTCAGCAGCTATGCTATGCACTGGGTCCGCCAGGC TCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACT ACGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTG TATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGA TTATTGTAGTAGTACCAGCTGCCAGAACTGGTTCGACCCCTGGGGCCAGGGCACCCTGG TCACCGTCTCCTCA
SEQ ID 139	CAGGTCCAGCTGGTGCAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACT CTCCTGTGCAGCCTCTGGATTCACCTTTAGCAACTATGTCATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTATTGGTGATACTACATACT ACGCGGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACACGCTG TATCTGCAAATGAACAGTCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCAAGAGG GCGCGTGGCGGGGGATGCTTTTGATATCTGGGGCCAAGGGACAATGGTGACCGTCTCTT CA
SEQ ID 140	CAGCTGCAGCTGCAGGAGTCGGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACT CTCCTGTGCAGCCTCTGGATTCACCTTTAGCAGCTATGCCATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACT ACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTG TATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAAAGA TCAAGGGGCAGCAGCTGGTACCCTGGGGTACTTTGACTACTGGGGCCAGGGAACCCTGG TGACCGTCTCCTCA
SEQ ID 141	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGT CTCCTGCAAGGCTTCTGGATACACCTTCACCAGTTATGATATCAACTGGGTGCGACAGGC CACTGGACAAGGGCTTGAGTGGATGGGATGGATGAACCCTAACAGTGGTAACACAGGCT ATGCACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGAACACCTCCATAAGCACAGCC TACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTACGAGAGG AATCTATGATAGTAGTGGTTCTTCCAATCCCTTTGACTCCTGGGGCCAGGGAACCCTGGT GACCGTCTCCTCA
SEQ ID 142	GAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGA TTTCCTGCGAGGCTTCTGGATACACCTTCACTGATTATGCTATACATTGGGTGCGCCAGG CCCCCGGACAAAGACTTGAGTGGATGGGATGGATCAACGCTGGCGATGGTGGCACAAA AAGTTCACGGGAGTTCCAGGGCAGAGTCACCATTACCAGGGACACATCCGCGACCACAG CCTACATGGAGGTGAGCAGTCTGAGATCTGAAGACACGGCTGTCTATTACTGTGCGAGA GGATATTGTAGTGGTGGTAGCTGCCCAGGAACGGATTTTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTCTCCTCA
SEQ ID 143	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGT TTCCTGCAAGGCATCTGGATACACCTTCACCAGCTACTATATGCACTGGGTGCGACAGGC CCCTGGACAAGGGCTTGAGTGGATGGGAATAATCAACCCTAGTGGTGGTAGCACAAGCT ACGCACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGT CTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAG ATGGTGTAGGAGGGAGAGATGGCTACAATTTTGACTACTGGGGCCAGGGAACCCTGGTC ACCGTCTCCTCA
SEQ ID 144	GAAGTGCAGCTGGTGCAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACT CTCCTGTGCAGCCTCTGGATTCACCGTCAGTAGCAACTACATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGGAGTGGGTCTCAGTTATTTATAGCGGTGGTAGCACATACTACG CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT CTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGCCCC CCTAGCAGCAGATGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTC A
SEQ ID 145	GAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGT CTCCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGG CCCCTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAAC TACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAG CCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA GCCCGGGGGCTACAGTACCTAATCTGGTACTTCGATCTCTGGGGCCGTGGCACCCTGGTG ACCGTCTCCTCA

SEQ ID 146	CAGGTCCAGCTGGTACAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGT TTCCTGCAAGGCATCTGGATACACCTTCACCAGCTACTATATGCACTGGGTGCGACAGGC CCCTGGACAAGGGCTTGAGTGGATGGGAATAATCAACCCTAGTGGTGGTAGCACAAGCT ACGCACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGT CTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGCC CGGGTATGGTTCGGGGAGTTATTACTGCCCCGCTTGACTACTGGGGCCAGGGCACCCTG GTCACCGTCTCCTCA
SEQ ID 147	GAGGTCCAGCTGGTACAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACT CTCCTGTGCAGCCTCTGGATTCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGC CCCTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATGTATGGTACAGCAAACT ACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGC CTACATGGAACTGAGCAGCCTGAGATCTGAGGACACGGCCCTCTATTACTGTGCGAGAG AAGCTAAGTGGGGAATGTACTACTTTGACTACTGGGGCCAGGGCACCCTGGTCACCGTC TCCTCA
SEQ ID 148	GAGGTGCAGCTGGTGGAGTCCGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACT CTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGCTATACACTGGGTCCGCCAGGC TCCAGGCAAGGGGCTGGAGTGGGTGGCAATTATATCAGATGATGGAAGTAAGAGTTACT ACGCAGACTCCGTGCAGGGCCGATTCACCATCTCCAGAGACAATTCGAGGAACACAGTA TATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATGTATTACTGTGCGAGAGA CAGGGGAACTAAATGGAACCAATTGAATGATGTTTTTGATATGTGGGGCCAAGGGACAA TGGTCACCGTCTCTTCA
SEQ ID 149	CAGATGCAGCTGGTGCAATCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGT CTCCTGCACGGCTTCTGGATACACCTTCACCAGTTCTGATATCAACTGGGTGCGACAGGC CACTGGACAAGGGCTTGAGTGGATGGGATGGATGAACCCTAACAGTGGTAACACCGGCT ATGCAGAGAAGTTCCAGGGCAGGGTCACCATGACCAGCGACTCCTCCATAAGCACCGCC TACATGGAGTTGAGAAGCCTGACCACTGAGGACACGGCCGTATATTACTGTGCGAGAGG TGGGGGTGCGAGCTATACTGACTCCTGGGGCCAGGGCACCCTGGTCACCGTCTCCTCA
SEQ ID 150	CAGGTCCAGCTGGTGCAGTCTGGGGGAGGCTTGGTACAGCCAGGGCGGTCCCTGAGACT CTCCTGTACAGCTTCTGGATTCACCTTTGGTGATTATGCTATGAGCTGGTTCCGCCAGGC TCCAGGGAAGGGGCTGGAGTGGGTAGGTTTCATTAGAAGCAAAGCTTATGGTGGGACAA CAGAATACGCCGCGTCTGTGAAAGGCAGATTCACCATCTCAAGAGATGATTCCAAAAGC ATCGCCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTACTGTAC CGCTAAGGGGGGCTACGTCGGATACAGCTATGGACCTTTTGGGGGCTACTGGGGCCAGG GAACCCTGGTCACCGTCTCCTCA
SEQ ID 151	CAGGTGCAGCTGGTGCAGTCTGGGGGAGGCTTGGTACAGCCAGGGCGGTCCCTGAGACT CTCCTGTACAGCTTCTGGATTCACCTTTGGTGATTATGCTATGAGCTGGTTCCGCCAGGC TCCAGGGAAGGGGCTGGAGTGGGTAGGTTTCATTAGAAGCAAAGCTTATGGTGGGACAA CAGAATACGCCGCGTCTGTGAAAGGCAGATTCACCATCTCAAGAGATGATTCCAAAAGC ATCGCCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTACTGTAC TAGAGGGGGGACTATGGTTCGGGGTTTCGGATTTAACTACTGGGGCCAGGGAACCCTGG TCACCGTCTCCTCA
SEQ ID 152	CAGGTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCT CACCTGCGCTGTCTATGGTGGGTCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCC CCCAGGGAAGGGGCTGGAGTGGATTGGGGAAATCAATCATAGTGGAAGCACCAACTAC AACCCGTCCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTC CCTGAAGCTGAGCTCTGTGACCGCCGCGGACACGGCTGTGTATTACTGTGCGAGAGCCC GGCGGGCTATGATAGGGCCGCTTCCGCGACTTGTCGGGTACTTCGATCTCTGGGGCCGTG GAACCCTGGTCACCGTCTCCTCA
SEQ ID 153	CAGGTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCT CACCTGCGCTGTCTATGGTGGGTCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCC CCCAGGGAAGGGGCTGGAGTGGATTGGGGAAATCAATCATAGTGGAAGCACCAACTAC AACCCGTCCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTC CCTGAAGCTGAGCTCTGTGACCGCCGCGGACACGGCTGTGTATTACTGTGCGAGAGGCC GCCCCGCCCCATCCTGGGTTAAAACCCGTAACTGGTTCGACCCCTGGGGCCAGGGAACC CTGGTCACCGTCTCCTCA

SEQ ID 154	CAGGTACAGCTGCAGCAGTCAGGTCCAGGACTGGTGAAGCCCTCGCAGACCCTCTCACT CACCTGTGCCATCTCCGGGGACAGTGTCTCTAGCAACAGTGCTGCTTGGAACTGGATCA GGCAGTCCCCATCGAGAGGCCTTGAGTGGCTGGGAAGGACATACTACAGGTCCAAGTGG TATAATGATTATGCAGTATCTGTGAAAAGTCGAATAACCATCAACCCAGACACATCCAA GAACCAGTTCTCCCTGCAGCTGAACTCTGTGACTCCCGAGGACACGGCTGTGTATTACTG TGCAAGAGAGGCTAGCAGTGGCTGGAACTGGGGCCAGGGAACCCTGGTCACCGTCTCCT CA
SEQ ID 155	CAGGTGCAGCTGCAGGAGTCCGGTCCAGGACTGGTGAAGCCCTCGCAGACCCTCTCACT CACCTGTGCCATCTCCGGGGACAGTGTCTCTAGCAACAATGCTGCTTGGAACTGGATCA GGCAGTCCCCATCGAGAGGCCTTGAGTGGCTGGGAAGGACATTCTACAGGTCCAAGTGG TATAATGACTATGCAGTTTCTGTGAAAAGTCGACTAACCGTCAACCCAGACACATCCAA GAACCAGTTCTCCCTGCGGTTGAACTCTGTGAGTCCCGAGGACACGGCTGTGTATTACTG TGCAAGAGGGGGAAGATATACCAAGGGAGGGTACTTTGACGACTGGGGCCAGGGAACC CTGGTGACCGTCTCCTCA
SEQ ID 156	CAGGTCACCTTGAAGGAGTCTGGTCCTACGCTGGTGAAACCCACACAGACCCTCACGCT GACCTGCACCTTCTCTGGGTTCTCACTCAGCACTAGTGGAGTGGGTGTGGGCTGGATCCG TCAGCCCCCAGGAAAGGCCCTGGAGTGGCTTGCACTCATTTATTGGGATGATGATAAGC GCTACAGCCCATCTCTGAAGAGCAGGCTCACCATCACCAAGGACACCTCCAAAAACCAG GTGGTCCTTACAATGACCAACATGGACCCTGTGGACACAGCCACATATTACTGTGCACA CAGATTGGATAGCAGTGGCCGTGGTGGTTACTTTGACTACTGGGGCCAGGGCACCCTGG TCACCGTCTCCTCA
SEQ ID 157	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACT CTCCTGTACAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGC TCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACT ATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTG TATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGA GTTGGTGGGTACCAGCTCTCCTTATTACTACTACTACGGTATGGACGTCTGGGGCCA AGGGACAATGGTCACCGTCTCTTCA
SEQ ID 158	CAGCTGCAGCTGCAGGAGTCGGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACT CTCCTGTGCAGCCTCTGGATTCACCGTCAGTAGCAACTACATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGGAGTGGGTCTCAGTTATTTATAGCGGTGGTAGCACATACTACG CAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT CTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACTA TTACTATGGTTCGGGGAGTTCTCCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
SEQ ID 159	CAGGTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCT CACCTGCGCTGTCTATGGTGGGTCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCC CCCAGGGAAGGGGCTGGAGTGGATTGGGGAAATCAATCATAGTGGAAGCACCAACTAC AACCCGTCCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTC CCTGAAGCTGAGCTCTGTGACCGCCGCGGACACGGCTGTGTATTACTGTGCGAGAGGCC GGCCATATTGTAGTAGTACCAGCTGCTACCCAGAGTGGTTCGACCCCTGGGGCCAGGGA ACCCTGGTCACCGTCTCCTCA
SEQ ID 160	CAGGTCACCTTGAAGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACT CTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGC TCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACT ATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTG TATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAATT AAGGGGTATAGATTACTATGATAGTAGTGGTTACCAACGGGGGTTTGACTACTGGGGCC AGGGAACCCTGGTCACCGTCTCCTCA
SEQ ID 161	CAGGTGCAGCTGCAGGAGTCCGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCT CACCTGCACTGTCTCTGGTGGCTCCATCAGTAGTTACTACTGGAGCTGGATCCGGCAGCC CCCAGGGAAGGGACTGGAGTGGATTGGCTATATCTATTACACTGGGAGCACCAACTACA ACCCCTCCCTCAAGAGCCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCC CTGAAGCTGAGCTCTGTGACCACTGCGGACACGGCCGTGTATTACTGTGCGAGAGGTGG GAGGGGGGATGGGGCCGCTTTTGACATCTGGGGCCAAGGGACAATGGTCACCGTCTCTT CA

SEQ ID 162	CAGGTGCAGCTGGTGCAATCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACT CTCCTGTGCAGCGTCTGGATTCACCTTCAGCAGCTCTGCCATGCACTGGGTCCGCCAGGC TCCAGGCAAGGGACTGGAGTGGGTGGCAATGATTTGGCATGATGAGAGTAAGAAATACT ATGCAGACTCCGTGAAGGGCCGATTCACTATCTCCAGAGACAATTCCAAGAACACGCTG TATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGACC CCCCGACGGTGGTAACTCCGGTCGCTGGTACTTCGATCTCTGGGGCCGTGGCACCCTGGT CACCGTCTCCTCA
SEQ ID 163	CAGATGCAGCTGGTGCAATCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACT CTCCTGTGCAGCCTCTGGATTCACCTTTAGCAGCTATGCCATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACT ACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTG TATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAAAGA CAAGAACGTCCGAAAACATGACTACGGTGACCACCCCTACGGGGGGTACTTTGACTACT GGGGCCAGGGCACCCTGGTGACCGTCTCCTCA
SEQ ID 164	GAGGTCCAGCTGGTACAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGT TTCCTGCAAGGCTTCTGGATACACCTTCACTAGCTATGCTATGCATTGGGTGCGCCAGGC CCCCGGACAAAGGCTTGAGTGGATGGGATGGATCAACGCTGGCAATGGTAACACAAAA TATTCACAGAAGTTCCAGGGCAGAGTCACCATTACCAGGGACACATCCGCGAGCACAGC CTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCTGTGTATTACTGTGCGAGAG TGGCGGGAGCTACTTCCCTATGGTACTGGGGCCAGGGCACCCTGGTCACCGTCTCCTCA
SEQ ID 165	CAGGTACAGCTGCAGCAGTCAGGTCCAGGACTGGTGAAGCCCTCGCAGAGCCTCTCACT CACCTGTGCCATCTCCGGGGACAGTGTCTCTAGCAACAGTGCTGCTTGGAACTGGATCA GGCAGTCCCCATCGAGAGGCCTTGAGTGGCTGGGAAGGACATACTACAGGTCCAAGTGG TATAATGATTATGCAGTATCTGTGAAGAGTCGAATAACCATCAAACCAGACACATCCAA GAACCAGTTCTCCCTGCAGCTGAACTCTGTGACTCCCGAGGACACGGCTGTGTATTACTG TACAAGGCTAGCTAATTCCGACGGTGTGGACGTCTGGGGCCAAGGGACAATGGTCACCG TCTCCTCA
SEQ ID 166	CAGGTACAGCTGCAGCAGTCAGGTCCAGGACTGGTGAAGCCCTCGCAGACCCTCTCACT CACCTGTGCCATCTCCGGGGACAGTGTCTCTAGCGACAGTGCTGTTTGGACCTGGATCAG GCAGTCCCCATCGAGAGGCCTTGAGTGGCTGGGAAGGACATACTACAAGTCGAAGTGGT ATAATGATTATGCAGCATCTGTGAAAAGTCGAATAACCATCAACCCAGACACATCCAAG AACCAGTTCTCCCTGCACCTGAACTCTGTGACTCCCGAGGACACGGCTGTGTATTACTGT GCAAGAGGTGTAACCCGGACCTTTGACTACTGGGGCCAGGGGACCACGGTCACCGTCTC CTCA
SEQ ID 167	CAGCTGCAGCTGCAGGAGTCGGGTCCAGGACTGGTGAAGCCCTCGCAGACCCTCTCACT CACCTGTGCCATCTCCGGGGACAGTGTCTCTAGCAACAGTGCTGCTTGGAACTGGATCA GGCAGTCCCCATCGAGAGGCCTTGAGTGGCTGGGAAGGACATACTACAGGTCCAAGTGG TATAATGATTATGCAGTATCTGTGAAAAGTCGAATAACCATCAACCCAGACACATCCAA GAACCAGTTCTCCCTGCAGCTGAACTCTGTGACTCCCGAGGACACGGCTGTGTATTACTG TGCAGAAGGCAATGGGCCGTTCGACCCCTGGGGCCAGGGAACCCTGGTGACCGTCTCCT CA
SEQ ID 168	CAGATCACCTTGAAGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACT CTCCTGTGTAGCCTCTGGATTCACCTTCAGTACCTATCCCATGCACTGGGTCCGCCAGGC TCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGACGTAATGAATACT ACGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAAAACACGCTG TATCTGCAAATGAACAGTCTGCGAGCTGAAGACACGGCTGTCTATTATTGTGCGACTCG GGATACACCTTTGGTTGGGGTTTCGATATACTGGGGCCAGGGCACCCTGGTCACCGTCTC CTCA
SEQ ID 169	CAGATGCAGCTGGTGCAATCTGGGGGAGGCCTGGTCAAGGCTGGGGGGTCCCTGAGACT CTCCTGTTCAGCCTCTGGATTCACCTTCAGTAGCTATGCTATGCACTGGGTCCGCCAGGC TCCAGGGAAGGGACTGGAATATGTTTCAGCTATTAGTAGTAATGGGGGTAGCACATACT ACGCAGACTCAGTGAAGGGCAGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTG TATCTTCAAATGAGCAGTCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGTGAATCG GGCGGGTTACGGTGACTACAGACACTTCCAGCACTGGGGCCAGGGCACCCTGGTCACCG TCTCCTCA

SEQ ID 170	GAGGTGCAGCTGGTGCAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACT CTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGC TCCAGGCAAGGGGCTGGAGTGGGTGGCATTTATATCATATGATGGAAGTAATAAATACT ACGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTG TATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGACAAC AGGGGACCGCTTCCAAGAGTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCT CA
SEQ ID 171	CAGATGCAGCTGGTGCAGTCTGGGGGAGTCTTGCTTCAGCCAGGGCGGTCCCTGAGACT CTCCTGTACAGCTTCTGGATTCACCTTTGCTGCTTATAATATCAACTGGTTCCGCCAGGGT CCTGGGGGGGGGCTGGAGTGGGTAGGTTTCATTAGAGCCAACGCTGATAGTGGGACAAC AGAGTACGCCGCGTCTGTGAAAGGCAGATTCTTCATCTCAAGAGATGATTCCAGAAGCA CCGCCTACCTGCAAATGACTAGCCTTAAAACCGAGGACACAGCCGTTTATTACTGTGCC AGAGATGATCGGGGTCGGGGAGATGACTTTGACTACTGGGGCCAGGGCACCCTGGTCAC CGTCTCCTCA
SEQ ID 172	CAGGTGCAGCTGGTGCAATCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACT CTCCTGTGCAGCCTCTGGATTCACCTTTAGCAGCTATGGCATGACGTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGGAGTGGGTCTCAACTATTAGTGGTAATGGTGTTGGCACATACT ACCCAGACTCCGTGAAGGACCGGTTCACCATCTCCAGAGACAGTTCCAAGAACACGGTG TATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGTGAAACA TGGTAGGGCCGGAATAAACTGGTACTTCGATCTCTGGGGCCGTGGCACCCTGGTGACCG TCTCCTCA
SEQ ID 173	CAGGTACAGCTGCAGCAGTCAGGTCCAGGACTGGTGAAGCCCTCGCAGACCCTCTCACT CACCTGTGCCATCTCCGGGGACAGTGTCTCTAGCAACAGTGCTGCTTGGAACTGGATCA GGCAGTCCCCATCGAGAGGCCTTGAGTGGCTGGGAAGGACATACTACAGGTCCAAGTGG TATAATGATTATGCAGTATCTGTGAAAAGTCGAATAACCATCAACCCAGACACATCCAA GAACCAGTTCTCCCTGCAGCTGAACTCTGTGACTCCCGAGGACACGGCTGTGTATTACTG TGCAAGAGGGGGAGGGCTTTGGGCTTTTGATATCTGGGGCCAAGGGACCACGGTCACCG TCTCCTCA
SEQ ID 174	GAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGT CTCCTGCAAGGCTTCTGGATACACCTTCACCGGCTACTATATGCACTGGGTGCGACAGGC CCCTGGACAAGGGCTTGAGTGGATGGGATGGATCAACCCTAACAGTGGTGGCACAAACT ATGCACAGAAGTTTCAGGGCAGGGTCACCATGACCAGGGACACGTCCATCAGCACAGCC TACATGGAGCTGAGCAGGCTGAGATCTGACGACACGGCCGTGTATTACTGTGCGAGAGA CAAGATCGGCAGCTGTCCTTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
SEQ ID 175	CAGGTCACCTTGAAGGAGTCTGGTCCTACGCTGGTGAAACCCACACAGACCCTCACGCT GACCTGCACCTTCTCTGGGTTCTCACTCAGCACTAGTGGAGTGGGTGTGGGCTGGATCCG TCAGCCCCCAGGAAAGGCCCTGGAGTGGCTTGCACTCATTTATTGGGATGATGATAAGC GCTACAGCCCATCTCTGAAGAGCAGGCTCACCATCACCAAGGACACCTCCAAAAACCAG GTGGTCCTTACAATGACCAACATGGACCCTGTGGACACAGCCACATATTACTGTGCACA CAGACCGGATAGCAGCAGTCAATGTTTTGACTACTGGGGCCAGGGAACCCTGGTCACCG TCTCCTCA
SEQ ID 176	CAGGTCACCTTGAAGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACT CTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGCTATGCACTGGGTCCGCCAGGC TCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACT ACGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTG TATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAG CAGTGGCTGGTCACTGCCTGAAGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCT CA
SEQ ID 177	CAGGTCCAGCTGGTACAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGT CTCCTGCAAGGTTTCCGGATACACCCTCACTGAATTATCCATGCACTGGGTGCGACAGGC TCCTGGAAAAGGGCTTGAGTGGATGGGAGGTTTTGATCCTGAAGATGGTGAAACAATCT ACGCACAGAAGTTCCAGGGCAGAGTCACCATGACCGAGGACACATCTACAGACACAGC CTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCAACGG ATGTGAACCCGGAGCTACTGGGGGCGGGATTTGACTACTGGGGCCAGGGCACCCTGGTC ACCGTCTCCTCA

SEQ ID 178	CAGGTCACCTTGAAGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGAGGGTCCCTGAGACT CTCCTGTGCAGCCTCTGGATTCACCTTCAGTGACCAGTACATGGACTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGGAGTGGGTTGGCCGTGTTAGAAACAAAGCTAACAGTTACACCA CAGAATACGCCGCGTCTGTGAAAGGCAGATTCACCATCTCAAGAGATGATTCAAAGAAC TCACTGTATCTGCAAATGAATAGTCTGAACACCGAGGACACGGCCATGTATTTCTGTGCT AGTAGTCTCAATAGTGGGGGCTACCGATGCTTCCATCACTGGGGCCAGGGCACCCTGGT GACCGTCTCCTCA
SEQ ID 179	CAGGTCCAGCTGGTGCAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACT CTCCTGTTCAGCCTCTGGATTCACCTTCAGTAGCTATGCTATGCACTGGGTCCGCCAGGC TCCAGGGAAGGGACTGGAATATGTTTCAGCTATTAGTAGTAATGGGGGTAGCACATACT ACGCAGACTCAGTGAAGGGCAGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTG TATCTTCAAATGAGCAGTCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGTGAAAGC GCCGAGGGGTGTAGTACCAGCTGCTATGCGGGGGGGCTACTGGGGCCAGGGAACCCTG GTCACCGTCTCCTCA
SEQ ID 180	CAGGTGCAGCTGCAGGAGTCGGGGGGAGGCTTGGTACAGCCAGGGCGGTCCCTGAGAC TCTCCTGTACAGCTTCTGGATTCACCTTTGGTGATTATGCTATGAGCTGGTTCCGCCAGG CTCCAGGGAAGGGGCTGGAGTGGGTAGGTTTCATTAGAAGCAAAGCTTATGGTGGGACA ACAGAATACGCCGCGTCTGTGAAAGGCAGATTCACCATCTCAAGAGATGATTCCAAAAG CATCGCCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTACTGTA CTAGATTGGTGGGCAATAGTGGGAGCTACTATCCGTTTGGGTACTGGGGCCAGGGAACC CTGGTGACCGTCTCCTCA
SEQ ID 181	CAGGTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCT CACCTGCGCTGTCTATGGTGGGTCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCC CCCAGGGAAGGGGCTGGAGTGGATTGGGGAAATCAATCATAGTGGAAGCACCAACTAC AACCCGTCCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTC CCTGAAGCTGAGCTCGGTGACCGCCGCGGACACGGCTGTGTATTACTGTGCGAGAGGCC GGTCCCTTCCCTACCGGGGGTTGGCTCCTAGATCTTTCGGAGGATACTACTTTGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
SEQ ID 182	CAGGTGCAGCTGCAGGAGTCGGGGGGAGGCTTGGTACGGCCTGGAGGGTCCCTGAGACT CTCCTGTGGAGACTCTGGATTCAACTTCAGTGGATATGAAATGAACTGGGTCCGCCAGG CTCCAGGGAAGGGGCTGGAGTGGGTTTCATACGTCAGTACTAGTGGTAGTACCAGATAC TACGCAGACTCTGTGAAGGGCCGATTTACCATCTCCAGAGACAACGCCAAGAACACCCT GTATTTGCAAATGAACAGTCTGAGAGTCGAGGACACGGCTGTGTATTACTGTGCAAGAG GACGGACTCACTGGGGCCCCCAGGACTTTGACTACTGGGGCCAGGGAACCCTGGTCACC GTCTCCTCA
SEQ ID 183	CAGGTGCAGCTGCAGGAGTCGGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACT CTCCTGTGCAGCCTCTGGATTCACCTTTAGCAGCTATGCCATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACT ACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTG TATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAAAGG AGGAATGTATTACTATGGTTCGGGGAGCTCGTACTTTGACTACTGGGGCCAGGGAACCC TGGTGACCGTCTCCTCA
SEQ ID 184	CAGGTGCAGCTGGTGCAATCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACT CTCCTGTGCAGCCTCTGGATTCACCTTTAGCAGCTATGCCATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGGAATGGGTCTCAGGTATTAGTGGTAGTGGTGGTAGCACATACT ACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACATGCTG TTTCTGCAAATGAACAGCCCGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAAGAA AATAGCAGCAGCTGGTAAGCAACCTGTTGACTACTGGGGCCAGGGAACCCTGGTCACCG TCTCCTCA
SEQ ID 185	CAGGTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCT CACCTGCGCTGTCTATGGTGGGTCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCC CCCAGGGAAGGGGCTGGAGTGGATTGGGGAAATCAATCATAGTGGAAGCACCAACTAC AACCCGTCCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTC CCTGAAGCTGAGCTCTGTGACCGCCGCGGACACGGCTGTGTATTACTGTGCGAGAAGGA AGGTGTATGATTACGTTTGGGGGAGTTATCGCCTCCCCGGGTCGGTATCGTACTACTTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA

SEQ ID 186	CAGGTCCAGCTGGTACAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCTCTGAAGA TCTCCTGTAAGGGTTCTGGATACAGCTTTACCAGCTACTGGATCGGCTGGGTGCGCCAGA TGCCCGGGAAAGGCCTGGAGTGGATGGGGATCATCTATCCTGGTGACTCTGATACCAGA TACAGCCCGTCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCACCGC CTACCTGCAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATGTATTACTGTGCGAGAC TCCCGGGGAGAGCAGCTCGTCCAGACTACTGGGGCCAGGGCACCCTGGTCACCGTCTCC TCA
SEQ ID 187	CAGGTCACCTTGAAGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACT CTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGCTATGCACTGGGTCCGCCAGGC TCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACT ACGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTG TATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGG CCCCGGGGCAGTGGCTGGTACTAAGCCAAAGTACTACTTTGACTACTGGGGCCAGGGAA CCCTGGTCACCGTCTCCTCA
SEQ ID 188	GAGGTCCAGCTGGTGCAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACT CTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGCTATGCACTGGGTCCGCCAGGC TCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACT ACGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTG TATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGGGC CACGTATTACTATGATAGTAGTGGTTATAGGTTTGACTACTGGGGCCAGGGAACCCTGGT CACCGTCTCCTCA
SEQ ID 189	GAGGTCCAGCTGGTACAGTCTGGGGGAGGCTTGGTAGAACCGGGGGGGTCCCTTAGACT CTCCTGTGCAGCCTCTCGATTCACTTTCAGTGACGCCTGGATGAGCTGGGTCCGCCAGGC TCCAGGTAAGGGGCTGGAGTGGGTTGGCCGTATTAAAAGCAAAATAAGTGGTGGGACA ACAGACTACGCTGCACCCGTGCAAGGCAGATTCACCATCTCAAGAGATGATTCAAAAAA CACGCTGTATCTGCAAATGGACAGCCTGAAAACCGAGGACACAGCCGTGTATTACTGTG CGAACCGAAACTTAGGCTACTGGGGCCAGGGCACCCTGGTGACCGTCTCCTCA
SEQ ID 190	GAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGT TTCCTGCAAGGCTTCTGGATACACCTTCACTAGCTATGCTATGCATTGGGTGCGCCAGGC CCCCGGACAAAGGCTTGAGTGGATGGGATGGATCAACGCTGGCAATGGTAACACAAAA TATTCACAGAAGTTCCAGGGCAGAGTCACCATGACCACAGACACATCCACGAGCACAGC CTACATGGAGCTGAGGAGCCTGAGATCTGACGACACGGCCGTGTATTACTGTGCGAGAG CTCGTTACTATGATAGTAGTGGTTATATTGCCCCATCGGGTTACTTTGACTACTGGGGCC AGGGAACCCTGGTCACCGTCTCCTCA
SEQ ID 191	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGT TTCCTGCAAGGCTTCTGGATACACCTTCACTAGCTATGCTATGCATTGGGTGCGCCAGGC CCCCGGACAAAGGCTTGAGTGGATGGGATGGATCAACGCTGGCAATGGTAACACAAAA TATTCACAGAAGTTCCAGGGCAGAGTCACCATTACCAGGGACACATCCGCGAGCACAGC CTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCTGTGTATTACTGTGCGAGAG ATGGCCCCGCCGTTGATGGTGCTGAATACTTCCAGCACTGGGGCCAGGGCACCCTGGTC ACCGTCTCCTCA
SEQ ID 192	CAGCTGCAGCTGCAGGAGTCGGGTCCAGGACTGGTGAAGCCCTCGCAGACCCTCTCACT CACCTGTGCCATCTCCGGGGACAGTGTCTCTAGCAACAGTGCTGCTTGGAACTGGATCA GGCAGTCCCCATCGCGAGGCCTTGAGTGGCTGGGAAGGACTTACTACAGGTCCAAGTGG TATAATGATTATGCAGTATCTCTGAAAAGTCGAATAACCATCAACCCGGACACATCCAA GAACCAGTTCTCCCTGCAGCTGAACTCTGTGACTCCCGAGGACACGGCTGTATATTACTG TGCAAGTTTGGCGAGTGGTTCCCCCCCTCCGGGGGACTACTGGGGCCAGGGAACCCTGG TGACCGTCTCCTCA
SEQ ID 193	CAGGTCACCTTGAAGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACT CTCCTGTGCAGCCTCTGGATTCACCTTCAGTACCTATGGCATGCACTGGGTCCGCCAGGC TCCAGGCAAGGGGCTGGAGTGGGTGGCACTTATATCATATGATGGAAGTAAAAAATACT ATGCAAACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGTTG TATCTGCAAATGAAAAGTCTGAGAGCTGAGGACACGGCTATGTATTACTGTGCGAAAGG CCCTATAGTGGGAGCGACTATGGACTACTGGGGCCAGGGAGCCCTGGTCACCGTCTCCT CA

SEQ ID 194	GAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGT CTCCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGG CCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCAGCGCTTACAATGGTAACACAAAC TATGCACAGAAGCTCCAGGGCAGAGTCACCATGACCACAGACACATCCACGAGCACAG CCTACATGGAGCTGAGGAGCCTGAGATCTGACGACACGGCCGTGTATTACTGTGCGAGA TGGTACGGTGACTACGGCCTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTC A
SEQ ID 195	GAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGT TTCCTGCAAGGCTTCTGGATACACCTTCACTAGCTATGCTATGCATTGGGTGCGCCAGGC CCCCGGACAAAGGCTTGCGTGGATGGGATGGATCAACGCTGGCAATGGTAACACAAAAT ATTCAGAGAAGTTCGAAGGCAGAGTCACCATCACCAGGGACACATCCGCGAGCACAGC CTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCTGTGTATTACTGTGCGAGGG TCGCCAAATATTATTACGAGAGTGGTGGTTATCGGGCCTCCAACTGGTTCGACCCCTGGG GCCAGGGCACCCTGGTCACCGTCTCCTCA
SEQ ID 196	CAGGTGCAGCTGCAGGAGTCAGGTCCAGGACTGGTGAAGCCCTCGCAGACCCTCTCACT CACCTGTGCCATCTCCGGGGACAGTGTCTCTAGCAACAGTGCTGCTTGGAACTGGATCA GGCAGTCCCCATCGAGAGGCCTTGAGTGGCTGGGAAGGACATACTACAGGTCCAAGTGG TATAATGATTATGCAGTATCTGTGAAAAGTCGAATAACCATCAACCCAGACACATCCAA GAACCAGTTCTCCCTGCAGCTGAACTCTGTGACTCCCGAGGACACGGCTGTGTATTACTG TGCAAGAGCGCCCCCTCCGACTGTTGGCTGGTACGCCCCCGTCTTTGACTACTGGGGCCA GGGAACCCTGGTCACCGTCTCCTCA
SEQ ID 197	CAGCTGCAGCTGCAGGAGTCCGGGGGAGGCTTAGTTCAGCCGGGGGGGTCCCTGAGACT CTCCTGCTCAGCCTCTGGAATCAGCTTCAGAGATTACTGGATGCACTGGATCCGCCAAAC TCCAGGGAAGGGGCTGGTGTGGGTCTCACGTATTAATCCTGATGGGAGTAGCACAAGCT ACGCGGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTG TATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGT TACGGGACGGAGAGTGGGAGCCCATGACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCA
SEQ ID 198	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGT CTCCTGCAAGGCTTCTGGATACACCTTCACCGGCTACTATATGCACTGGGTGCGACAGGC CCCTGGACAAGGGCTTGAGTGGATGGGATGGATCAACCCTAACAGTGGTGGCACAAACT ATGCACAGAAGTTTCAGGGCAGGGTCACCATGACCAGGGACACGTCCATCAGCACAGCC TACATGGAGCTGAGCAGGCTGAGATCTGACGACACGGCCGTGTATTACTGTGCCTTTGC CCAGCCGGGCGCTGAGACGTTGAACTTCGATCTCTGGGGCCGTGGCACCCTGGTCACCG TCTCCTCA
SEQ ID 199	CAGGTACAGCTGCAGCAGTCAGGTCCAGGACTGGTGAAGCCCTCGCAGACCCTCTCACT CACCTGTGCCATCTCCGGGGACAGTGTCTCTAGCAAAAGTGCTGCTTGGAACTGGATCA GGCAGTCCCCATCGAGAGGCCTTGAGTGGCTGGGAAGGACATACTACAGGTCCAAATGG AATAATGATTATGCATTATCTGTGAAAAGTCGAATAACCATCAACCCAGACACATCCAA GAACCAGTTCTCCCTGCAGCTGAAGTCTGTGACTCCCGAGGACACGGCTCTGTATTACTG TGTAAGACAAGTCGCGGGCGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCT CCTCA
SEQ ID 200	CAGGTGCAGCTGGTGCAATCTGGGGGAGGCTTGGTACAGCCAGGGCGGTCCCTGAGACT CTCCTGTACAGCTTCTGGATTCACCTTTGGTGATTATGCTATGAGCTGGTTCCGCCAGGC TCCAGGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACT ATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTG TATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGG ATCGGTATATAGTGGGAGCTACTATATGCTCATTGACTACTGGGGCCAGGGCACCCTGG TCACCGTCTCCTCA
SEQ ID 201	CAGGTACAGCTGCAGCAGTCAGGTCCAGGACTGGTGAGGCCCTCGCAGACCCTCTCACT CACCTGTGTCATCTCCGGGGACAGTGTCTCTAGCGGCAGTGCTGCTTGGAACTGGATCAG GCAGTCCCCATCGAGAGGCCTTGAGTGGCTGGGAAGGACATATTATAGGGCCAAGTGGT ATAATGAATATGCAGGGTCTGTGAAAAGCCGAATAACCATCAGTCCGGACACATCCAAG AACCAGTTCTCCCTGCAACTGAACTCTGTGACTCCCGAGGACACGGCTGTGTATTTCTGT ACAAGACAAGACAAAGACAACACGAGATATTCCGGTTTGGGCGTCTGGGGCCAAGGGA CCACGGTGACCGTCTCCTCA

SEQ ID 202	GAGGTGCAGCTGGTGGAGACCGGGGGAGGCTTAGTTCAGCCTGGGGGGTCCCTGAGACT CTCCTGTGCAGCCTCTGAATTCACCCTTAGGAACTATGGCGTGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGGAGTGGGTCTCAGGTATGAGTGGTAGTGGTTATAGTACATACT ACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAGTTCCAAGAACACGCTG TTTCTGCAAATGGACAGCCTGAGAGCCGAGGACACGGCCATATATTACTGTGCGAGAGG GCCCCGAATGTGGAGCAGTGGCATTGATGCTTTTGATATCTGGGGCCACGGGACAATGG TGACCGTCTCTTCA
SEQ ID 203	CAGGTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCT CACCTGCGCTGTCTATGGTGGGTCCGTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCC CCCAGGGAAGGGGCTGGAGTGGATGGGGGAAATCCATCATAGTGGAAGCACCAACTAC AACCCGTCCCTCAAGAGTCGAGTCACCATATCACTAGACACGCCCAAGAACCAGTTCTC CCTGAAGCTAAGCTCTGTGACCGCCGCGGACACGGCTGTATATTACTGTGCGAGACGGG ATTGGGCAGGAAAAAGGGTCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
SEQ ID 204	CAGGTACAGCTGCAGCAGTCAGGTCCAGGACTATTAAAGCCCTCGCAGACCCTCTCACT CACCTGTGCCATCTCCGGGGACAGTGTCTCTAGCAACACTGCTACTTGGAACTGGATCAG GCAGTCCCCATCGAGAGGCCTTGAGTGGCTGGGAAGGACATACTACAGGTCCAAGTGGT ATAAGGATAATGCACTGTCTGTGAAAAGTCGAATAACCATCAACCCAGACACATCCAAG AACCAGTTCTCCCTGCAGCTGAACTCTGTGACTCCCGAGGACACGGCTGTGTATTACTGT GCAGGAGGTCGGGCTGGTATTGCCGCTTTTGATATCTGGGGCCAAGGGACCACGGTCAC CGTCTCCTCA
SEQ ID 205	CAGGTGCAGCTGGTGCAATCTGGAGGAGGCTTGATCCAGCCTGGGGGGTCCCTGAGACT CTCCTGTGCAGCCTCTGGGTTCACCGTCAGTAGCAACTACATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGGAATGGGTCTCACTTATTTATAGTGATGGTCGCACAAACTATG CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT CTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAAGGGGG CCCTACAGGGCGAATGGCGGAGATTTGACTACTGGGGCCAGGGCACCCTGGTCACCGTC TCCTCA
SEQ ID 206	CAGGTGCAGCTACAGCAGTCAGGTCCAGGACTGGTGAAGCCCTCGCAGACCCTCTCACT CACCTGTGCCATCTCCGGGGACAGTGTCTCTAGCAACAGTGCTGCTTGGAACTGGATCA GGCAGTCCCCATCGAGAGGCCTTGAGTGGCTGGGAAGGACATATTACAGGTCCAAGTGG TATAATGATTATGCAGTATCTGTGAAAAGTCGAATAACCATCAACCCAGACACATCCAA GAACCAGTTCTCCCTGCAGCTGAACTCTGTGACTCCCGAGGACACGGCTGTGTATTACTG TACAAGAACCAACCAGGGATACGGTGGTAACTCCGGGGTATTTGACTACTGGGGCCAGG GAACCCTGGTCACCGTCTCCTCA
SEQ ID 207	CAGGTGCAGCTACAGCAGTCAGGTCCAGGACTGGTGAAGCCCTCGCAGACCCTCTCACT CACCTGTGCCATCTCCGGGGACAGTGTCTCTGGCAACAGTGCTGCTTGGAACTGGATCA GGCAGTCCCCATCGAGAGGCCTTGAGTGGCTGGGAAGGACATACTACAGGTCCAAGTGG TATAATGATTATGCAGTATCTGTGAAAAGTCGAATAACCATCAACCCAGACACATCCAA GAACCAGTTCTCCCTGCAGTTGAATTCTGTGACTCCCGAGGACACGGCTGTGTATTACTG TGCGAGGATAGTGGGAGGTGCCGTTGACTGCTGGGGCCAGGGAACCCTGGTGACCGTCT CCTCA
SEQ ID 208	GAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGG TTTCCTGCAAGGCTTCTGGATACACCTTCACTAGCTATGCTATGCATTGGGTGCGCCAGG CCCCCGGACAAAGGCTTGAGTGGATGGGATGGATCAACGCTGGCAATGGTAACACAAA ATATTCACAGAAGTTCCAGGGCAGAGTCACCATTACCAGGGACACATCCGCGAGCACAG CCTACATGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCTGTGTATTACTGTGCGAGA GTTAGAGTGGGAGCTACTACTGTTTACGACAGCTGGTTCGACCCCTGGGGCCAGGGAAC CCTGGTGACCGTCTCCTCA
SEQ ID 209	CAGGTGCAGCTGGTGCAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACT CTCCTGTGCAGCCTCTGGATTCACCTTTAGCAGCTATGCCATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACT ACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTG TATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAAAGA TGGGGGGTCCAGCCCATACTATGATAGTAGTGGTTTACTACCCTGGTACTTCGATCTCTG GGGCCGTGGCACCCTGGTCACCGTCTCCTCA

SEQ ID 210	CAGGTGCAGCTGCAGGAGTCGGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACT CTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGCTATGCACTGGGTCCGCCAGGC TCCAGGGAAGGGACTGGAATATGTTTCAGCTATTAGTAGTAATGGGGGTAGCACATATT ATGCAAACTCTGTGAAGGGCAGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTG TATCTTCAAATGGGCAGCCTGAGAGCTGAGGACATGGCTGTGTATTACTGTGCGAGAGC TAAGTTTTGGACATACTACTTTGACTACTGGGGCCAGGGAACCCTGGTGACCGTCTCCTC A
SEQ ID 211	CAGGTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCT CACCTGCGCTGTCTATGGTGGGTCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCC CCCAGGGAAGGGGCTGGAGTGGATTGGGGAAATCAATCATAGTGGAAGCACCAACTAC AACCCGTCCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTC CCTGAAGCTGAGCTCTGTGACCGCCGCGGACACGGCTGTGTATTACTGTGCGAGAGGCG GTGGTTCGGGGAGTTATTATAAGAGGTTCTTTGACTACTGGGGCCAGGGAACCCTGGTC ACCGTCTCCTCA
SEQ ID 212	GAGGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGAGGAAGCCTGGGGCCTCAGTGAAGG TCTCCTGCAAGGCTTCTGGTTACACATTTACCAGTTATGCCATCAGCTGGGTGCGACAGG CCCCTGGACAAGGGCTTGAGTGGATGGGGTGGATCAGCGCTTACGACGGTAACACAAAC TATGCACAGAAGCTCCAGGGCAGAGTCACCATGACCACAGACACATCCACGAGCACAG CCTACATGGAGGTGAGGAGCCTGAGATCTGACGACACGGCCGTGTATTACTGTGCGAGA GATGGTACGGTCCGAAGGGTAGTGGGAGCTACTACCCCTGGAAACTTTGACTACAGGGG CCAGGGAACCCTGGTCACCGTCTCCTCA
SEQ ID 213	GAGGTGCAGCTGGTGCAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACT CTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGC TCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACT ATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTG TATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGA TCTGAATCGAGGATATTGTAGTGGTGGTAGCTGCTTTGGCTACTGGGGCCAGGGAACCC TGGTCACCGTCTCCTCA
SEQ ID 214	CAGGTGCAGCTGCAGGAGTCTGGGGGAGGCTTGGTACAGCCGGGGGGGTCCCTGAGACT CTCCTGTGCAGCCTCTGGATTCACCTTTAGCAGCTATGCCATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGGAGTGGGTTTCATACATTAGTAGTAGTGGTACTACCATATACT ACGCAGACTCTGTGAAGGGCCGATTCACCGTCTCCAGAGACAATGCCAAGAACTCACTG TATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGGGA TTATAGCAGCTCGGGGGAGTGCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCA
SEQ ID 215	GAGGTGCAGCTGGTGCAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACT CTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGC TCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACT ATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTG TATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGA TCAGGCAGCTATGGTAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCA
SEQ ID 216	CAGGTCACCTTGAAGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACT CTCCTGTGCAGCCTCTGGATTCATCTTCAGTAACTATGCTATACACTGGGTCCGCCAGGC TCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACT ACGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTG TATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGGAC TTTTGCGGGGTATAGCAGCAAACTGGGGTACTTCGATCTCTGGGGCCGTGGCACCCTGGT CACCGTCTCCTCA

[167] Exemplary VL amino acid sequences of CLEC2D antibodies of the disclosure are shown in Table 4 below. VL amino acid sequences having at least 50% identity, at least 55% identity, at least 60% identity, at least 65% identity, at least 70% identity, at least 75% identity, at least 80% identity, at least 85% identity, at least 90% identity, at least 91% identity, at least 92% identity,

at least 93% identity, at least 94% identity, at least 95% identity, at least 96% identity, at least 97% identity, at least 98% identity, at least 99% identity, at least 99.5% identity, at least 99.8% identity, at least 99.9% identity or 100 % identity to the sequences listed in Table 4 are considered within the scope of the disclosure.

Table 4. VL Amino Acid Sequences

SEQ ID	VL Amino Acid Sequence
SEQ ID 217	ETTLTQSPATLSVSLGERATLSCRASQSIGSNLVWYQLKPGQGPRLVIYSATSRATGIPARFSGSG SGTEFILSISNLQSEDLAVYYCQQYGSSPPTTFGQGTRLEIKR
SEQ ID 218	EIVMTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGRAPRLLIYGASNRATGIPDRFSGS GSGTDFTLIISRLEPEDFALYYCQQYGSSPGTFGQGTKVDIKR
SEQ ID 219	DVVMTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRSNWPRTFGQGTKLEIKR
SEQ ID 220	EIVLTQSPDSLAVSLGERATITCKSSRNILYSGNNKNFLAWYQHKPGQPPKLLIYWASTRESGVP DRFSGSGSGTDFTLTINSLEAEDAATYYCHQSSSLPHTFGPGTKVDIKR
SEQ ID 221	ETTLTQSPGTLSLSPGQRATLSCRASESVSKSYLLWYQQKPGQAPRLLIYGASTRASGIPNRFSGS GSGTDFTLTISRLEPEDSAVYYCQHYGSSRTFGQGTRLEIKR
SEQ ID 222	ETTLTQSPGTLSLSPGERATLSCRASQSISSTYLAWYQQKPGQAPRLLIYGASTRATGIPDRFSGS GSGTDFTLSISRLEPEDFAVYYCQQYGNSPPGATFGQGTRLEIKR
SEQ ID 223	DIQLTQSPSSLSASVGERVTITCRSSQALRNVVGLGDDLAWYQHTPGSAPKILIYSTSTLQSGVSS RFSGGKSGRDFTLTIDRLQPGDSATYYCLQHHDFPFTFGPGTKVEIKR
SEQ ID 224	DVVMTQSPLSLPVTPGEPASISCRSSQSLLNSNGYNYLEWYLQKPGQSPQLLIYLGSNRASGVPD RFSGSGSGTDFTLKISRVEADDAGVYYCMQSLQTPLTFGGGTKLEIKR
SEQ ID 225	ETTLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQYGSSPRITFGQGTRLEIKR
SEQ ID 226	DVVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPARFSGS GSGTEFTLTISSLQSEDFAVYYCQQYNNWPPMYTFGQGTKLEIKR
SEQ ID 227	DVVMTQSPATLSVSPGERVTLSCRASQSVRDNVGWYKQKPGQPPRLVIYGASTRATGIPARISG SGSGTEFTLTISSLQSEDFAVYYCQQFNNWPYTFGQGTKLEIKR
SEQ ID 228	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPNLLIYAASSLHTGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSYSIPRTFGQGTKVEIKR
SEQ ID 229	DVVMTQSPATLSVTPGERATLSCRASQSVNSNVAWYQQKPGQAPRLLIYDVSTRATDIPARFSG SGSGTDFTLTISRLDPEDFAVYYCQQCASSPPVTFGGGTKLEIKR
SEQ ID 230	EIVMTQSPATLSLSPGERATLSCGASQSVSSSYLAWYQQKPGLAPRLLIYDASSRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQYGSSPRVTFGGGTKVDIKR

SEQ ID 231	DVVMTQSPGTLSLSPGERATLSCRASQSVSSSALAWFQQKPGQAPRLLIYDSSSRATGIPDSFSGS GSGTEFTLTISSLQPEDFATYYCQQFNTYPNTFGQGTKLEIKR
SEQ ID 232	DIQMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWFLQKPGQSPRLLIYMGSSRASGVPER FSGSGSGTDFTLKISRVEAEDVGVYYCMQTLHTVTFGGGTKVEIKR
SEQ ID 233	ETTLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQYGSSLLFGQGTRLEIKR
SEQ ID 234	DIQLTQSPSFLSASVGDRVTITCRASQGISSSLAWYQQKPGKAPKLLIYAASTLQSGVPSRFSGSG SGTDFTFTISSLQPEDIATYYCQQYDNLPPLTFGGGTKVEIKR
SEQ ID 235	DVVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPD RFSGSGSGTDFTVKISRVEAEDVGVYYCMQALQTPYTFGQGTKLEIKR
SEQ ID 236	EIVLTQSPLSLPVTLGQPASISCRSCQSLVYSDGNTYLNCFQQRPGQSPRRLIYKVSNRDSGVPDR FSGSGSGTDFTLEISRVEAEDVGIYFCMQGLQTPFTFGPGTKVDIKR
SEQ ID 237	DVVMTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSG SGSGTDFTLTISRLEPEDFAVYYCQQYGSSPALTFGGGTKLEIKR
SEQ ID 238	EIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSTRASGVPDR FSGSGSGTDFTLKISRAEAEDVGVYYCMQALHTPWTFGLGTKVDIKR
SEQ ID 239	DIQMTQSPATLSVSPGERATLFCRASEGLTTNLAWYQHKPGQAPRLLIYAASTRATGVPARFSG SGSGTDFTLTISSLQSEDSAVYYCQQYNHWPLYTFGQGTKVEIKR
SEQ ID 240	DIQLTQSPSTLSLSPGERATLSCRASQSVSSYLAWYQQKSGQAPRLLIYDASNRATGIPARFSGSG SGTDFTLTISSLEPEDFAVYYCQQGSNWPLTFGGGTKVEIKR
SEQ ID 241	DIVMTHTPLSSPVTLGQPASISCRSSQSLEHTDGNTYLSWLHQRPGQPPRLLIYKVSTRFSGVPDR FSGSGAGTDFTLKISRVEAEDVGVYYCVQATHYPRTFGHGTKVEIKR
SEQ ID 242	EIVLTQSPGTLSLSPGERATLSCRASQSISGSYLAWYQQKRGQAPRLLIYDASSRAEGIPDRFIGSG SGTDFTLTISRLEPEDFAMYYCQQYGSSPIFTFGPGTKVDIKR
SEQ ID 243	EIVLTQSPDSLPVTPGEPASISCRSSQSLLHSNGNNYLDWYLQKPGQSPQLLIYLGSNRASGVPDR FSGSGSGTDFTLKLSRVEAEDVGVYYCMQGLQIPITFGPGTKVDIKR
SEQ ID 244	DIQMTQSPSSVSASVGDRVTITCRASQNIRHWLVWYQQKLGQAPKLLIYAASNLQSGVPSRFSG SGSGTEFTLTINSLQAEDFATYYCLQHNSYPWTFGQGTKVEIKR
SEQ ID 245	EIVLTQSPDFQSVTPKQKVTITCRASQSIGGSLHWYQQKPGQSPKLIIKYASQSFSGVPSRFSGSGS GTDFTLTIDSLEAEDAATYYCHQSISLPLTFGGGTKVDIKR
SEQ ID 246	ETTLTQSPGTLSLSPGEGATLSCRASQSVTSNYLAWYQQKPGQAPRLLIYGASYRATGIPDRFSG SGSGTDFTLTISRLEPEDFAVYYCQQYASSVTFGQGTRLEIKR
SEQ ID 247	DVVMTQSPATLSVSPGERATLSCRASQSISSNLAWYQQKPGQAPRLLIYGASTRATGIPARFSGS GSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKLEIKR
SEQ ID 248	DIQLTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASARESGV PDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQFYSPPRTFGQGTKVEIKR

SEQ ID 249	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQYGSSPPGTFGGGTKVDIKR
SEQ ID 250	EIVLTQSPGTLSLSPGERATLSCRASQSLSTNLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSG SGTEFTLTITSLQSEDFAVYYCQQYHNWPPYTFGQGTKVEIKR
SEQ ID 251	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYKASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQYNSYWTFGQGTKVEIKR
SEQ ID 252	ETTLTQSPGTLSLSPGEGATLSCRASHSVGANYIAWYQQKPGQAPRLLIHTASKRATGVPERFSG SGSGTDFTLSISRLEPEDFAVYHCQQYAAAPITFGQGTRLEIKR
SEQ ID 253	EIVMTQSPSSLSASVGDRVIITCRASQGIANYLAWYQQKPGKGPKLLIYASSTLQSGVPSRFSGSG SGTDFTLTISGLQPEDVATYYCQKYNSVPLTFGGGTKVDIKR
SEQ ID 254	DVVMTQSPVSLAVSLGERATINCKSSQSVLYRTNNKNYLAWYQQKPGQPPKLLIYWASTRESG VPDRFSGSGSGTDFTLTISSLQPEDVAVYYCQQYYNLPRSFGQGTKLEIKR
SEQ ID 255	DIVMTHTPDSLAVSLGERATINCKSNRSVLYSPNNQNYLGWYQQKPGQPPKLLIYWASTRDSG APDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYASTPYTFGQGTKVEIKR
SEQ ID 256	DVVMTQSPATLSLSPGERATLSCRASESVNSNFLAWYQQKPGQAPRLLIYAASTRATGIPARFSG SGSGTEFTLIITSLQSEDFAVYYCQQYNNWPLTFGGGTKLEIKR
SEQ ID 257	DVVMTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRSNWSLTFGGGTKLEIKR
SEQ ID 258	ETTLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASTRATGIPDRFSGS GSGTDFTLTIGRLEPEDFAVYYCQHYGPSRRITFGQGTRLEIKR
SEQ ID 259	ETTLTQSPDTLSVSPGGRATLSCRASQSIGSNLAWYQQKPGQSPRLLIYDASTRATGIPARFSGSG SGTEFTLTISSLESEDFVLYYCQQHGEWPTFGQGTRLEIKR
SEQ ID 260	DVVMTQSPATLSLSPGERATLSCRASQSVGNSLAWYQQKPGQAPRLLIYDASNRATGIPARFSG SGSGTDFTLTITSLEPEDFAIYYCQQRGTWPPLTFGGGTKLEIKR
SEQ ID 261	DVVMTQSPSSLSASVGDTVTITCRASQSITNWLAWYQQKPGKAPKRLIYGASSLQSGVPSRFSGS GSGTEFTLTISSLQPEDFATYYCQQYTNYPRTFGQGTKLEIKR
SEQ ID 262	DIQMTQSPSTLSASVGDRVTITCRARQSISNRLAWYQQKPGRAPNVLIYKASTLANGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQYQSYWTFGPGTKVEIKR
SEQ ID 263	DIQLTQSPATLSLSPGERATLSCKASQSVSSYLAWYQQKLGQAPRLLIYDASNRATGIPARFSAS GSGTDFTLTISSLQPEDVATYYCQKYNSPPRTFGQGTKVEIKR
SEQ ID 264	ETTLTQSPGTLSLSPGERVSLSCRASQNVYSNFLAWYQQRPGQAPSLLIYGASSRAAGVPDRFSG SGSGTDFALTISRVEPEDFAVYYCQQYGTSPITFGQGTRLEIKR
SEQ ID 265	EIVLTQSPRSSPVTLGQPASISCRSSQSLEHGDGNTYLSWLQQRPGQPPRLLIYKVSNRLSGVPDR FSGSGAGTDFTLKISRVEAEDVGVYYCMQGIYWPRTFGQGTRLEIKR
SEQ ID 266	ETTLTQSPVTLSLSPGDRATLSCRASQSVSSTSLAWYQHKPGQAPRLLIYGASRRATGIPDRFSGS GSGTDFTLTINRLEPEDFAVYYCQHYGSSPPITFGQGTRLEIKR

SEQ ID 267	ETTLTQSPATLSVSPGERATLSCRASQSVGSKLAWYQQKPGQAPRLLIYGASTRATGVPVRFSGS GSGTEFTLTISSLQSEDFAVYYCQQYNNWPPITFGQGTRLEIKR
SEQ ID 268	EIVLTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDR FSGSGSGTDFTLKISRVEAEDVGVYYCMQTLQTPLTFGGGTKVDIKR
SEQ ID 269	DVVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESG VPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSSTPYTFGQGTKLEIKR
SEQ ID 270	DIVMTHTPLSLSVTPGQPASISCKSSQSLLGGDGKTYLYWYLQKPGQPPQLLLYEVSNRFSGVPD RFSGSGAATDFTLKISRVEAEDVGVYYCMQSTQFPWTFGQGTKVEIKR
SEQ ID 271	ETTLTQSPGTLSLSAGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYAASYRATGIPDRFSG RGSGTEFTLTISSLQSEDFAVYYCQQYNNWPPITFGQGTRLEIKR
SEQ ID 272	DVVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYDASTRATGIPARFSGS GSGTEFTLTISSLQSEDFAVYYCQHYNNWPHTFGQGTKLEIKR
SEQ ID 273	ETTLTQSPGTLSLSPGERATLSCRASQSVSSNSLAWYQQKPGQAPRLLIYGASSRASGIPDRFNGS GSGTDFTLTINRLEPEDFAVYYCQQYGNSQTFGQGTRLEIKR
SEQ ID 274	DVVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPARFSGS GSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKLEIKR
SEQ ID 275	DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWFQQRPGQSPRRLIYKVSNRDSGVP DRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWPRTFGGGTKLEIKR
SEQ ID 276	DIQMTQSPSTLSASVGDRVTITCRASQSISRWLAWYQQKPGKAPKLLIYKASTIKSGVPSRFSAS GSGTEFTLTISSLQPEDFATYYCQHYKSDSRTFGQGTKVEIKR
SEQ ID 277	DVVMTQSPSSLAASVGDRITITCRPSQDIGTYLNWYQQKAGEAPKLLIYAASNLHSGVSSRFRG VGSGTQFTLTISSLQPEDFATYYCHQSYGPRTFGQGTKLEIKR
SEQ ID 278	ETTLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPARFSGS GSGTEFTLTISSLQSEDFAVYYCQQYNNWPPITFGQGTRLEIKR
SEQ ID 279	DVVMTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSG SGSGTDFTLTISRLEPEDFAVYYCQQYGSSGYTFGQGTKLEIKR
SEQ ID 280	ETTLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQYGSSFGQGTRLEIKR
SEQ ID 281	EIVLTQSPSTLSASVGDRVTITCRASQSISSCLAWYQQKPGKAPKLLIYAASTLQSGVPSRFSGSG SGTEFTLTISTLQPEDFATYYCQQLNSYPQTFGQGTKVDIKR
SEQ ID 282	DIVMTHTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLYWYLQKPGQPPQLLIYEVSNRFSGVPD RFSGSGSGTDFTLKISRVEAEDVGVYYCMQSIQLPLTFGGGTKVEIKR
SEQ ID 283	DVVMTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSG SGSGTDFTLTISRLEPEDFAVYYCQQYNNWPLTFGGGTKLEIKR
SEQ ID 284	DIQLTQSPDSLAVSLGERATINCTSSQSVLYSSNNKNYIAWYQQKPGQPPKLLIYWASTRESGVP DRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYYIPRTFGQGTKVEIKR

SEQ ID 285	DVVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRAPGVPD RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTRTFGQGTKLEIKR
SEQ ID 286	ETTLTQSPGTLSLSPGERATLSCRASQSLTSSYLAWYQQKPGQAPRLLIYRASSRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQYGSSPNTFGQGTRLEIKR
SEQ ID 287	EIVLTQSPLSLPVTLGQPASISCRSSQSLVHSNGHTYLSWFQQRPGQSPRRLIYEVSNRDSGVPDR FSGSGSGTDFTLRISRVEAEDVGVYYCLQGTHWPPLTVGGGTKVDIKR
SEQ ID 288	DVVMTQSPATLSLSPGERATLSCRASQSVGSDLAWYQQKPGQAPRLLIYRASTRAAGIPARFSG SGSGTDFTLTISRLEPEDFAVFYCQQYGRSPYTSGQGTKLEIKR
SEQ ID 289	DIVMTHTPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGV PDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPLTFGGGTKVEIKR
SEQ ID 290	EIVMTQSPLSLSVTPGEPASISCRSSQSLLHSSGYNYLDWYLQKPGQSPQLLIYLGSTRASGVPDR FSGSGSGTDFTLKISRVEAEDVGVYYCMQGLQIPLTFGGGTKVDIKR
SEQ ID 291	DIVMTHTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLYWYLQKPGQPPQLLIYEVSNRFSGVPD RFSGSGSGTDFTLKISRVEAEDVGVYYCMQSIQLPWTFGQGTKVEIKR
SEQ ID 292	ETTLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPARFSGS GSGTEFTLTISSLQSEDFAVYYCQQYNNWPRFGQGTRLEIKR
SEQ ID 293	DVVMTQSPSTLSASVGDRVTITCRASQTINSWLAWYQQKPGKAPKLLISRASRLESGVPSRFSGS ASGTEYILTINSLQPDDFAMYFCHQYNSYSPTFGQGTKLEIKR
SEQ ID 294	ETTLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRYNWPITFGQGTRLEIKR
SEQ ID 295	EIVLTQSPATLSLSPGETATLSCRASQTIGPKSFGWYQQRPGQAPRLLIYDSNRATGIPARFSGSGS GTDFTLTISSLEPEDFAVYYCQQRSRWPLTFGPGTKVDIKR
SEQ ID 296	DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLYWFQQRAGQSPRRLIYKVSKRDSGVP DRFSGSGSGTDFTLKISRVEAEDVGIYYCVQGRHWPYTLGQGTKLEIKR
SEQ ID 297	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTEFTLTISSLQPDDFATYYCQQYNSYSRTFGQGTKVDIKR
SEQ ID 298	DVVMTQSPSTLSASVGDRVTITCRASQSITTWLAWSQQQPGKAPKLLIYKASSLTSGVPSRFSGS GSGTEFTLTISSLQPDDFASYYCHHYNGASRMFGQGTKLEIKR
SEQ ID 299	ETTLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRSNWPFFGQGTRLEIKR
SEQ ID 300	ETTLTQSPATLTLSPGERVTLSCRASQSIGTYVAWYQQKPGQAPRFLIYDSSNRATGIPARFSGSG SGTDFTLTISSLEPEDFAFYYCQQRAEWPLTFGQGTRLEIKR
SEQ ID 301	DVVMTQSPGTLSLSPGERATLSCRASQSVNSGYLAWYQQKPGQPPRLLISGVSTRATGIPDRFSG SGSGTDFTLTISRLEPEDFAVYYCQEYGNSAMYNFGQGTKLEIKR
SEQ ID 302	ETTLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPARFSGS GSGTEFTLTISSLQSEDFAVYYCQQYNNWPPFTFGQGTRLEIKR

SEQ ID 303	DVVMTQSPGTLSLSPGERATLSCRASQSVSSSYLGWYQQKSGQAPRLLIYGASSRATDIPDRFSG SGSGTDFTLTISKLEAEDSAVYYCQQYGISPLAFGQGTKLEIKR
SEQ ID 304	ETTLTQSPATLSVSPGERATLSCRASQSISNNLAWYQQKPGQAPRLLIYGTSTRATGIPARFSGSG SGTEFTLTISSLQSEDFAVYYCQQYNFWPSITFGQGTRLEIKR
SEQ ID 305	ETTLTQSPGTLSLSPGERATLSCRASQSVSSSSLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQYGSSQTFGQGTRLEIKR
SEQ ID 306	DVVMTQSPLSLPVSLGQPASISCRSNQSLVYSDGGTYLNWFQQRAGQSPRRLVYKVSNRDSGVP DRFSGSGSGTDFTLRISRVEAEDVGVYYCMQGTHWPYTFGQGTKLEIKR
SEQ ID 307	DIQLTQSPSSLSASVGDRVTVTCRASQSISSYLNWYQQKPGKAPQLLIYDASNLETGVPSRFSGS GSGTDFTFTISSLQPEDFATYYCQQFDNVPVTFGGGTKVEIKR
SEQ ID 308	EIVLTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWFQQRPGQSPRRLIYKVSNRDSGVPDR FSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWPRTFGQGTKLEIKR
SEQ ID 309	DVVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGS GSGTDFTLTINRLEPEDFAVYYCQQYGSSSMYTFGQGTKLEIKR
SEQ ID 310	DVVMTQSPSSLSASVGDSVAITCRASQSISNYLNWYQQRPGKAPKLLIFAASSLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYSCQQSYITPWTFGQGTKLEIKR
SEQ ID 311	DVVMTQSPGTLSLSPGERATLSCRASQSVSTLLAWYQQKPGQAPRLLIYDASNRATGIPGRFSAS GSGTDFSLTISSLETEDSAVYYCQHRYVWPFTFGGGTKLEIKR
SEQ ID 312	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYGASSLQSGVPSRFSGS GSGTEFTLTIRSLQPEDFATYYCLQHNSYPRTFGQGTKVEIKR
SEQ ID 313	DVVMTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGS GSGTDFTLTISSLEPEDFAVYYCQQRSNWPWTFGQGTKLEIKR
SEQ ID 314	DVVMTQSPLSLPVTLGQAASISCRSSHSLTTTDGRTYVAWFQQRPGQSPRRLLYEVSKRDSGAP DRFSGSGSGTDFTLKISRVEADDVGIYHCMQGTHGPHTFGQGTKLEIKR
SEQ ID 315	ETTLTQSPATLSVSPGERATLSCRASQSVTSNLAWYQQKPGQAPRLLIYGASNRATGIPARFSVS GSGTDFTLTISRLEPEDFAVYYCQQYGSPPPTTFGQGTRLEIKR
SEQ ID 316	DVVMTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSG SGSGTDFTLTISRLEPEDFAVYYCQQYGSSRRTFGQGTKLEIKR
SEQ ID 317	ETTLTQSPGTLSLSPGERATLSCRASQSVFNNYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSG GGSGTDFTLTISRLEPEDFAVYCCQQYGSSPITFGQGTRLEIKR
SEQ ID 318	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSG SGTDFTLTISRLEPEDFAVYYCQQYGSSLRYTFGQGTKLEIKR
SEQ ID 319	EIVLTQSPDSLAVSLGERATINCKSSQSVLYDSNSKNYLSWYQQKPGQPPKLLISWASTRGSGVP DRFSGSGSGTDFTLTISSLQAEDVAVYYCQQFYGIPHFGQGTRLEIKR
SEQ ID 320	DVVMTQSPATLSLSPGERATLSCRASQSVGTNLAWYQQKPGQAPRLLIYDASNRATGIPARFSG SGSGTEFTLTISSLQSEDFAVYYCQQYNNWPPITFGGGTKLEIKR

SEQ ID 321	DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLSWLQQRPGQPPRLLIYKISNRFSGVPDR FSGSGAGTDFTLKISRVEAEDVGVYYCMQGTQFPQTFGQGTKLEIKR
SEQ ID 322	EIVLTQSPGTLSLSPGERATLSCRASQSVISRYLAWYQQKPGQAPRLLIHGASTRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQYGSSPPYTFGQGTKVEIKR
SEQ ID 323	DIQLTQSPSTLAASVGDRVTITCRASQSISSWLAWYQQKPGKAPKVLIYKASSLESGVPSRFSGS GSGTEFTLTISSLQPDDFATYYCQQYNSYSGTFGQGTKVEIKR
SEQ ID 324	DVVMTQSPAILSVSPGERATLSCRASQSVSSSLAWYQQKPGQPPRLLIYGASTRATAIPARFSGS GSGTEFTLTISSLQSEDFAVYYCQRYDNWPPLFGQGTKLEIKR

[168] A VL amino acid sequence of the disclosure may be encoded by a polynucleotide shown in Table 5 below.

Table 5. VL DNA Sequences

SEQ ID	**VL DNA Sequence**
SEQ ID 325	GAAACGACACTCACGCAGTCTCCAGCCACCCTATCTGTGTCTCTAGGAGAAAGAGCCACCC TTTCTTGCAGGGCCAGTCAGAGTATTGGCAGCAACTTAGTCTGGTACCAGCTGAAACCTGGC CAGGGTCCCAGGCTCGTCATATATAGTGCAACCTCTAGGGCCACTGGAATCCCAGCCAGGT TCAGCGGCAGTGGGTCTGGGACAGAGTTCATTCTCTCCATCAGCAACCTGCAGTCTGAAGAT CTTGCAGTTTATTACTGTCAGCAGTATGGTAGTTCACCTCCGACCACCTTCGGCCAAGGGAC ACGACTGGAGATTAAACGT
SEQ ID 326	GAAATTGTGATGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCCTGGTACCAGCAAAAACCT GGCCGGGCTCCCAGGCTCCTCATCTATGGCGCATCCAACAGGGCCACAGGCATCCCAGACA GGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCATCATCAGCAGACTGGAGCCTGA AGATTTTGCCTTGTATTACTGTCAGCAGTATGGAAGCTCACCGGGAACGTTCGGCCAAGGG ACCAAAGTGGATATCAAACGT
SEQ ID 327	GATGTTGTGATGACTCAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCTACTTAGCCTGGTACCAACAGAAACCTGGC CAGGCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGAAGAT TTTGCAGTTTATTACTGTCAGCAGCGTAGCAACTGGCCTCGGACGTTCGGCCAAGGGACCAA GCTGGAGATCAAACGT
SEQ ID 328	GAAATTGTGTTGACGCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCAT CACCTGCAAGTCCAGCCGGAATATTTTATACAGCGGCAACAATAAAAACTTCTTGGCTTGGT ATCAGCACAAACCAGGACAGCCTCCTAAGTTGCTCATTTACTGGGCATCTACCCGGGAATCC GGGGTCCCTGACCGATTTAGTGGCAGCGGGTCTGGGACAGATTTCACCCTCACCATCAATA GCCTGGAAGCTGAAGATGCTGCAACGTATTACTGTCATCAGAGTAGTAGTTTACCTCACACT TTCGGCCCTGGGACCAAAGTGGATATCAAACGT
SEQ ID 329	GAAACGACACTCACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGCAAAGAGCCACCC TCTCCTGCAGGGCCAGTGAGAGTGTTAGCAAGAGCTACTTACTCTGGTACCAGCAGAAACC TGGCCAGGCTCCCAGACTCCTCATCTATGGTGCATCCACCAGGGCCAGTGGCATCCCAAAC AGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTG AAGATTCTGCAGTGTATTACTGTCAGCACTATGGCAGCTCTCGCACCTTCGGCCAAGGGACA CGACTGGAGATTAAACGT
SEQ ID 330	GAAACGACACTCACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCC TCTCCTGCAGGGCCAGTCAGAGTATTAGCAGCACCTACTTAGCCTGGTACCAGCAGAAACC TGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGCATCCCAGACA GGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCAGCATCAGCAGACTGGAGCCTGA

	AGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAACTCACCTCCGGGAGCCACCTTCGGCC AAGGGACACGACTGGAGATTAAACGT
SEQ ID 331	GACATCCAGTTGACCCAGTCTCCTTCCTCCCTGTCTGCATCTGTGGGAGAAAGAGTCACCAT CACTTGCCGGTCCAGCCAGGCCCTGCGAAATGTTGTCGGCCTTGGCGATGATTTAGCCTGGT ATCAACACACGCCAGGCAGCGCCCCCAAGATCCTGATCTACTCTACATCGACTTTACAAAGT GGAGTCTCATCAAGATTCAGCGGCGGAAAGTCTGGGAGAGACTTCACTCTCACGATCGATC GTCTGCAGCCTGGAGATTCTGCAACTTATTACTGTCTCCAGCACCATGATTTCCCTTTCACTT TCGGCCCTGGGACCAAGGTGGAAATCAAACGT
SEQ ID 332	GATGTTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCAT CTCCTGCAGGTCTAGTCAGAGCCTCCTGAATAGTAATGGATACAACTATTTGGAGTGGTACC TGCAGAAGCCGGGGCAGTCTCCACAGCTCCTGATCTATTTGGGTTCTAATCGGGCCTCCGGG GTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAG TGGAGGCTGACGATGCTGGTGTTTATTACTGCATGCAGTCTCTACAAACTCCTCTCACTTTC GGCGGTGGGACCAAGCTGGAGATCAAACGT
SEQ ID 333	GAAACGACACTCACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCC TCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACC TGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGAC AGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTG AAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCACCCCGGATCACCTTCGGCCAA GGGACACGACTGGAGATTAAACGT
SEQ ID 334	GATGTTGTGATGACTCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGC CAGGCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTT CAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGAT TTTGCAGTTTATTACTGTCAGCAGTATAATAACTGGCCTCCTATGTACACTTTTGGCCAGGG GACCAAGCTGGAGATCAAACGT
SEQ ID 335	GATGTTGTGATGACTCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGTCACACT CTCCTGCAGGGCCAGTCAGAGTGTTAGAGACAACGTAGGTTGGTACAAGCAGAAACCTGGC CAACCTCCCAGGCTCGTCATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGAT CAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGAT TTTGCAGTTTATTACTGTCAGCAGTTTAATAATTGGCCTTACACTTTTGGCCAGGGGACCAA GCTGGAGATCAAACGT
SEQ ID 336	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCAT CACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGG AAAGCCCCTAACCTCCTGATCTATGCTGCATCCAGTTTGCACACTGGGGTCCCATCAAGGTT CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATT TTGCAACTTACTACTGTCAACAGAGTTACAGTATTCCTCGAACGTTCGGCCAAGGGACCAAG GTGGAAATCAAACGT
SEQ ID 337	GATGTTGTGATGACTCAGTCTCCAGCCACCCTGTCTGTGACTCCAGGGGAAAGGGCCACCCT CTCCTGCAGGGCCAGTCAAAGTGTTAACAGCAACGTAGCCTGGTACCAGCAGAAACCTGGC CAGGCTCCCAGGCTCCTCATCTATGATGTATCCACCAGGGCCACTGATATCCCAGCCAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTTGACCCTGAAGAT TTTGCAGTGTATTACTGTCAGCAGTGTGCTAGCTCACCTCCTGTCACTTTCGGCGGAGGGAC CAAGCTGGAGATCAAACGT
SEQ ID 338	GAAATTGTGATGACGCAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCT CTCCTGCGGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCT GGCCTGGCGCCCAGGCTCCTCATCTATGATGCATCCAGCAGGGCCACTGGCATCCCAGACA GGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGA AGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCACCTCGGGTCACTTTCGGCGGAG GGACCAAAGTGGATATCAAACGT
SEQ ID 339	GATGTTGTGATGACTCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCGCCTTAGCCTGGTTCCAGCAGAAACCT GGCCAGGCTCCCAGGCTCCTCATCTATGATTCATCCAGCAGGGCCACTGGCATCCCAGACA GCTTCAGCGGCAGTGGATCTGGGACAGAATTCACACTCACAATCAGTAGCCTGCAGCCTGA

	AGATTTTGCAACTTATTACTGTCAACAGTTTAATACCTACCCCAACACTTTTGGCCAGGGGA CCAAGCTGGAGATCAAACGT
SEQ ID 340	GACATCCAGATGACCCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCAT CTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACAACTATTTGGATTGGTTCC TGCAGAAGCCAGGGCAGTCTCCACGGCTCCTGATCTATATGGGTTCTAGTCGGGCCTCCGGG GTCCCTGAGAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAG TGGAGGCTGAGGATGTTGGGGTCTATTACTGCATGCAAACTTTACACACTGTCACTTTCGGC GGCGGGACCAAGGTGGAAATCAAACGT
SEQ ID 341	GAAACGACACTCACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCC TCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACC TGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGAC AGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTG AAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCACTCCTCTTCGGCCAAGGGACA CGACTGGAGATTAAACGT
SEQ ID 342	GACATCCAGTTGACCCAGTCTCCATCCTTCCTGTCTGCATCTGTTGGAGACAGAGTCACCAT CACTTGCCGGGCCAGTCAGGGCATTAGCAGTTCTTTGGCCTGGTATCAGCAAAAGCCAGGG AAAGCCCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAAAGTGGGGTCCCATCAAGGTT CAGTGGAAGTGGATCTGGGACAGATTTTACTTTCACCATCAGCAGCCTGCAGCCTGAAGAT ATTGCAACATATTACTGTCAACAGTATGATAATCTCCCTCCTCTCACTTTCGGCGGAGGGAC CAAGGTGGAAATCAAACGT
SEQ ID 343	GATGTTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCAT CTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACAACTATTTGGATTGGTACC TGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGGGTTCTAATCGGGCCTCCGGG GTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTCACAGTGAAAATCAGCAGAG TGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGCTCTACAAACTCCGTACACTTTT GGCCAGGGGACCAAGCTGGAGATCAAACGT
SEQ ID 344	GAAATTGTGTTGACGCAGTCTCCACTCTCCCTGCCCGTCACCCTTGGACAGCCGGCCTCCAT CTCCTGCAGGTCTTGTCAAAGCCTCGTATACAGTGATGGCAACACCTACTTGAATTGCTTTC AGCAGAGGCCAGGCCAATCTCCAAGGCGCCTAATTTATAAGGTTTCTAACCGGGACTCTGG GGTCCCAGACAGATTCAGCGGCAGTGGGTCAGGCACAGATTTTACACTGGAAATCAGCAGA GTGGAGGCTGAGGATGTTGGGATTTATTTCTGCATGCAAGGTCTACAAACTCCATTCACTTT CGGCCCTGGGACCAAAGTGGATATCAAACGT
SEQ ID 345	GATGTTGTGATGACTCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCT GGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACA GGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGA AGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCACCTGCGCTCACTTTCGGCGGAG GGACCAAGCTGGAGATCAAACGT
SEQ ID 346	GAAATTGTGATGACGCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCAT CTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACAACTATTTGGATTGGTACC TGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGGGTTCTACTCGGGCCTCCGGG GTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGACTTTACACTGAAAATCAGCAGAG CGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGCTCTACACACTCCGTGGACGTTC GGCCTAGGGACCAAAGTGGATATCAAACGT
SEQ ID 347	GACATCCAGATGACCCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGGGCCACCC TCTTTTGCCGGGCCAGTGAAGGTCTTACCACCAACTTAGCCTGGTACCAGCACAAACCTGGC CAGGCTCCCAGGCTCCTCATCTATGCTGCCTCCACCAGGGCCACTGGTGTCCCAGCCAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGAT TCCGCAGTTTATTACTGTCAGCAGTATAATCACTGGCCTCTCTACACTTTTGGCCAGGGGAC CAAGGTGGAAATCAAACGT
SEQ ID 348	GACATCCAGTTGACCCAGTCTCCTTCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCTACTTAGCCTGGTACCAACAGAAATCTGGC CAGGCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGAAGAT

	TTTGCAGTTTATTACTGTCAGCAGGGTAGCAACTGGCCGCTCACTTTCGGCGGAGGGACCAA GGTGGAAATCAAACGT
SEQ ID 349	GATATTGTGATGACCCACACTCCACTCTCCTCACCTGTCACCCTTGGACAGCCGGCCTCCAT CTCCTGCAGGTCTAGTCAAAGCCTCGAACACACTGATGGAAACACCTACTTAAGTTGGCTTC ACCAGAGGCCAGGCCAGCCCCCAAGACTGTTAATTTATAAGGTTTCTACCCGGTTCTCTGGG GTCCCAGACAGATTCAGTGGCAGTGGGGCAGGGACAGATTTCACACTGAAAATCAGCAGGG TGGAGGCTGAGGATGTCGGCGTTTATTACTGCGTGCAGGCTACACACTATCCTCGGACGTTC GGCCATGGGACCAAGGTGGAGATCAAACGT
SEQ ID 350	GAAATTGTGCTGACTCAGTCTCCAGGCACCCTGTCCTTGTCTCCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAGTATTAGCGGCAGTTACTTAGCCTGGTACCAGCAGAAACGT GGCCAGGCTCCCAGGCTCCTCATCTATGATGCGTCCAGCAGGGCCGAAGGCATCCCAGACA GGTTCATTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGA AGACTTTGCTATGTATTACTGTCAGCAGTATGGTAGCTCACCAATATTCACTTTCGGCCCTG GGACCAAAGTGGATATCAAACGT
SEQ ID 351	GAAATTGTGCTGACTCAGTCTCCAGACTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCAT CTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGAAACAACTATTTGGATTGGTACC TGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGGGTTCTAATCGGGCCTCCGGG GTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAACTCAGCAGAG TGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGGTCTACAAATCCCTATCACTTTC GGCCCTGGGACCAAAGTGGATATCAAACGT
SEQ ID 352	GACATCCAGATGACCCAGTCTCCATCTTCTGTGTCTGCATCTGTGGGAGACAGAGTCACCAT CACTTGTCGGGCGAGTCAGAACATTCGCCACTGGTTAGTCTGGTATCAGCAAAAATTAGGG CAAGCCCCTAAACTCCTGATCTATGCTGCGTCCAATTTGCAAAGTGGGGTCCCGTCAAGGTT CAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACAATCAACAGCCTGCAGGCTGAAGAT TTTGCAACCTATTACTGTCTACAGCATAACAGTTACCCGTGGACGTTCGGCCAAGGGACCAA GGTGGAAATCAAACGT
SEQ ID 353	GAAATTGTGTTGACGCAGTCTCCAGACTTTCAGTCTGTGACTCCAAAGCAGAAAGTCACCAT CACCTGCCGGGCCAGTCAGAGCATTGGTGGTAGCTTACACTGGTACCAGCAGAAACCAGGT CAGTCTCCAAAGCTCATCATCAAGTATGCTTCCCAGTCCTTCTCAGGGGTCCCCTCGAGGTT CAGTGGCAGTGGATCTGGGACAGATTTCACCCTCACCATCGATAGCCTGGAGGCTGAAGAT GCTGCAACGTACTATTGTCATCAGAGTATCAGTTTACCGCTCACTTTCGGCGGAGGGACCAA AGTGGATATCAAACGT
SEQ ID 354	GAAACGACACTCACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAGGAGCCACCC TCTCCTGCAGGGCCAGTCAGAGTGTTACCAGCAACTACTTAGCCTGGTACCAGCAGAAACC TGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCTACAGGGCCACTGGCATCCCTGACA GGTTCAGCGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGA AGATTTTGCAGTGTATTACTGTCAGCAGTATGCTAGCTCAGTCACCTTCGGCCAAGGGACAC GACTGGAGATTAAACGT
SEQ ID 355	GATGTTGTGATGACTCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAGTATTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGC CAGGCTCCCAGGCTCCTCATCTATGGTGCCTCCACCAGGGCCACTGGTATCCCAGCCAGGTT CAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGAT TTTGCAGTTTATTACTGTCAGCAGTATAATAACTGGCCTAGAACGTTCGGCCAAGGGACCAA GCTGGAGATCAAACGT
SEQ ID 356	GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCAT CAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCTTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTGCCCGGGAATC CGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAAC AGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATTTTATAGTCCTCCTCGGAC GTTCGGCCAAGGGACCAAGGTGGAAATCAAACGT
SEQ ID 357	GAAATTGTGTTGACACAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCT GGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACA GGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGA

	AGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCACCCCCGGGCACTTTCGGCGGAG GGACCAAAGTGGATATCAAACGT
SEQ ID 358	GAAATTGTGCTGACTCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAGTTTAAGTACCAACTTAGCCTGGTACCAGCAGAAACCTGGC CAGGCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTT CAGTGGCAGTGGGTCTGGCACAGAGTTCACTCTCACCATCACCAGCCTGCAGTCTGAAGATT TTGCAGTTTATTACTGTCAGCAGTATCATAACTGGCCTCCGTACACTTTTGGCCAGGGGACC AAGGTGGAGATCAAACGT
SEQ ID 359	GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCAT CACTTGCCGGGCCAGTCAGAGTATTAGTAGCTGGTTGGCCTGGTATCAGCAGAAACCAGGG AAAGCCCCTAAGCTCCTGATCTATAAGGCGTCTAGTTTAGAAAGTGGGGTCCCATCAAGGTT CAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAGCCTGATGAT TTTGCAACTTATTACTGCCAACAGTATAATAGTTATTGGACGTTCGGCCAAGGGACCAAGGT GGAAATCAAACGT
SEQ ID 360	GAAACGACACTCACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAGGCGCCACCC TCTCCTGCAGGGCCAGTCACAGTGTTGGCGCCAACTACATAGCCTGGTACCAGCAGAAACC TGGCCAGGCTCCCAGGCTCCTTATCCATACTGCATCCAAAAGGGCCACTGGCGTCCCAGAG AGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCAGTATCAGCAGACTGGAGCCTG AAGACTTTGCCGTGTATCACTGTCAGCAGTATGCTGCCGCACCGATTACCTTCGGCCAAGGG ACACGACTGGAGATTAAACGT
SEQ ID 361	GAAATTGTGATGACACAGTCTCCATCCTCCCTGTCTGCATCTGTGGGGGACAGAGTCATCAT CACTTGCCGGGCGAGTCAGGGCATTGCCAATTATTTAGCCTGGTATCAGCAGAAACCAGGG AAAGGTCCTAAACTCCTGATCTATGCTTCATCTACTTTGCAATCAGGGGTCCCATCTCGGTT CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCGGCCTGCAGCCTGAAGAT GTTGCAACTTATTACTGTCAGAAGTATAACAGTGTCCCTCTCACTTTCGGCGGAGGGACCAA AGTGGATATCAAACGT
SEQ ID 362	GATGTTGTGATGACTCAGTCTCCAGTCTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCAT CAACTGCAAGTCCAGCCAGAGTGTTTTATACAGAACCAACAATAAGAACTACTTGGCTTGG TATCAGCAGAAACCAGGACAGCCTCCTAAGTTGCTCATTTACTGGGCATCTACCCGGGAATC CGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGC AGCCTGCAGCCTGAGGATGTGGCAGTGTACTACTGTCAGCAATATTACAATCTTCCTCGATC TTTTGGCCAGGGGACCAAGCTGGAGATCAAACGT
SEQ ID 363	GATATTGTGATGACCCACACTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCAT CAACTGCAAGTCCAACCGGAGTGTTTTATACAGCCCCAACAATCAGAACTACTTAGGTTGGT ACCAGCAGAAGCCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGACTC CGGGGCCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAAC AGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATGCAAGTACTCCATACAC TTTTGGCCAGGGGACCAAGGTGGAGATCAAACGT
SEQ ID 364	GATGTTGTGATGACTCAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTGAGAGTGTTAATAGCAACTTCTTAGCCTGGTACCAGCAGAAACCT GGCCAGGCTCCCAGGCTCCTCATCTATGCTGCATCCACCAGGGCCACTGGTATCCCAGCCAG GTTCAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCATCATCACCAGCCTGCAGTCTGAAG ATTTTGCAGTTTATTACTGTCAGCAGTATAATAACTGGCCGCTCACTTTCGGCGGAGGGACC AAGCTGGAGATCAAACGT
SEQ ID 365	GATGTTGTGATGACTCAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCTACTTAGCCTGGTACCAACAGAAACCTGGC CAGGCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGAAGAT TTTGCAGTTTATTACTGTCAGCAGCGTAGCAACTGGTCGCTCACTTTCGGCGGAGGGACCAA GCTGGAGATCAAACGT
SEQ ID 366	GAAACGACACTCACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCC TCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCCTGGTACCAACAGAAACC TGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCTTCCACCAGGGCCACTGGCATCCCAGACA GGTTCAGTGGCAGTGGGTCTGGGACGGACTTCACTCTCACCATCGGCAGACTGGAGCCTGA

	AGATTTTGCAGTGTATTACTGTCAACACTATGGTCCCTCACGTCGGATCACCTTCGGCCAAG GGACACGACTGGAGATTAAACGT
SEQ ID 367	GAAACGACACTCACGCAGTCTCCAGACACCCTGTCTGTGTCTCCAGGGGGAAGAGCCACCC TCTCCTGTAGGGCCAGTCAGAGCATTGGGAGCAATTTAGCCTGGTACCAACAGAAACCTGG CCAGTCTCCCAGGCTCCTCATCTATGATGCATCCACCAGGGCCACGGGAATCCCAGCCAGGT TCAGTGGCAGTGGGTCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGGAGTCTGAAGA TTTTGTACTTTATTACTGTCAGCAGCATGGTGAATGGCCCACCTTCGGCCAAGGGACACGAC TGGAGATTAAACGT
SEQ ID 368	GATGTTGTGATGACTCAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAGTGTCGGTAACTCCTTAGCCTGGTACCAGCAGAAGCCTGGC CAGGCTCCCCGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCCGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCACCAGCCTAGAGCCTGAAGAT TTTGCAATTTATTACTGTCAACAACGTGGCACCTGGCCTCCCCTCACTTTCGGCGGAGGGAC CAAGCTGGAGATCAAACGT
SEQ ID 369	GATGTTGTGATGACTCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACACAGTCACCAT CACTTGCCGGGCCAGTCAGAGTATAACTAACTGGTTGGCCTGGTATCAGCAGAAACCAGGG AAAGCCCCCAAGCGCCTGATCTATGGTGCGTCCAGTTTGCAGAGTGGGGTCCCATCAAGGT TCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGA TTTTGCAACTTATTACTGTCAACAGTATACTAATTACCCTCGTACGTTCGGCCAAGGGACCA AGCTGGAGATCAAACGT
SEQ ID 370	GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCAT CACTTGTCGGGCCAGGCAGAGCATCAGTAACCGGTTGGCCTGGTATCAGCAGAAACCAGGG AGAGCCCCTAATGTCCTGATCTATAAGGCGTCTACTTTAGCAAATGGGGTCCCATCAAGGTT CAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAGCCTGATGAC TTTGCAACTTATTACTGCCAACAGTATCAAAGTTACTGGACGTTCGGCCCAGGGACCAAGGT GGAAATCAAACGT
SEQ ID 371	GACATCCAGTTGACCCAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCT CTCCTGCAAGGCCAGTCAGAGTGTTAGTAGCTACTTAGCCTGGTACCAACAGAAACTTGGC CAGGCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTT CAGTGCCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGAT GTTGCAACTTATTACTGTCAAAAGTATAACAGTCCCCCTCGGACGTTCGGCCAGGGGACCA AGGTGGAAATCAAACGT
SEQ ID 372	GAAACGACACTCACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGGGTCAGCC TTTCCTGCAGGGCCAGTCAGAATGTTTACAGCAATTTCTTAGCCTGGTATCAACAGAGACCT GGCCAGGCTCCCAGTCTCCTCATCTATGGTGCCTCCAGCAGGGCCGCTGGCGTCCCAGACAG GTTCAGTGGCAGTGGGTCTGGGACAGACTTCGCTCTCACCATCAGCAGAGTGGAGCCTGAA GATTTTGCAGTCTATTACTGTCAACAATATGGAACCTCACCGATCACCTTCGGCCAAGGGAC ACGACTGGAGATTAAACGT
SEQ ID 373	GAAATTGTGCTGACTCAGTCTCCACGCTCCTCACCCGTCACCCTTGGACAGCCGGCCTCCAT CTCCTGTAGGTCTAGTCAAAGTCTCGAACACGGTGATGGAAACACGTACTTGAGTTGGCTTC AGCAGAGGCCAGGCCAGCCTCCAAGACTCCTGATTTATAAGGTTTCTAACCGGTTGTCTGGG GTCCCAGACAGATTCAGTGGCAGTGGGGCAGGGACTGATTTCACACTGAAAATCAGCAGGG TGGAAGCTGAGGATGTCGGGGTTTATTACTGCATGCAAGGTATATACTGGCCTCGAACCTTC GGCCAAGGGACACGACTGGAGATTAAACGT
SEQ ID 374	GAAACGACACTCACGCAGTCTCCAGTCACCCTGTCTTTGTCTCCAGGGGACAGAGCCACCCT CTCTTGCAGGGCCAGTCAGAGTGTTAGCAGCACCTCCTTAGCCTGGTACCAGCACAAACCTG GCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGGAGGGCCACTGGCATCCCAGACAG GTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAACAGACTGGAGCCTGAA GATTTTGCAGTGTATTACTGTCAGCACTATGGTAGTTCACCTCCAATCACCTTCGGCCAAGG GACACGACTGGAGATTAAACGT
SEQ ID 375	GAAACGACACTCACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCC TCTCCTGCAGGGCCAGTCAGAGTGTTGGCAGCAAATTAGCCTGGTACCAGCAGAAACCTGG CCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGTGTCCCAGTCCGGT TCAGTGGCAGTGGGTCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGA

	TTTTGCAGTTTATTACTGTCAGCAGTATAATAACTGGCCCCCGATCACCTTCGGCCAAGGGA CACGACTGGAGATTAAACGT
SEQ ID 376	GAAATTGTGTTGACGCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCAT CTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACAACTATTTGGATTGGTACC TGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGGGTTCTAATCGGGCCTCCGGG GTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAG TGGAGGCTGAGGATGTTGGGGTGTATTACTGCATGCAAACTCTTCAAACTCCGCTCACTTTC GGCGGAGGGACCAAAGTGGATATCAAACGT
SEQ ID 377	GATGTTGTGATGACTCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCAT CAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCTTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATC CGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGC AGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTAGTACTCCGTA CACTTTTGGCCAGGGGACCAAGCTGGAGATCAAACGT
SEQ ID 378	GATATTGTGATGACCCACACTCCCCTCTCTCTGTCCGTCACCCCTGGACAGCCGGCCTCCAT CTCCTGCAAGTCTAGTCAGAGCCTCCTGGGTGGTGATGGAAAGACCTATTTGTATTGGTACC TGCAGAAGCCAGGCCAGCCTCCACAGCTCCTGCTCTATGAAGTTTCCAACCGATTCTCTGGA GTGCCAGATAGGTTCAGTGGCAGCGGGGCAGCGACAGATTTCACACTGAAAATCAGCAGGG TGGAAGCTGAGGATGTCGGGGTTTATTACTGCATGCAATCTACACAATTTCCGTGGACGTTC GGCCAAGGGACCAAGGTGGAGATCAAACGT
SEQ ID 379	GAAACGACACTCACGCAGTCTCCAGGCACCCTGTCTTTGTCTGCAGGGGAAAGAGCCACCC TCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACC TGGCCAGGCTCCCAGGCTCCTCATCTATGCTGCATCCTACAGGGCCACTGGCATCCCAGACA GGTTCAGTGGCCGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGA AGATTTTGCAGTTTATTACTGTCAGCAGTATAATAACTGGCCTCCCATCACCTTCGGCCAAG GGACACGACTGGAGATTAAACGT
SEQ ID 380	GATGTTGTGATGACTCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGC CAGGCTCCCAGGCTCCTCATCTATGATGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTT CAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGAT TTTGCAGTTTATTACTGTCAGCACTATAATAACTGGCCTCATACCTTCGGCCAAGGGACCAA GCTGGAGATCAAACGT
SEQ ID 381	GAAACGACACTCACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCC TCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTCCTTAGCCTGGTACCAGCAGAAACC TGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCTCTGGCATCCCAGACA GGTTCAATGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAATAGGCTGGAGCCTGA AGACTTTGCAGTGTATTACTGTCAGCAGTATGGTAACTCACAGACCTTCGGCCAAGGGACA CGACTGGAGATTAAACGT
SEQ ID 382	GATGTTGTGATGACTCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGC CAGGCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTT CAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGAT TTTGCAGTTTATTACTGTCAGCAGTATAATAACTGGCCCCGGACGTTCGGCCAAGGGACCAA GCTGGAGATCAAACGT
SEQ ID 383	GATGTTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCTTGGACAGCCGGCCTCCAT CTCCTGCAGGTCTAGTCAAAGCCTCGTATACAGTGATGGAAACACCTACTTGAATTGGTTTC AGCAGAGGCCAGGCCAATCTCCAAGGCGCCTAATTTATAAGGTTTCTAACCGGGACTCTGG GGTCCCAGACAGATTCAGCGGCAGTGGGTCAGGCACTGATTTCACACTGAAAATCAGCAGG GTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGGTACACATTGGCCTCGGACTTT CGGCGGAGGGACCAAGCTGGAGATCAAACGT
SEQ ID 384	GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCAT CACTTGCCGGGCCAGTCAGAGTATTAGTAGGTGGTTGGCCTGGTATCAGCAGAAGCCAGGG AAAGCCCCTAAGCTCCTGATCTATAAGGCGTCTACTATAAAAAGTGGGGTCCCATCAAGAT TCAGCGCCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGA

	TTTTGCAACTTATTACTGCCAACACTATAAAAGTGATTCCCGGACGTTCGGCCAAGGGACCA AGGTGGAAATCAAACGT
SEQ ID 385	GATGTTGTGATGACTCAGTCTCCATCCTCCCTCGCTGCATCTGTTGGAGACAGAATTACCAT CACTTGCCGGCCAAGTCAGGACATAGGCACTTATTTAAATTGGTATCAACAGAAGGCAGGG GAAGCCCCTAAGCTCCTCATCTATGCTGCCTCCAATCTGCACAGTGGCGTCTCATCAAGGTT CAGAGGCGTTGGGTCTGGGACACAATTCACTCTCACCATCAGCAGTCTGCAACCTGAGGAT TTTGCAACTTACTACTGTCATCAGAGTTACGGTCCTCGGACATTCGGCCAAGGGACCAAGCT GGAGATCAAACGT
SEQ ID 386	GAAACGACACTCACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCC TCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGG CCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGCATCCCAGCCAGGT TCAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGA TTTTGCAGTTTATTACTGTCAGCAGTATAATAACTGGCCTCCGATCACCTTCGGCCAAGGGA CACGACTGGAGATTAAACGT
SEQ ID 387	GATGTTGTGATGACTCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCT GGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACA GGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGA AGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCAGGGTACACTTTTGGCCAGGGGA CCAAGCTGGAGATCAAACGT
SEQ ID 388	GAAACGACACTCACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCC TCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACC TGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGAC AGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTG AAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCGTTCGGCCAAGGGACACGACTG GAGATTAAACGT
SEQ ID 389	GAAATTGTGTTGACACAGTCTCCTTCCACCCTGTCTGCATCTGTAGGGGACAGAGTCACCAT CACTTGCCGGGCCAGTCAGAGTATTAGTAGCTGCTTGGCCTGGTATCAGCAGAAACCAGGG AAAGCCCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAAAGTGGGGTCCCATCAAGGTT CAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACAATCAGCACCCTGCAGCCTGAAGAT TTTGCAACTTATTACTGTCAACAGCTTAATAGTTACCCTCAGACGTTCGGCCAAGGGACCAA AGTGGATATCAAACGT
SEQ ID 390	GATATTGTGATGACCCACACTCCACTCTCTCTGTCCGTCACCCCTGGACAGCCGGCCTCCAT CTCCTGCAAGTCTAGTCAGAGCCTCCTGCATAGTGATGGAAAGACCTATTTGTATTGGTACC TGCAGAAGCCAGGCCAGCCTCCACAGCTCCTGATCTATGAAGTTTCCAACCGGTTCTCTGGA GTGCCAGATAGGTTCAGTGGCAGCGGGTCAGGGACAGATTTCACACTGAAAATCAGCCGGG TGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAAGTATACAGCTTCCGCTCACTTTC GGCGGAGGGACCAAGGTGGAGATCAAACGT
SEQ ID 391	GATGTTGTGATGACTCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCT GGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACA GGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGA AGATTTTGCAGTGTATTACTGTCAGCAGTATAATAACTGGCCTCTCACTTTCGGCGGAGGGA CCAAGCTGGAGATCAAACGT
SEQ ID 392	GACATCCAGTTGACCCAGTCTCCCGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCAT CAACTGCACGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACATAGCTTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATC CGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGC AGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATTATATTCCTCGGAC GTTCGGCCAAGGGACCAAGGTGGAAATCAAACGT
SEQ ID 393	GATGTTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCAT CTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACAACTATTTGGATTGGTACC TGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGGGTTCTAATCGGGCCCCCGGG GTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAG

	TGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGCTCTACAAACTCGGACATTCGGC CAAGGGACCAAGCTGGAGATCAAACGT
SEQ ID 394	GAAACGACACTCACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCC TCTCCTGCAGGGCCAGTCAGAGTCTTACCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCT GGCCAGGCTCCCAGACTCCTCATCTATCGTGCATCCAGCAGGGCCACTGGCATCCCAGACC GGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGA AGATTTTGCAGTTTATTACTGTCAGCAGTATGGTAGTTCACCTAACACCTTCGGCCAAGGGA CACGACTGGAGATTAAACGT
SEQ ID 395	GAAATTGTGTTGACACAGTCTCCACTCTCCCTGCCCGTCACCCTTGGACAGCCGGCCTCCAT CTCCTGCAGGTCTAGTCAAAGCCTCGTACACAGTAATGGACACACCTACTTGAGTTGGTTTC AGCAGAGGCCAGGCCAATCTCCAAGGCGCCTCATTTATGAGGTTTCTAACCGGGACTCTGG TGTCCCAGACAGATTCAGCGGCAGTGGGTCAGGCACTGATTTCACACTAAGAATCAGCAGG GTGGAGGCTGAGGATGTTGGGGTTTATTACTGCTTGCAAGGAACACACTGGCCCCCCCTCAC TGTCGGCGGAGGGACCAAAGTGGATATCAAACGT
SEQ ID 396	GATGTTGTGATGACTCAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAGTGTTGGCAGCGACTTAGCCTGGTACCAGCAGAAACCTGGC CAGGCTCCCAGGCTCCTCATCTACCGTGCATCCACCAGGGCCGCTGGTATCCCAGCCAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGAT TTTGCAGTGTTTTACTGTCAGCAGTATGGTAGATCACCGTACACTTCTGGCCAGGGGACCAA GCTGGAGATCAAACGT
SEQ ID 397	GATATTGTGATGACCCACACTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCAT CAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCTTGGT ACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATC CGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGC AGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACTCCGCTCAC TTTCGGCGGAGGGACCAAGGTGGAGATCAAACGT
SEQ ID 398	GAAATTGTGATGACGCAGTCTCCACTCTCCCTGTCCGTCACCCCTGGAGAGCCGGCCTCCAT CTCCTGCAGGTCTAGTCAGAGCCTCCTACATAGTAGTGGATACAACTATTTGGATTGGTACC TGCAGAAGCCAGGCCAGTCTCCACAGCTCCTGATCTATTTGGGTTCTACTCGGGCCTCCGGG GTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAG TGGAGGCTGAGGATGTTGGGGTTTATTATTGCATGCAAGGTCTACAAATTCCGCTCACTTTC GGCGGAGGGACCAAAGTGGATATCAAACGT
SEQ ID 399	GATATTGTGATGACCCACACTCCACTCTCTCTGTCCGTCACCCCTGGACAGCCGGCCTCCAT CTCCTGCAAGTCTAGTCAGAGCCTCCTGCATAGTGATGGAAAGACCTATTTGTATTGGTACC TGCAGAAGCCAGGCCAGCCTCCACAGCTCCTGATCTATGAAGTTTCCAACCGGTTCTCTGGA GTGCCAGATAGGTTCAGTGGCAGCGGGTCAGGGACAGATTTCACACTGAAAATCAGCCGGG TGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAAGTATACAGCTTCCGTGGACGTTC GGCCAAGGGACCAAGGTGGAGATCAAACGT
SEQ ID 400	GAAACGACACTCACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCC TCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGG CCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGCATCCCAGCCAGGT TCAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGA TTTTGCAGTTTATTACTGTCAGCAGTATAATAACTGGCCTCGGTTCGGCCAAGGGACACGAC TGGAGATTAAACGT
SEQ ID 401	GATGTTGTGATGACTCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGGGACAGAGTCACCAT CACTTGCCGGGCCAGTCAGACTATTAATAGTTGGTTGGCCTGGTATCAGCAGAAACCAGGG AAGGCCCCTAAGCTCCTCATCTCTAGGGCGTCTCGTTTAGAAAGTGGGGTCCCATCAAGGTT CAGCGGCAGTGCATCTGGCACAGAATACATTCTCACCATCAACAGCCTGCAGCCTGATGAT TTTGCAATGTACTTCTGCCATCAATATAATAGTTATTCTCCCACTTTTGGCCAGGGGACCAA GCTGGAGATCAAACGT
SEQ ID 402	GAAACGACACTCACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCC TCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACC TGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGCCA GGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGA

	AGATTTTGCAGTTTATTACTGTCAGCAGCGTTACAACTGGCCTATCACCTTCGGCCAAGGGA CACGACTGGAGATTAAACGT
SEQ ID 403	GAAATTGTGTTGACGCAGTCTCCAGCCACCCTGTCTTTGTCTCCGGGGGAAACAGCCACCCT CTCCTGCAGGGCCAGTCAGACTATTGGTCCCAAGTCCTTCGGCTGGTACCAACAGAGACCTG GCCAGGCTCCCAGGCTCCTCATCTATGACTCCAACAGGGCCACTGGCATCCCAGCCAGGTTC AGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGAAGATT TTGCAGTTTATTACTGTCAGCAGCGTAGCAGGTGGCCTCTCACTTTCGGCCCTGGGACCAAA GTGGATATCAAACGT
SEQ ID 404	GATGTTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCTTGGACAGCCGGCCTCCAT CTCCTGCAGGTCTAGTCAAAGCCTCGTGTACAGTGATGGAAACACCTACTTGTATTGGTTTC AGCAGAGGGCAGGCCAATCTCCAAGGCGCCTGATTTATAAGGTTTCTAAGCGGGACTCTGG GGTCCCAGACAGGTTCAGCGGCAGTGGGTCAGGCACTGATTTCACACTGAAAATCAGCAGG GTGGAGGCTGAGGATGTTGGAATTTATTACTGCGTGCAAGGTAGACACTGGCCGTACACTC TTGGCCAGGGGACCAAGCTGGAGATCAAACGT
SEQ ID 405	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCT GGCCAGGCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCA GGTTCAGTGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAGCCTGA TGATTTTGCAACTTATTACTGCCAACAGTATAATAGTTATTCAAGGACGTTCGGCCAGGGGA CCAAAGTGGATATCAAACGT
SEQ ID 406	GATGTTGTGATGACTCAGTCTCCTTCCACCCTGTCTGCATCTGTGGGAGACAGAGTCACCAT CACTTGCCGGGCCAGTCAGAGTATTACTACCTGGTTGGCCTGGTCTCAGCAGCAACCAGGG AAAGCCCCTAAGCTCCTCATCTATAAGGCCTCTAGTTTAACAAGTGGGGTCCCATCAAGGTT CAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGCCTGATGAT TTTGCAAGTTATTACTGCCATCATTATAATGGTGCTTCTCGTATGTTCGGCCAAGGGACCAA GCTGGAGATCAAACGT
SEQ ID 407	GAAACGACACTCACGCAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCC TCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCTACTTAGCCTGGTACCAACAGAAACCTGG CCAGGCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGT TCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGAAGA TTTTGCAGTTTATTACTGTCAGCAGCGTAGCAACTGGCCTTTCTTCGGCCAAGGGACACGAC TGGAGATTAAACGT
SEQ ID 408	GAAACGACACTCACGCAGTCTCCAGCCACCCTGACTTTGTCTCCAGGGGAAAGAGTCACCC TCTCCTGCAGGGCCAGTCAGAGTATTGGCACTTACGTCGCCTGGTATCAGCAGAAACCTGGC CAGGCTCCCAGATTCCTCATCTATGATTCATCGAATAGGGCCACTGGCATCCCAGCCAGGTT CAGTGGTAGTGGGTCTGGGACAGACTTCACTCTCACGATCAGCAGCCTGGAGCCTGAAGAT TTTGCATTTTATTACTGTCAACAGCGTGCCGAGTGGCCTCTCACCTTCGGCCAAGGGACACG ACTGGAGATTAAACGT
SEQ ID 409	GATGTTGTGATGACTCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACTCT CTCCTGCAGGGCCAGTCAGAGTGTTAATAGCGGCTACTTAGCCTGGTACCAGCAGAAACCT GGCCAACCTCCCAGACTCCTCATCTCTGGTGTTTCCACCAGGGCCACTGGCATCCCAGACAG GTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAA GATTTTGCAGTGTATTACTGTCAGGAGTATGGTAACTCAGCTATGTACAATTTTGGCCAGGG GACCAAGCTGGAGATCAAACGT
SEQ ID 410	GAAACGACACTCACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCC TCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGG CCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGT TCAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGA TTTTGCAGTTTATTACTGTCAGCAGTATAATAACTGGCCTCCCTTCACCTTCGGCCAAGGGA CACGACTGGAGATTAAACGT
SEQ ID 411	GATGTTGTGATGACTCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGGCTGGTATCAGCAGAAATCC GGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGACATCCCAGACA GGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAAACTGGAGGCAGA

	AGATTCTGCAGTGTATTACTGTCAGCAGTATGGTATCTCACCTCTCGCGTTCGGCCAAGGGA CCAAGCTGGAGATCAAACGT
SEQ ID 412	GAAACGACACTCACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAGAGAGCCACCC TCTCCTGCAGGGCCAGTCAGAGTATTAGCAACAACTTAGCCTGGTACCAGCAGAAACCTGG CCAGGCTCCCAGGCTCCTCATCTATGGTACATCCACCAGGGCCACTGGTATCCCAGCCAGGT TCAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGA TTTTGCAGTTTATTACTGTCAGCAGTATAATTTCTGGCCTTCGATCACCTTCGGCCAAGGGAC ACGACTGGAGATTAAACGT
SEQ ID 413	GAAACGACACTCACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCC TCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTCCTTAGCCTGGTACCAGCAGAAACC TGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGAC AGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTG AAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCACAGACCTTCGGCCAAGGGAC ACGACTGGAGATTAAACGT
SEQ ID 414	GATGTTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCTCCCTTGGACAGCCGGCCTCCATC TCCTGCAGGTCTAATCAAAGCCTCGTATACAGTGATGGAGGCACCTACTTGAATTGGTTTCA GCAGAGGGCAGGCCAGTCTCCAAGGCGCCTAGTTTATAAGGTTTCTAACCGGGACTCTGGG GTCCCAGACAGATTCAGCGGCAGTGGGTCAGGCACTGATTTCACACTGAGAATCAGCAGGG TGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGGGACACACTGGCCGTACACTTTT GGCCAGGGGACCAAGCTGGAGATCAAACGT
SEQ ID 415	GACATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCGT CACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGG AAAGCCCCTCAACTCCTGATCTACGATGCATCCAATTTGGAAACAGGGGTCCCCTCAAGGTT CAGTGGAAGTGGATCTGGGACAGATTTTACTTTCACCATCAGCAGCCTGCAGCCTGAAGATT TTGCAACATATTACTGTCAGCAGTTTGATAATGTCCCAGTCACTTTCGGCGGAGGGACCAAG GTGGAAATCAAACGT
SEQ ID 416	GAAATTGTGCTGACTCAGTCTCCACTCTCCCTGCCCGTCACCCTTGGACAGCCGGCCTCCAT CTCCTGCAGGTCTAGTCAAAGCCTCGTATACAGTGATGGAAACACCTACTTGAATTGGTTTC AGCAGAGGCCAGGCCAATCTCCAAGGCGCCTAATTTATAAGGTTTCTAACCGGGACTCTGG GGTCCCAGACAGATTCAGCGGCAGTGGGTCAGGCACTGATTTCACACTGAAAATCAGCAGG GTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGGTACACACTGGCCTCGAACGT TCGGCCAAGGGACCAAGCTGGAGATCAAACGT
SEQ ID 417	GATGTTGTGATGACTCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGC CAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAACAGACTGGAGCCTGAAGAT TTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCATCCATGTACACTTTTGGCCAGGGGAC CAAGCTGGAGATCAAACGT
SEQ ID 418	GATGTTGTGATGACTCAGTCTCCATCCTCCCTGTCTGCATCTGTGGGGGACAGCGTCGCCAT CACTTGCCGGGCAAGTCAGAGCATTAGCAACTATTTAAATTGGTATCAGCAGAGACCAGGG AAAGCCCCTAAGCTCCTGATCTTTGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATT TTGCAACTTACTCCTGTCAACAGAGTTACATTACCCCGTGGACGTTCGGCCAAGGGACCAAG CTGGAGATCAAACGT
SEQ ID 419	GATGTTGTGATGACTCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAGTGTTAGCACCCTCTTAGCCTGGTACCAACAGAAACCTGGC CAGGCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGGCAGGTT CAGTGCCAGTGGGTCTGGGACAGACTTCAGTCTCACCATCAGCAGCCTAGAGACTGAAGAT TCTGCAGTTTATTACTGTCAGCACCGTTACGTGTGGCCGTTCACTTTCGGCGGAGGGACCAA GCTGGAGATCAAACGT
SEQ ID 420	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCAT CACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTTAGGCTGGTATCAGCAGAAACCAGGG AAAGCCCCTAAGCGTCTGATCTATGGTGCATCCAGTTTGCAAAGTGGAGTCCCATCAAGGTT CAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACAATCAGGAGCCTGCAGCCTGAAGAT

	TTTGCAACTTATTATTGTCTACAGCATAATTCCTACCCTCGAACATTCGGCCAAGGGACCAA GGTGGAAATCAAACGT
SEQ ID 421	GATGTTGTGATGACTCAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCTACTTAGCCTGGTACCAACAGAAACCTGGC CAGGCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGAAGAT TTTGCAGTTTATTACTGTCAGCAGCGTAGCAACTGGCCGTGGACGTTCGGCCAAGGGACCA AGCTGGAGATCAAACGT
SEQ ID 422	GATGTTGTGATGACTCAGTCTCCGCTCTCCCTGCCCGTCACCCTTGGACAGGCGGCCTCCAT CTCCTGCAGGTCTAGTCATAGCCTCACAACTACTGATGGACGTACTTACGTGGCTTGGTTTC AGCAGAGGCCAGGCCAATCTCCAAGGCGCCTTCTTTATGAGGTTTCTAAGCGGGACTCTGG GGCCCCAGACAGATTCAGCGGCAGTGGGTCAGGCACTGATTTCACTCTGAAAATCAGCAGG GTGGAGGCTGACGATGTTGGAATTTATCATTGCATGCAAGGAACACATGGGCCTCACACGT TCGGCCAAGGGACCAAGCTGGAGATCAAACGT
SEQ ID 423	GAAACGACACTCACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCC TCTCCTGCAGGGCCAGTCAAAGTGTTACCAGCAACTTAGCCTGGTACCAGCAGAAACCTGG CCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAACAGGGCCACTGGTATCCCAGCCAGGT TCAGTGTCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGA TTTTGCAGTGTATTACTGTCAGCAGTATGGTAGTCCACCTCCGACCACCTTCGGCCAAGGGA CACGACTGGAGATTAAACGT
SEQ ID 424	GATGTTGTGATGACTCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCT GGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACA GGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGA AGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCACGTCGGACGTTCGGCCAAGGGA CCAAGCTGGAGATCAAACGT
SEQ ID 425	GAAACGACACTCACGCAGTCTCCAGGCACCCTGTCCTTGTCTCCAGGGGAAAGAGCCACCC TCTCCTGCAGGGCCAGTCAGAGTGTTTTCAACAACTACTTAGCCTGGTACCAACAGAGACCT GGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACA GGTTCAGTGGCGGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGA AGATTTCGCAGTGTATTGCTGTCAGCAGTATGGTAGTTCACCGATCACCTTCGGCCAAGGGA CACGACTGGAGATTAAACGT
SEQ ID 426	GAAATTGTGCTGACTCAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCTACTTAGCCTGGTACCAACAGAAACCTGGC CAGGCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGAT TTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCACTCAGGTACACTTTTGGCCAGGGGAC CAAGCTGGAGATCAAACGT
SEQ ID 427	GAAATTGTGCTGACTCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCAT CAACTGCAAGTCCAGCCAGAGTGTTTTATATGATTCCAACAGTAAGAACTACTTAAGTTGGT ATCAGCAGAAACCAGGCCAGCCTCCTAAGTTGCTCATTTCCTGGGCGTCTACCCGGGGGTCC GGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCA GCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATTTTATGGTATTCCCCACTTC GGCCAAGGGACACGACTGGAGATTAAACGT
SEQ ID 428	GATGTTGTGATGACTCAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAGTGTTGGTACCAATTTAGCCTGGTACCAGCAGAAACCTGGC CAGGCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTT CAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGAT TTTGCAGTTTATTACTGTCAGCAGTATAATAACTGGCCTCCGATAACTTTCGGCGGAGGGAC CAAGCTGGAGATCAAACGT
SEQ ID 429	GATGTTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCTTGGACAGCCGGCCTCCAT CTCCTGCAGGTCTAGTCAAAGCCTCGTATACAGTGATGGAAACACCTACTTGAGTTGGCTTC AGCAGAGGCCAGGCCAGCCTCCAAGACTCCTAATTTATAAGATTTCTAACCGGTTCTCTGGG GTCCCAGACAGATTCAGTGGCAGTGGGGCAGGGACAGATTTCACACTGAAAATCAGCAGGG

	TGGAAGCTGAGGATGTCGGGGTTTATTACTGCATGCAAGGTACACAATTTCCTCAAACGTTC GGCCAAGGGACCAAGCTGGAGATCAAACGT
SEQ ID 430	GAAATTGTGCTGACTCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAGTGTAATAAGCAGGTACTTAGCCTGGTATCAGCAGAAACCT GGCCAGGCTCCCAGGCTCCTCATCCATGGTGCATCCACCAGGGCCACTGGCATCCCAGACA GGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGA AGACTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCACCTCCGTACACTTTTGGCCAGG GGACCAAGGTGGAAATCAAACGT
SEQ ID 431	GACATCCAGTTGACCCAGTCTCCTTCCACCCTGGCTGCATCTGTAGGAGACAGAGTCACCAT CACTTGCCGGGCCAGTCAGAGTATTAGTAGCTGGTTGGCCTGGTATCAGCAGAAACCAGGG AAAGCCCCTAAGGTCCTGATCTATAAGGCGTCTAGTTTAGAAAGTGGGGTCCCATCAAGGT TCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAGCCTGATGA TTTTGCAACTTATTACTGCCAACAGTATAATAGTTATTCGGGGACGTTCGGCCAAGGGACCA AGGTGGAAATCAAACGT
SEQ ID 432	GATGTTGTGATGACTCAGTCTCCAGCCATCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCT CTCCTGCAGGGCCAGTCAGAGTGTTAGTAGCAGCTTAGCCTGGTACCAGCAGAAACCTGGC CAGCCTCCCAGGCTCCTCATCTATGGTGCCTCCACCAGGGCCACTGCTATCCCAGCCAGGTT CAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGAT TTTGCAGTTTATTACTGTCAGCGCTATGATAACTGGCCTCCCCTTTTTGGCCAGGGGACCAA GCTGGAGATCAAACGT

[169] Exemplary CDR amino acid sequences of CLEC2D antibodies of the disclosure are shown in Table 6 below.

Table 6. CDR Amino Acid Sequences

VH						VL					
SEQ ID	CDRH1	SEQ ID	CDRH2	SEQ ID	CDRH3	SEQ ID	CDRL1	SEQ ID	CDRL2	SEQ ID	CDRL3
SEQ ID 433	GYTFTSYAMH	SEQ ID 486	WINAGNGNTKYSQKFQG	SEQ ID 547	GSLSRSGWYAGLFDY	SEQ ID 654	ASQSIGSNLVW	SEQ ID 727	SATSRATG	SEQ ID 784	YGSSPPTTF
SEQ ID 434	GFTFSSYSMN	SEQ ID 487	IISDDGSKSYYADSVQG	SEQ ID 548	DRGTKWNQLNDVFDM	SEQ ID 655	ASQSVSSSYLAW	SEQ ID 728	GASNRATG	SEQ ID 785	YGSSPGTF
SEQ ID 435	GYTFTSYYMH	SEQ ID 488	IINPSGGSTSYAQKFQG	SEQ ID 549	GRGYSSSRLYYFDY	SEQ ID 656	ASQSVSSYLAW	SEQ ID 729	DASNRATG	SEQ ID 786	RSNWPRTF
SEQ ID 436	GFTFSDPYMD	SEQ ID 489	RITNKRTGYATTYAASVKD	SEQ ID 550	DVSGSFAAY	SEQ ID 657	SSRNILYSGNNKNFLAW	SEQ ID 730	WASTRESG	SEQ ID 787	SSSLPHTF
SEQ ID 437	GFTFSSYAMH	SEQ ID 490	WINAGNGNTKYSQKFQG	SEQ ID 551	EGGAVAGTVY	SEQ ID 658	ASESVSKSYLLW	SEQ ID 731	GASTRASG	SEQ ID 788	YGSSRTF
SEQ ID 438	GFTFSNAWMS	SEQ ID 491	RIKSKTDGGTTDYAAPVKG	SEQ ID 552	DEYFY	SEQ ID 659	ASQSISSTYLAW	SEQ ID 732	GASTRATG	SEQ ID 789	YGNSPPGATF
SEQ ID 439	GGSFSGYYWS	SEQ ID 492	EINHSGSTNYNPSLKS	SEQ ID 553	VNPGSYTREVSNFDY	SEQ ID 660	SSQALRNVVGLGDDLAW	SEQ ID 733	STSTLQSG	SEQ ID 790	HHDFPFTF
SEQ ID 440	GDSVSSNSVTWN	SEQ ID 493	RTYYRSQWYYNYAVSVKS	SEQ ID 554	RGHNYGVDY	SEQ ID 661	SSQSLLNSNGYNYLEW	SEQ ID 734	LGSNRASG	SEQ ID 791	SLQTPLTF
SEQ ID 441	GYTFAAYYLH	SEQ ID 494	RIKSKTDGETTDYAAPVKG	SEQ ID 555	GVGWSPFQY	SEQ ID 662	ASQSVSSNLAW	SEQ ID 735	GASSRATG	SEQ ID 792	YGSSPRITF
SEQ ID 442	GFTFSSHLMH	SEQ ID 495	FIRSKAYGGTTEYAASVKG	SEQ ID 556	DDKIAAAGFTYWYFDL	SEQ ID 663	ASQSVRDNVGW	SEQ ID 736	AASSLHTG	SEQ ID 793	YNNWPPMYTF
SEQ ID 443	GGSISSGGYSWS	SEQ ID 496	RISPGNGVTSYAQKFQG	SEQ ID 557	EAADDPFDH	SEQ ID 664	ASQSISSYLNW	SEQ ID 737	DVSTRATD	SEQ ID 794	FNNWPYTF
SEQ ID 444	GDSVSNNRAAWN	SEQ ID 497	VISYDGTSKYYGDSVKG	SEQ ID 558	ADYKYD	SEQ ID 665	ASQSVNSNVAW	SEQ ID 738	DASSRATG	SEQ ID 795	SYSIPRTF
SEQ ID 445	GYTFTSYGIS	SEQ ID 498	YIYHSGSTYYNPSLKS	SEQ ID 559	HRRPIYDILTGFDY	SEQ ID 666	ASQSVSSSALAW	SEQ ID 739	DSSSRATG	SEQ ID 796	CASSPPVTF
SEQ ID 446	GYSFTSYWIG	SEQ ID 499	YISSSGSYTNYADSVKG	SEQ ID 560	EDTMVRGVIP	SEQ ID 667	SSQSLLHSNGYNYLDW	SEQ ID 740	MGSSRASG	SEQ ID 797	YGSSPRVTF
SEQ ID 447	GYSFTSYWIA	SEQ ID 500	WISAYNGNTNYAQKLQG	SEQ ID 561	DRRYYDSSGYYPAYYFDY	SEQ ID 668	ASQGISSSLAW	SEQ ID 741	AASTLQSG	SEQ ID 798	FNTYPNTF

SEQ ID 448	GFTFT DAWM N	SEQ ID 501	IIYPGDSDT RYSPSFQG	SEQ ID 562	DGGYDSSGF HFDY	SEQ ID 669	SCQSLVY SDGNTYL NC	SEQ ID 742	KVS NRD SG	SEQ ID 799	TLHT VTF
SEQ ID 449	GFTFS NNWM T	SEQ ID 502	WIIPIFGIA NYAQKFQ G	SEQ ID 563	LPSSGYLQD HHYYGMDV	SEQ ID 670	ASEGLTT NLAW	SEQ ID 743	LGS TRA SG	SEQ ID 800	YGSS LLF
SEQ ID 450	GFTFS SYGM H	SEQ ID 503	VIYPGDSD TRYSPSFQ G	SEQ ID 564	AAVGDGYSY GRLD	SEQ ID 671	SSQSLEH TDGNTYL SW	SEQ ID 744	AAS TRA TG	SEQ ID 801	YDNL PPLT F
SEQ ID 451	GFTFD DYAM H	SEQ ID 504	RVKNKAD GETTDYA APVKG	SEQ ID 565	LPSYYYDSS GYFTWYFDL	SEQ ID 672	ASQSISGS YLAW	SEQ ID 745	KVS TRF SG	SEQ ID 802	ALQT PYTF
SEQ ID 452	GFTFS NYVM S	SEQ ID 505	NIKQDGTE KHYVDSV KG	SEQ ID 566	ELYNYGSKD YFDY	SEQ ID 673	SSQSLLH SNGNNYL DW	SEQ ID 746	DAS SRA EG	SEQ ID 803	GLQT PFTF
SEQ ID 453	GFTFS SYAMS	SEQ ID 506	VISYDGSN KYYADSV KG	SEQ ID 567	GGTWDTAM VTGFDY	SEQ ID 674	ASQNIRH WLVW	SEQ ID 747	AAS NLQ SG	SEQ ID 804	YGSS PALT F
SEQ ID 454	GYTFT SYDIN	SEQ ID 507	AISGSGGS TYYADSV KG	SEQ ID 568	PHYDILTGSR APFDY	SEQ ID 675	ASQSIGG SLHW	SEQ ID 748	YAS QSF SG	SEQ ID 805	ALHT PWTF
SEQ ID 455	GYTFT DYAIH	SEQ ID 508	YISSTSSTI YYADSVK G	SEQ ID 569	ARVESKDGY FDY	SEQ ID 676	ASQSVTS NYLAW	SEQ ID 749	GAS YRA TG	SEQ ID 806	YNH WPLY TF
SEQ ID 456	GFTVS SNYMS	SEQ ID 509	AISGIGDTT YYADSVK G	SEQ ID 570	DLRLSTWDA YDF	SEQ ID 677	ASQSISSN LAW	SEQ ID 750	WAS ARE SG	SEQ ID 807	GSN WPLT F
SEQ ID 457	GGTFS SYAIS	SEQ ID 510	WMNPNSG NTGYAQK FQG	SEQ ID 571	NSQRSFDY	SEQ ID 678	SSQSVLY SSNNKNY LAW	SEQ ID 751	TAS KRA TG	SEQ ID 808	ATHY PRTF
SEQ ID 458	GFTFS SYAIS	SEQ ID 511	WINAGDG GTKSSREF QG	SEQ ID 572	DLGDPRGGIL NY	SEQ ID 679	ASQSLST NLAW	SEQ ID 752	ASS TLQ SG	SEQ ID 809	YGSS PIFTF
SEQ ID 459	GFTFS SYAIH	SEQ ID 512	VIYSGGST YYADSVK G	SEQ ID 573	SSPWGELSL YQGAFDI	SEQ ID 680	ASQSISS WLAW	SEQ ID 753	WAS TRD SG	SEQ ID 810	GLQI PITF
SEQ ID 460	GYTFT SSDIN	SEQ ID 513	GIIPIFGTA NYAQKFQ G	SEQ ID 574	DNDFWSGKV FDY	SEQ ID 681	ASHSVGA NYIAW	SEQ ID 754	DAS TRA TG	SEQ ID 811	HNSY PWTF
SEQ ID 461	GDSVS SNSAA WN	SEQ ID 514	GIIPMYGT ANYAQKF QG	SEQ ID 575	EGGSGWRHY FDY	SEQ ID 682	ASQGIAN YLAW	SEQ ID 755	GAS SLQ SG	SEQ ID 812	SISLP LTF
SEQ ID 462	GDSVS SNNAA WN	SEQ ID 515	WMNPNSG NTGYAEK FQG	SEQ ID 576	DYCSSTSCQ NWFDP	SEQ ID 683	SSQSVLY RTNNKN YLAW	SEQ ID 756	KAS TLA NG	SEQ ID 813	YASS VTF
SEQ ID 463	GFSLS TSGVG VG	SEQ ID 516	RTYYRSK WYNDYAV SVKS	SEQ ID 577	GRVAGDAFD I	SEQ ID 684	SNRSVLY SPNNQNY LGW	SEQ ID 757	GAS SRA AG	SEQ ID 814	YNN WPRT F

SEQ ID 464	GGSISSYYWS	SEQ ID 517	RTFYRSKWYNDYAVSVKS	SEQ ID 578	DQGAAAGTLGYFDY	SEQ ID 685	ASESVNSNFLAW	SEQ ID 758	KVSNRLSG	SEQ ID 815	FYSPPRTF
SEQ ID 465	GFTFSSSAMH	SEQ ID 518	LIYWDDDKRYSPSLKS	SEQ ID 579	GIYDSSGSSNPFDS	SEQ ID 686	ASQSIGSNLAW	SEQ ID 759	GASRRATG	SEQ ID 816	YGSSPPGTF
SEQ ID 466	GDSVSSDSAVWT	SEQ ID 519	YIYYTGSTNYNPSLKS	SEQ ID 580	GYCSGGSCPGTDFDY	SEQ ID 687	ASQSVGNSLAW	SEQ ID 760	EVSNRFSG	SEQ ID 817	YHNWPPYTF
SEQ ID 467	GFTFSTYPMH	SEQ ID 520	MIWHDESKKYYADSVKG	SEQ ID 581	DGVGGRDGYNFDY	SEQ ID 688	ASQSITNWLAW	SEQ ID 761	AASYRATG	SEQ ID 818	YNSYWTF
SEQ ID 468	GFTFAAYNIN	SEQ ID 521	RTYYKSKWYNDYAASVKS	SEQ ID 582	APLAADGYFDY	SEQ ID 689	ARQSISNRLAW	SEQ ID 762	GASSRASG	SEQ ID 819	YAAAPITF
SEQ ID 469	GFTFSSYGMT	SEQ ID 522	VISYDGRNEYYADSVKG	SEQ ID 583	ARGLQYLIWYFDL	SEQ ID 690	ASQNVYSNFLAW	SEQ ID 763	KASTIKSG	SEQ ID 820	YNSVPLTF
SEQ ID 470	GYTFTGYYMH	SEQ ID 523	FISYDGSNKYYADSVKG	SEQ ID 584	PGMVRGVITAPLDY	SEQ ID 691	SSQSLEHGDGNTYLSW	SEQ ID 764	AASNLHSG	SEQ ID 821	YYNLPRSF
SEQ ID 471	GYTLTELSMH	SEQ ID 524	FIRANADSGTTEYAASVKG	SEQ ID 585	EAKWGMYYFDY	SEQ ID 692	ASQSVSSTSLAW	SEQ ID 765	LGSNRAPG	SEQ ID 822	YASTPYTF
SEQ ID 472	GFTFSDQYMD	SEQ ID 525	TISGNGVGTYYPDSVKD	SEQ ID 586	GGGASYTDS	SEQ ID 693	ASQSVGSKLAW	SEQ ID 766	RASSRATG	SEQ ID 823	YNNWPLTF
SEQ ID 473	GFTFGDYAMS	SEQ ID 526	WINPNSGGTNYAQKFQG	SEQ ID 587	KGGYVGYSYGPFGGY	SEQ ID 694	SSQSLLGGDGKTYLYW	SEQ ID 767	EVSNRDSG	SEQ ID 824	RSNWSLTF
SEQ ID 474	GFNFSGYEMN	SEQ ID 527	GFDPEDGETIYAQKFQG	SEQ ID 588	GGTMVRGFGFNY	SEQ ID 695	ASQSVSSNSLAW	SEQ ID 768	RASTRAAG	SEQ ID 825	YGPSRRITF
SEQ ID 475	RFTFSDAWMS	SEQ ID 528	RVRNKANSYTTEYAASVKG	SEQ ID 589	ARRAMIGPLPRLVGYFDL	SEQ ID 696	SSQSLVYSDGNTYLNW	SEQ ID 769	RASRLESG	SEQ ID 826	HGEWPTF
SEQ ID 476	GFTFSTYGMH	SEQ ID 529	AISSNGGSTYYADSVKG	SEQ ID 590	GRPAPSWVKTRNWFDP	SEQ ID 697	ASQSISRWLAW	SEQ ID 770	DSNRATG	SEQ ID 827	RGTWPPLTF
SEQ ID 477	GISFRDYWMH	SEQ ID 530	YVSTSGSTRYYADSVKG	SEQ ID 591	EASSGWN	SEQ ID 698	PSQDIGTYLNW	SEQ ID 771	KVSKRDSG	SEQ ID 828	YTNYPRTF
SEQ ID 478	GDSVSSKSAAWN	SEQ ID 531	GISGSGGSTYYADSVKG	SEQ ID 592	GGRYTKGGYFDD	SEQ ID 699	ASQSISSCLAW	SEQ ID 772	KASSLTSG	SEQ ID 829	YQSYWTF
SEQ ID 479	GDSVSSGSAAWN	SEQ ID 532	RIKSKISGGTTDYAAPVQG	SEQ ID 593	RLDSSGRGGYFDY	SEQ ID 700	SSQSLLHSDGKTYLYW	SEQ ID 773	DSSNRATG	SEQ ID 830	YNSPPRTF

SEQ ID 480	EFTLR NYGVS	SEQ ID 533	RTYYRSK WYNDYAV SLKS	SEQ ID 594	ELVGTSSPYY YYYYGMDV	SEQ ID 701	SSQSVLY SSNNKNY IAW	SEQ ID 774	GVS TRA TG	SEQ ID 831	YGTS PITF
SEQ ID 481	GGSVS GYYW S	SEQ ID 534	LISYDGSK KYYANSV KG	SEQ ID 595	DYYYGSGSS P	SEQ ID 702	ASQSLTS SYLAW	SEQ ID 775	GAS SRA TD	SEQ ID 832	GIYW PRTF
SEQ ID 482	GDSVS SNTAT WN	SEQ ID 535	WINAGNG NTKYSEKF EG	SEQ ID 596	GRPYCSSTSC YPEWFDP	SEQ ID 703	SSQSLVH SNGHTYL SW	SEQ ID 776	GTS TRA TG	SEQ ID 833	YGSS PPITF
SEQ ID 483	GDSVS GNSAA WN	SEQ ID 536	RINPDGSS TSYADSVK G	SEQ ID 597	LRGIDYYDSS GYQRGFDY	SEQ ID 704	ASQSVGS DLAW	SEQ ID 777	DAS NLE TG	SEQ ID 834	YNN WPPI TF
SEQ ID 484	GYTFT SYAIS	SEQ ID 537	RTYYRSK WNNDYAL SVKS	SEQ ID 598	GGRGDGAAF DI	SEQ ID 705	SSQSLLH SSGYNYL DW	SEQ ID 778	AAS SLQ SG	SEQ ID 835	TLQT PLTF
SEQ ID 485	GFIFSN YAIH	SEQ ID 538	RTYYRAK WYNEYAG SVKS	SEQ ID 599	PPDGGNSGR WYFDL	SEQ ID 706	ASQTINS WLAW	SEQ ID 779	EVS KRD SG	SEQ ID 836	YYSS TPYT F
		SEQ ID 539	GMSGSGY STYYADSV KG	SEQ ID 600	DKNVRKHD YGDHPYGGY FDY	SEQ ID 707	ASQTIGP KSFGW	SEQ ID 780	WAS TRG SG	SEQ ID 837	STQF PWTF
		SEQ ID 540	EIHHSGST NYNPSLKS	SEQ ID 601	VAGATSLWY	SEQ ID 708	SSQSLVY SDGNTYL YW	SEQ ID 781	KIS NRF SG	SEQ ID 838	YNN WPHT F
		SEQ ID 541	RTYYRSK WYKDNAL SVKS	SEQ ID 602	LANSDGVDV	SEQ ID 709	ASQSITT WLAW	SEQ ID 782	KAS SLE SG	SEQ ID 839	YGNS QTF
		SEQ ID 542	LIYSDGRT NYADSVK G	SEQ ID 603	GVTRTFDY	SEQ ID 710	ASQSIGT YVAW	SEQ ID 783	GAS TRA TA	SEQ ID 840	GTH WPRT F
		SEQ ID 543	AISSNGGS TYYANSV KG	SEQ ID 604	GNGPFDP	SEQ ID 711	ASQSVNS GYLAW			SEQ ID 841	YKSD SRTF
		SEQ ID 544	WISAYDG NTNYAQK LQG	SEQ ID 605	RDTPLVGVSI Y	SEQ ID 712	ASQSVSS SYLGW			SEQ ID 842	SYGP RTF
		SEQ ID 545	YISSSGTTI YYADSVK G	SEQ ID 606	RAGYGDYRH FQH	SEQ ID 713	ASQSISN NLAW			SEQ ID 843	YGSS GYTF
		SEQ ID 546	VIWYDGS NKYYADS VKG	SEQ ID 607	TGDRFQEFD Y	SEQ ID 714	ASQSVSS SSLAW			SEQ ID 844	YGSS F
				SEQ ID 608	DDRGRGDDF DY	SEQ ID 715	SNQSLVY SDGGTYL NW			SEQ ID 845	LNSY PQTF
				SEQ ID 609	HGRAGINWY FDL	SEQ ID 716	ASQSISN YLNW			SEQ ID 846	SIQLP LTF
				SEQ ID 610	GGGLWAFDI	SEQ ID 717	ASQSVST LLAW			SEQ ID 847	YYYI PRTF

				SEQ ID 611	DKIGSCPY	SEQ ID 718	ASQGIRNDLGW			SEQ ID 848	ALQTRTF
				SEQ ID 612	RPDSSSQCFDY	SEQ ID 719	SSHSLTTTDGRTYVAW			SEQ ID 849	YGSSPNTF
				SEQ ID 613	SSGWSLPEDY	SEQ ID 720	ASQSVTSNLAW			SEQ ID 850	GTHWPPLTV
				SEQ ID 614	DVNPELLGAGFDY	SEQ ID 721	ASQSVFNNYLAW			SEQ ID 851	YGRSPYTS
				SEQ ID 615	SLNSGGYRCFHH	SEQ ID 722	SSQSVLYDSNSKNYLSW			SEQ ID 852	YYSTPLTF
				SEQ ID 616	APRGVVPAAMRGGY	SEQ ID 723	ASQSVGTNLAW			SEQ ID 853	GLQIPLTF
				SEQ ID 617	LVGNSGSYYPFGY	SEQ ID 724	SSQSLVYSDGNTYLSW			SEQ ID 854	SIQLPWTF
				SEQ ID 618	GRSLPYRGLAPRSFGGYYFDY	SEQ ID 725	ASQSVISRYLAW			SEQ ID 855	YNNWPRF
				SEQ ID 619	GRTHWGPQDFDY	SEQ ID 726	ASQSVSSSLAW			SEQ ID 856	YNSYSPTF
				SEQ ID 620	GGMYYYGSGSSYFDY					SEQ ID 857	RYNWPITF
				SEQ ID 621	KIAAAGKQPVDY					SEQ ID 858	RSRWPLTF
				SEQ ID 622	RKVYDYVWGSYRLPGSVSYYFDY					SEQ ID 859	GRHWPYTL
				SEQ ID 623	LPGRAARPDY					SEQ ID 860	YNSYSRTF
				SEQ ID 624	GPGAVAGTKPKYYFDY					SEQ ID 861	YNGASRMF
				SEQ ID 625	ATYYYDSSGYRFDY					SEQ ID 862	RSNWPFF
				SEQ ID 626	RNLGY					SEQ ID 863	RAEWPLTF
				SEQ ID 627	ARYYDSSGYIAPSGYFDY					SEQ ID 864	YGNSAMYNF

				SEQ ID 628	DGPAVDGAEYFQH					SEQ ID 865	YNNWPPFTF
				SEQ ID 629	LASGSPPPGDY					SEQ ID 866	YGISPLAF
				SEQ ID 630	GPIVGATMDY					SEQ ID 867	YNFWPSITF
				SEQ ID 631	WYGDYGLDY					SEQ ID 868	YGSSQTF
				SEQ ID 632	VAKYYYESGGYRASNWFDP					SEQ ID 869	GTHWPYTF
				SEQ ID 633	APPPTVGWYAPVFDY					SEQ ID 870	FDNVPVTF
				SEQ ID 634	VTGRRVGAHDY					SEQ ID 871	YGSSSMYTF
				SEQ ID 635	AQPGAETLNFDL					SEQ ID 872	SYITPWTF
				SEQ ID 636	QVAGGMDV					SEQ ID 873	RYVWPFTF
				SEQ ID 637	GSVYSGSYYMLIDY					SEQ ID 874	HNSYPRTF
				SEQ ID 638	QDKDNTRYSGLGV					SEQ ID 875	RSNWPWTF
				SEQ ID 639	GPRMWSSGIDAFDI					SEQ ID 876	GTHGPHTF
				SEQ ID 640	RDWAGKRV					SEQ ID 877	YGSPPPTTF
				SEQ ID 641	GRAGIAAFDI					SEQ ID 878	YGSSRRTF
				SEQ ID 642	GALQGEWRRFDY					SEQ ID 879	YGSSPITF
				SEQ ID 643	TNQGYGGNSGVFDY					SEQ ID 880	YGSSLRYTF
				SEQ ID 644	IVGGAVDC					SEQ ID 881	FYGIPHF

				SEQ ID 645	VRVGATTVY DSWFDP					SEQ ID 882	GTQF PQTF
				SEQ ID 646	DGGSSPYYD SSGLLPWYF DL					SEQ ID 883	YGSS PPYT F
				SEQ ID 647	AKFWTYYFD Y					SEQ ID 884	YNSY SGTF
				SEQ ID 648	GGGSGSYYK RFFDY					SEQ ID 885	YDN WPPL F
				SEQ ID 649	DGTVRRVVG ATTPGNFDY						
				SEQ ID 650	DLNRGYCSG GSCFGY						
				SEQ ID 651	DYSSSGECFD Y						
				SEQ ID 652	DQAAMVGY FDY						
				SEQ ID 653	TFAGYSSKL GYFDL						

Table 7. Heavy Chain CDR DNA Sequences

SEQ ID	CDRH1 DNA Seq	SEQ ID	CDRH2 DNA Seq	SEQ ID	CDRH3 DNA Seq
SEQ ID 1004	GGGGACAGTGTCTCTAGCAACACTGCTACTTGGAAC	SEQ ID 1062	AGGACATACTACAGGTCCAAGTGGTATAAGGATAATGCACTGTCTGTGAAAAGT	SEQ ID 1127	GCCCGGCGGGCTATGATAGGGCCGCTTCCGCGACTTGTCGGGTACTTCGATCTC
SEQ ID 1005	GGATTCACCTTCAGTTCCCATCTTATGCAC	SEQ ID 1063	GTTATATCATATGATGGAACTAGTAAATATTACGGAGACTCCGTGAAGGGC	SEQ ID 1128	GGCCGCCCCGCCCCATCCTGGGTTAAAACCCGTAACTGGTTCGACCCC
SEQ ID 1006	GGGGACAGTGTCTCTAGCGGCAGTGCTGCTTGGAAC	SEQ ID 1064	AGGACATATTATAGGGCCAAGTGGTATAATGAATATGCAGGGTCTGTGAAAAGC	SEQ ID 1129	GGAGGAATGTATTACTATGGTTCGGGGAGCTCGTACTTTGACTAC
SEQ ID 1007	GGTTACACCTTTACCAGCTACGGTATCAGC	SEQ ID 1065	TGGATCAGCGCTTACAATGGTAACACAAACTATGCACAGAAGCTCCAGGGC	SEQ ID 1130	AGGAAGGTGTATGATTACGTTTGGGGGAGTTATCGCCTCCCCGGGTCGGTATCGTACTACTTTGACTAC
SEQ ID 1008	GGATTCACCTTCAGTAGCTATGCTATACAC	SEQ ID 1066	CTCATTTATTGGGATGATGATAAGCGCTACAGCCCATCTCTGAAGAGC	SEQ ID 1131	AAGGGGGGCTACGTCGGATACAGCTATGGACCTTTTGGGGGCTAC
SEQ ID 1009	GGGTTCTCACTCAGCACTAGTGGAGTGGGTGTGGGC	SEQ ID 1067	TGGATGAACCCTAACAGTGGTAACACCGGCTATGCAGAGAAGTTCCAGGGC	SEQ ID 1132	GGTCGGGCTGGTATTGCCGCTTTTGATATC
SEQ ID 1010	GGATACACCTTCACCAGTTCTGATATCAAC	SEQ ID 1068	GTTATATCATATGATGGAAGTAATAAATACTACGCAGACTCCGTGAAGGGC	SEQ ID 1133	GCAGATTATAAATATGACT
SEQ ID 1011	GGATTCACCTTCAGTAGCTATGCTATGCAC	SEQ ID 1069	ACTATTAGTGGTAATGGTGTTGGCACATACTACCCAGACTCCGTGAAGGAC	SEQ ID 1134	AGCAGTGGCTGGTCACTGCCTGAAGACTAC
SEQ ID 1012	GGATTCACCTTTAGCAGCTATGGCATGACG	SEQ ID 1070	GTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGC	SEQ ID 1135	CAAGACAAAGACAACACGAGATATTCCGGTTTGGGCGTC

SEQ ID 1013	GGATACACCTTCGCCGC CTATTATTTACAC	SEQ ID 1071	CGGATCAGCCCTGGTAACGGT GTCACAAGTTATGCACAGAAA TTTCAGGGC	SEQ ID 1136	GCCGCGGTGGGGGATGGATACAGCT ATGGTCGGCTCGATT
SEQ ID 1014	GGATACACCTTCACCGG CTACTATATGCAC	SEQ ID 1072	TGGATCAACCCTAACAGTGGT GGCACAAACTATGCACAGAAG TTTCAGGGC	SEQ ID 1137	GATCAGGCAGCTATGGTAGGCTACT TTGACTAC
SEQ ID 1015	GGATACACCTTCACCAG TTATGATATCAAC	SEQ ID 1073	TGGATGAACCCTAACAGTGGT AACACAGGCTATGCACAGAAG TTCCAGGGC	SEQ ID 1138	GGCCGGCCATATTGTAGTAGTACCA GCTGCTACCCAGAGTGGTTCGACCC C
SEQ ID 1016	GGATTCATCTTCAGTAAC TATGCTATACAC	SEQ ID 1074	CGTGTTAAAAACAAAGCTGAT GGTGAGACAACGGACTACGCT GCACCCGTCAAAGGC	SEQ ID 1139	AGATTGGATAGCAGTGGCCGTGGTG GTTACTTTGACTAC
SEQ ID 1017	GGATTCACTTTCACTGAT GCCTGGATGAAC	SEQ ID 1075	GCTATTAGTGGTAGTGGTGGTA GCACATACTATGCAGACTCCGT GAAGGGC	SEQ ID 1140	GACAAGAACGTCCGAAAACATGAC TACGGTGACCACCCCTACGGGGGGT ACTTTGACTAC
SEQ ID 1018	GGTGGGTCCGTCAGTGG TTACTACTGGAGC	SEQ ID 1076	GAAATCCATCATAGTGGAAGC ACCAACTACAACCCGTCCCTCA AGAGT	SEQ ID 1141	GAGTTGGTGGGTACCAGCTCTCCTT ATTACTACTACTACTACGGTATGGA CGTC
SEQ ID 1019	GGATTCAACTTCAGTGG ATATGAAATGAAC	SEQ ID 1077	TACGTCAGTACTAGTGGTAGTA CCAGATACTACGCAGACTCTGT GAAGGGC	SEQ ID 1142	GGTGGGGGTGCGAGCTATACTGACT CC
SEQ ID 1020	GGGGACAGTGTCTCTAG CAACAGTGTTACTTGGA AC	SEQ ID 1078	AGGACTTACTACCGGTCCCAGT GGTATTATAATTATGCGGTGTC TGTGAAAAGT	SEQ ID 1143	TCGAGCCCCTGGGGGGAGTTATCGT TATACCAGGGGGCTTTTGATATC
SEQ ID 1021	GGATTCACCTTCAGCAG CTATGCTATGCAC	SEQ ID 1079	CGTATTAATCCTGATGGGAGTA GCACAAGCTACGCGGACTCCG TGAAGGGC	SEQ ID 1144	GTGGCGGGAGCTACTTCCCTATGGT AC
SEQ ID 1022	GGAATCAGCTTCAGAGA TTACTGGATGCAC	SEQ ID 1080	TGGATCAACGCTGGCAATGGT AACACAAAATATTCACAGAAG TTCCAGGGC	SEQ ID 1145	CATGGTAGGGCCGGAATAAACTGGT ACTTCGATCTC

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SEQ ID 1023	GGATACACCTTCACTAG CTATGCTATGCAT	SEQ ID 1081	CTTATTTATAGTGATGGTCGCA CAAACTATGCAGACTCCGTGA AGGGC	SEQ ID 1146	GCGCCCCCTCCGACTGTTGGCTGGT ACGCCCCCGTCTTTGACTAC
SEQ ID 1024	GGGTTCACCGTCAGTAG CAACTACATGAGC	SEQ ID 1082	AACATAAAGCAAGATGGAACT GAGAAACACTATGTGGACTCT GTGAAGGGC	SEQ ID 1147	GACTATTACTATGGTTCGGGGAGTT CTCCC
SEQ ID 1025	GGATTCACCTTTAGTAAC AATTGGATGACC	SEQ ID 1083	GGTATGAGTGGTAGTGGTTATA GTACATACTACGCAGACTCCGT GAAGGGC	SEQ ID 1148	GATCTGAATCGAGGATATTGTAGTG GTGGTAGCTGCTTTGGCTAC
SEQ ID 1026	GAATTCACCCTTAGGAA CTATGGCGTGAGC	SEQ ID 1084	GCTATTAGTAGTAATGGGGGT AGCACATACTACGCAGACTCA GTGAAGGGC	SEQ ID 1149	GCCCAGCCGGGCGCTGAGACGTTGA ACTTCGATCTC
SEQ ID 1027	GGTTACACATTTACCAGT TATGCCATCAGC	SEQ ID 1085	TGGATCAGCGCTTACGACGGT AACACAAACTATGCACAGAAG CTCCAGGGC	SEQ ID 1150	CCGGGTATGGTTCGGGGAGTTATTA CTGCCCCGCTTGACTAC
SEQ ID 1028	GGATTCACCTTCAGTACC TATCCCATGCAC	SEQ ID 1086	GTTATATCATATGATGGACGTA ATGAATACTACGCAGACTCCGT GAAGGGC	SEQ ID 1151	GGGGGGACTATGGTTCGGGGTTTCG GATTTAACTAC
SEQ ID 1029	GGATTCACCTTTGATGAT TATGCCATGCAC	SEQ ID 1087	GCTATTAGTGGTAGTGGTGGTA GCACATACTACGCAGACTCCGT GAAGGGC	SEQ ID 1152	GCCACGTATTACTATGATAGTAGTG GTTATAGGTTTGACTAC
SEQ ID 1030	GGGGACAGTGTCTCTAA CAACAGGGCTGCTTGGA AC	SEQ ID 1088	AGGACATACTACAGGTCCAAG TGGTATAATGAATATGCAGTCT CTGTGAAAAGT	SEQ ID 1153	GAGGCTGCCGACGACCCGTTTGACC AT
SEQ ID 1031	GGATTCACCTTCAGTGA CCCCTACATGGAC	SEQ ID 1089	CGAATTACAAATAAGCGTACC GGTTACGCCACAACATATGCC GCGTCTGTGAAGGAC	SEQ ID 1154	GGCCCCGGGGCAGTGGCTGGTACTA AGCCAAAGTACTACTTTGACTAC
SEQ ID 1032	GGATTCACTTTCAGTAAC GCCTGGATGAGC	SEQ ID 1090	CGTATTAAAAGCAAAACTGAT GGTGGGACAACAGACTACGCT GCACCCGTGAAAGGC	SEQ ID 1155	GACAAGATCGGCAGCTGTCCTTAC

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SEQ ID 1033	GGGGACAGTGTCTCTAGCAACAGTGCTGCTTGGAAC	SEQ ID 1091	AGGACATACTACAGGTCCAAGTGGTATAATGATTATGCAGTATCTGTGAAAAGT	SEQ ID 1156	GGAATCTATGATAGTAGTGGTTCTTCCAATCCCTTTGACTCC
SEQ ID 1034	GGATTCACCTTCAGTAGCTATGCTATGCAT	SEQ ID 1092	TACATCTATCATAGTGGGAGCACCTACTACAACCCGTCCCTCAAGAGT	SEQ ID 1157	ACTTTTGCGGGGTATAGCAGCAAACTGGGGTACTTCGATCTC
SEQ ID 1035	GGTGGCTCCATCAGCAGTGGTGGTTACTCCTGGAGC	SEQ ID 1093	AGGACTTACTACAGGTCCAAGTGGTATAATGATTATGCAGTATCTCTGAAAAGT	SEQ ID 1158	GCCCGAGTGGAATCCAAGGATGGGTACTTTGACTAC
SEQ ID 1036	GGGGACAGTGTCTCTGGCAACAGTGCTGCTTGGAAC	SEQ ID 1094	TTCATTAGAGCCAACGCTGATAGTGGGACAACAGAGTACGCCGCGTCTGTGAAAGGC	SEQ ID 1159	GACCTGCGACTTTCTACGTGGGATGCTTATGATTTC
SEQ ID 1037	GGATTCACCTTTGCTGCTTATAATATCAAC	SEQ ID 1095	AGGACATACTACAGGTCCAAGTGGTATAATGATTATGCAGTATCTGTGAAGAGT	SEQ ID 1160	GGATCGGTATATAGTGGGAGCTACTATATGCTCATTGACTAC
SEQ ID 1038	GGGGACAGTGTCTCTAGCAACAATGCTGCTTGGAAC	SEQ ID 1096	AGGACATTCTACAGGTCCAAGTGGTATAATGACTATGCAGTTTCTGTGAAAAGT	SEQ ID 1161	CGGGATTGGGCAGGAAAAAGGGTC
SEQ ID 1039	GGTTACACCTTTACCAGCTATGGTATCAGC	SEQ ID 1097	TGGATCATCCCTATCTTTGGTATAGCAAACTACGCACAGAAGTTCCAGGGC	SEQ ID 1162	GATGGGGGGTCCAGCCCATACTATGATAGTAGTGGTTTACTACCCTGGTACTTCGATCTC
SEQ ID 1040	GGATTCACCTTTAGCAGCTATGCCATGAGC	SEQ ID 1098	TGGATCAACGCTGGCAATGGTAACACAAAATATTCAGAGAAGTTCGAAGGC	SEQ ID 1163	GGCAATGGGCCGTTCGACCCC
SEQ ID 1041	GGATTCACCTTTAGCAACTATGTCATGAGC	SEQ ID 1099	TACATCAGTAGTACTAGTAGTACCATATACTACGCAGACTCCGTGAAGGGC	SEQ ID 1164	GGACGGACTCACTGGGGCCCCCAGGACTTTGACTAC
SEQ ID 1042	GGATTCACCTTCAGCAGCTCTGCCATGCAC	SEQ ID 1100	GCTATTAGTGGTATTGGTGATACTACATACTACGCGGACTCCGTGAAGGGC	SEQ ID 1165	AGGGGACATAACTACGGTGTAGATTAC

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SEQ ID 1043	GGAGGCACCTTCAGCAG CTATGCTATCAGC	SEQ ID 1101	AGGACATATTACAGGTCCAAG TGGTATAATGATTATGCAGTAT CTGTGAAAAGT	SEQ ID 1166	GATTATTGTAGTAGTACCAGCTGCC AGAACTGGTTCGACCCC
SEQ ID 1044	GGATACAGCTTTACCAG CTACTGGATCGCC	SEQ ID 1102	ATGATTTGGCATGATGAGAGT AAGAAATACTATGCAGACTCC GTGAAGGGC	SEQ ID 1167	TGGTACGGTGACTACGGCCTTGACT AC
SEQ ID 1045	CGATTCACTTTCAGTGAC GCCTGGATGAGC	SEQ ID 1103	GGGATCATCCCTATCTTTGGTA CAGCAAACTACGCACAGAAGT TCCAGGGC	SEQ ID 1168	GTTACGGGACGGAGAGTGGGAGCC CATGACTAC
SEQ ID 1046	GGATTCACCTTCAGTACC TATGGCATGCAC	SEQ ID 1104	GTCATCTATCCTGGTGACTCTG ATACCAGATACAGCCCGTCCTT CCAAGGC	SEQ ID 1169	GGCTCCTTGTCCCGAAGTGGCTGGT ACGCCGGACTCTTTGACTAC
SEQ ID 1047	GGATTCACCGTCAGTAG CAACTACATGAGC	SEQ ID 1105	CGTATTAAAAGCAAAATAAGT GGTGGGACAACAGACTACGCT GCACCCGTGCAAGGC	SEQ ID 1170	GGGGCCCTACAGGGCGAATGGCGG AGATTTGACTAC
SEQ ID 1048	GGATTCACCTTCAGTAG CTATAGCATGAAC	SEQ ID 1106	GCTATTAGTAGTAATGGGGGT AGCACATATTATGCAAACTCTG TGAAGGGC	SEQ ID 1171	AACAGTCAACGTTCGTTTGACTAC
SEQ ID 1049	GGGGACAGTGTCTCTAG CGACAGTGCTGTTTGGA CC	SEQ ID 1107	GGTATTAGTGGTAGTGGTGGTA GCACATACTACGCAGACTCCGT GAAGGGC	SEQ ID 1172	GGGCCCCGAATGTGGAGCAGTGGC ATTGATGCTTTTGATATC
SEQ ID 1050	GGATTCACCTTTGGTGAT TATGCTATGAGC	SEQ ID 1108	CTTATATCATATGATGGAAGTA AAAAATACTATGCAAACTCCG TGAAGGGC	SEQ ID 1173	CGGGCGGGTTACGGTGACTACAGAC ACTTCCAGCAC
SEQ ID 1051	GGATTCACCTTCAGTAGT TATAGCATGAAC	SEQ ID 1109	GTTATTTATAGCGGTGGTAGCA CATACTACGCAGACTCCGTGA AGGGC	SEQ ID 1174	CATAGACGCCCAATTTACGATATTT TGACTGGTTTTGACTAC
SEQ ID 1052	GGATACACCTTCACTGA TTATGCTATACAT	SEQ ID 1110	TACATTAGTAGTAGTGGTAGTT ACACAAACTACGCAGACTCTG TGAAGGGC	SEQ ID 1175	GATGGTACGGTCCGAAGGGTAGTGG GAGCTACTACCCCTGGAAACTTTGA CTAC

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SEQ ID 1053	GGTGGCTCCATCAGTAG TTACTACTGGAGC	SEQ ID 1111	CGTATTAAAAGCAAAACTGAT GGTGAGACAACAGACTACGCT GCACCCGTGAAAGGC	SEQ ID 1176	CGGGATACACCTTTGGTTGGGGTTT CGATATAC
SEQ ID 1054	GGATTCACCTTCAGTAG CTATGGCATGCAC	SEQ ID 1112	AGGACATACTACAAGTCGAAG TGGTATAATGATTATGCAGCAT CTGTGAAAAGT	SEQ ID 1177	GATAACGATTTTTGGAGTGGGAAAG TCTTTGACTAC
SEQ ID 1055	GGATTCACCTTCAGTGA CCAGTACATGGAC	SEQ ID 1113	TTCATTAGAAGCAAAGCTTATG GTGGGACAACAGAATACGCCG CGTCTGTGAAAGGC	SEQ ID 1178	GGCCGGTCCCTTCCCTACCGGGGGT TGGCTCCTAGATCTTTCGGAGGATA CTACTTTGACTAC
SEQ ID 1056	GGTGGGTCCTTCAGTGG TTACTACTGGAGC	SEQ ID 1114	TACATTAGTAGTAGTGGTACTA CCATATACTACGCAGACTCTGT GAAGGGC	SEQ ID 1179	TTGCCTAGTAGTGGTTATCTACAGG ACCACCACTACTACGGTATGGACGT C
SEQ ID 1057	GGATTCACCTTCAGCAG CTATGCTATCAGC	SEQ ID 1115	ATTATATCAGATGATGGAAGT AAGAGTTACTACGCAGACTCC GTGCAGGGC	SEQ ID 1180	GATGTCAGTGGGTCCTTCGCGGCCT AC
SEQ ID 1058	GGATACACCTTCACCAG CTACTATATGCAC	SEQ ID 1116	TGGATCAACGCTGGCGATGGT GGCACAAAAAGTTCACGGGAG TTCCAGGGC	SEQ ID 1181	GACGAGTATTTCTAC
SEQ ID 1059	GGGGACAGTGTCTCTAG CAAAAGTGCTGCTTGGA AC	SEQ ID 1117	TATATCTATTACACTGGGAGCA CCAACTACAACCCCTCCCTCAA GAGC	SEQ ID 1182	GAGGCTAGCAGTGGCTGGAAC
SEQ ID 1060	GGATACAGCTTTACCAG CTACTGGATCGGC	SEQ ID 1118	GTTATATCATATGATGGAAGTA ATAAATACTATGCAGACTCCGT GAAGGGC	SEQ ID 1183	GAGGGCGGAGCAGTGGCTGGTACT GTCTAC
SEQ ID 1061	GGATACACCCTCACTGA ATTATCCATGCAC	SEQ ID 1119	CGTGTTAGAAACAAAGCTAAC AGTTACACCACAGAATACGCC GCGTCTGTGAAAGGC	SEQ ID 1184	GATCGGCGTTACTATGATAGTAGTG GTTATTATCCCGCCTACTACTTTGAC TAC
		SEQ ID 1120	GAAATCAATCATAGTGGAAGC ACCAACTACAACCCGTCCCTCA AGAGT	SEQ ID 1185	GGCGGTACTTGGGATACAGCTATGG TTACGGGCTTTGACTAC

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		SEQ ID 1121	GGGATCATCCCTATGTATGGTACAGCAAACTACGCACAGAAGTTCCAGGGC	SEQ ID 1186	ATAGTGGGAGGTGCCGTTGACTGC
		SEQ ID 1122	ATAATCAACCCTAGTGGTGGTAGCACAAGCTACGCACAGAAGTTCCAGGGC	SEQ ID 1187	GAGGATACTATGGTTCGGGGAGTTATTCCC
		SEQ ID 1123	AGGACATACTACAGGTCCAAATGGAATAATGATTATGCATTATCTGTGAAAAGT	SEQ ID 1188	TTGGCGAGTGGTTCCCCCCCTCCGGGGGACTAC
		SEQ ID 1124	ATCATCTATCCTGGTGACTCTGATACCAGATACAGCCCGTCCTTCCAAGGC	SEQ ID 1189	GTTAGAGTGGGAGCTACTACTGTTTACGACAGCTGGTTCGACCCC
		SEQ ID 1125	TTTATATCATATGATGGAAGTAATAAATACTACGCAGACTCCGTGAAGGGC	SEQ ID 1190	GATGATCGGGGTCGGGGAGATGACTTTGACTAC
		SEQ ID 1126	GGTTTTGATCCTGAAGATGGTGAAACAATCTACGCACAGAAGTTCCAGGGC	SEQ ID 1191	CTAGCTAATTCCGACGGTGTGGACGTC
				SEQ ID 1192	GGCGGTGGTTCGGGGAGTTATTATAAGAGGTTCTTTGACTAC
				SEQ ID 1193	GGGGGAAGATATACCAAGGGAGGGTACTTTGACGAC
				SEQ ID 1194	GAACTATACAACTATGGTTCAAAGGACTACTTTGACTAC
				SEQ ID 1195	GATGGCCCCGCCGTTGATGGTGCTGAATACTTCCAGCAC
				SEQ ID 1196	GTCGCCAAATATTATTACGAGAGTGGTGGTTATCGGGCCTCCAACTGGTTCGACCCC
				SEQ ID 1197	GAAGGGGGCAGTGGCTGGCGCCACTACTTTGACTAC

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				SEQ ID 1198	GATCAAGGGGCAGCAGCTGGTACCC TGGGGTACTTTGACTAC
				SEQ ID 1199	GGGCGCGTGGCGGGGGATGCTTTTG ATATC
				SEQ ID 1200	ACCAACCAGGGATACGGTGGTAACT CCGGGGTATTTGACTAC
				SEQ ID 1201	CCCCCCGACGGTGGTAACTCCGGTC GCTGGTACTTCGATCTC
				SEQ ID 1202	GCCCGGGGGCTACAGTACCTAATCT GGTACTTCGATCTC
				SEQ ID 1203	GCTCGTTACTATGATAGTAGTGGTT ATATTGCCCCATCGGGTTACTTTGA CTAC
				SEQ ID 1204	GATGGTGTAGGAGGGAGAGATGGC TACAATTTTGACTAC
				SEQ ID 1205	CCCCATTACGATATTTTGACTGGTTC CCGGGCGCCCTTTGACTAC
				SEQ ID 1206	CGAAACTTAGGCTAC
				SEQ ID 1207	GCTAAGTTTTGGACATACTACTTTG ACTAC
				SEQ ID 1208	AAAATAGCAGCAGCTGGTAAGCAA CCTGTTGACTAC
				SEQ ID 1209	GGCCCTATAGTGGGAGCGACTATGG ACTAC
				SEQ ID 1210	AGACCGGATAGCAGCAGTCAATGTT TTGACTAC
				SEQ ID 1211	GCCCCCCTAGCAGCAGATGGCTACT TTGACTAC
				SEQ ID 1212	GACGGGGGCTATGATAGTAGTGGTT TTCACTTTGACTAC

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				SEQ ID 1213	GGGGTGGGATGGTCGCCCTTCCAATAC
				SEQ ID 1214	GGTGTAACCCGGACCTTTGACTAC
				SEQ ID 1215	GACGACAAAATAGCAGCAGCTGGATTCACATACTGGTACTTCGATCTC
				SEQ ID 1216	GATTATAGCAGCTCGGGGGAGTGCTTTGACTAC
				SEQ ID 1217	TTAAGGGGTATAGATTACTATGATAGTAGTGGTTACCAACGGGGGTTTGACTAC
				SEQ ID 1218	GCGCCGAGGGGTGTAGTACCAGCTGCTATGCGGGGGGGCTAC
				SEQ ID 1219	GACAGGGGAACTAAATGGAACCAATTGAATGATGTTTTTGATATG
				SEQ ID 1220	GGATATTGTAGTGGTGGTAGCTGCCCAGGAACGGATTTTGACTAC
				SEQ ID 1221	GGTGGGAGGGGGGATGGGGCCGCTTTTGACATC
				SEQ ID 1222	GATTTAGGGGATCCCCGGGGTGGTATTTTGAACTAC
				SEQ ID 1223	AGTCTCAATAGTGGGGGCTACCGATGCTTCCATCAC
				SEQ ID 1224	GTAAATCCGGGGAGTTATACGAGGGAGGTGAGCAACTTTGACTAC
				SEQ ID 1225	CTCCCGGGGAGAGCAGCTCGTCCAGACTAC
				SEQ ID 1226	GAAGCTAAGTGGGGAATGTACTACTTTGACTAC
				SEQ ID 1227	GGCCGAGGGTATAGCAGCAGTCGGCTCTACTACTTTGACTAC

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				SEQ ID 1228	TTGGTGGGCAATAGTGGGAGCTACT ATCCGTTTGGGTAC
				SEQ ID 1229	CAAGTCGCGGGCGGTATGGACGTC
				SEQ ID 1230	GGGGGAGGGCTTTGGGCTTTTGATA TC
				SEQ ID 1231	CTCCCCTCGTATTACTATGATAGTA GTGGTTACTTTACCTGGTACTTCGAT CTC
				SEQ ID 1232	ACAGGGGACCGCTTCCAAGAGTTTG ACTAC
				SEQ ID 1233	GATGTGAACCCGGAGCTACTGGGGG CGGGATTTGACTAC

Table 8. Light Chain CDR DNA Sequences

SEQ ID	CDRL1 DNA Seq	SEQ ID	CDRL2 DNA Seq	SEQ ID	CDRL3DNASeq
SEQ ID 1234	GCCAGTCAGAGTGTCGGTAACTCCTTA GCCTGG	SEQ ID 1308	GGTGCGTCCAGTTTGCAG AGTGGG	SEQ ID 1373	CAACGTGGCACCTGGCCT CCCCTCACTTTC
SEQ ID 1235	GCCAGTCAGAGTATAACTAACTGGTTG GCCTGG	SEQ ID 1309	AGGGCGTCTCGTTTAGAA AGTGGG	SEQ ID 1374	CAGTATACTAATTACCCTC GTACGTTC
SEQ ID 1236	GCCAGTCAGACTATTAATAGTTGGTTG GCCTGG	SEQ ID 1310	GGTGCTTCCACCAGGGCC ACTGGC	SEQ ID 1375	CAAAGTATACAGCTTCCG TGGACGTTC
SEQ ID 1237	GCAAGTCAGGGCATTAGAAATGATTTA GGCTGG	SEQ ID 1311	GGTGCATCCAGTTTGCAA AGTGGA	SEQ ID 1376	CAATATAATAGTTATTCTC CCACTTTT
SEQ ID 1238	GCAAGTCAGAGCATTAGCAGCTATTTA AATTGG	SEQ ID 1312	GCTGCATCCAGTTTGCAC ACTGGG	SEQ ID 1377	CACTATGGTCCCTCACGTC GGATCACCTTC
SEQ ID 1239	TCCAGCCAGAGTGTTTTATACAGCTCC AACAATAAGAACTACATAGCTTGG	SEQ ID 1313	GCTGCATCCACTTTGCAA AGTGGG	SEQ ID 1378	CAGCATAATTCCTACCCTC GAACATTC
SEQ ID 1240	GCCAGTCAGGGCATTAGCAGTTCTTTG GCCTGG	SEQ ID 1314	GCTGCATCCACCAGGGCC ACTGGT	SEQ ID 1379	CAGAGTTACAGTATTCCTC GAACGTTC
SEQ ID 1241	GCCAGTGAGAGTGTTAATAGCAACTTC TTAGCCTGG	SEQ ID 1315	GGTGCCTCCAGCAGGGCC GCTGGC	SEQ ID 1380	CAATATTATTATATTCCTC GGACGTTC
SEQ ID 1242	GCCAGTCAGAGTGTTGGCAGCAAATTA GCCTGG	SEQ ID 1316	GCTGCATCCTACAGGGCC ACTGGC	SEQ ID 1381	CAGTATGGTAGCTCATCC ATGTACACTTTT
SEQ ID 1243	GCCAGTCAGAATGTTTACAGCAATTTC TTAGCCTGG	SEQ ID 1317	AAGGTTTCTAACCGGTTG TCTGGG	SEQ ID 1382	CAGTATGATAATCTCCCTC CTCTCACTTTC

SEQ ID 1244	TCTAGTCAAAGTCTCGAACACGGTGAT GGAAACACGTACTTGAGTTGG	SEQ ID 1318	GATGCATCCACCAGGGCC ACTGGT	SEQ ID 1383	CAGTATAATAACTGGCCG CTCACTTTC
SEQ ID 1245	TCTAGTCAGAGCCTCCTGCATAGTAAT GGAAACAACTATTTGGATTGG	SEQ ID 1319	GGTACATCCACCAGGGCC ACTGGT	SEQ ID 1384	CAGTATAATAGTTATTCGG GGACGTTC
SEQ ID 1246	GCCAGTCAGAGTATTAGCAACAACTTA GCCTGG	SEQ ID 1320	GGTGCATCCAGGAGGGC CACTGGC	SEQ ID 1385	CAGTATAATAACTGGCCC CCGATCACCTTC
SEQ ID 1247	GCCAGTCAGAGTGTTAGCAGCACCTCC TTAGCCTGG	SEQ ID 1321	AAGATTTCTAACCGGTTC TCTGGG	SEQ ID 1386	CAATATGGAACCTCACCG ATCACCTTC
SEQ ID 1248	TCTAGTCAAAGCCTCGTATACAGTGAT GGAAACACCTACTTGAGTTGG	SEQ ID 1322	GATGCATCCACCAGGGCC ACGGGA	SEQ ID 1387	CAGTATAATAACTGGCCT CCCATCACCTTC
SEQ ID 1249	TCTAATCAAAGCCTCGTATACAGTGAT GGAGGCACCTACTTGAATTGG	SEQ ID 1323	AAGGTTTCTAAGCGGGAC TCTGGG	SEQ ID 1388	CAAGGTATATACTGGCCT CGAACCTTC
SEQ ID 1250	TCCAGCCAGAGTGTTTTATACAGAACC AACAATAAGAACTACTTGGCTTGG	SEQ ID 1324	GACTCCAACAGGGCCACT GGC	SEQ ID 1389	CAGCGTAGCAACTGGTCG CTCACTTTC
SEQ ID 1251	GCCAGTCAGAGCATTGGGAGCAATTTA GCCTGG	SEQ ID 1325	GAAGTTTCCAACCGGTTC TCTGGA	SEQ ID 1390	CAAGGTCTACAAATCCCT ATCACTTTC
SEQ ID 1252	TCTAGTCAAAGCCTCGTGTACAGTGAT GGAAACACCTACTTGTATTGG	SEQ ID 1326	GGTGCCTCCACCAGGGCC ACTGCT	SEQ ID 1391	CACTATAATAACTGGCCTC ATACCTTC
SEQ ID 1253	GCCAGTCAGAGTGTTAGAGACAACGTA GGTTGG	SEQ ID 1327	GCTGCCTCCACCAGGGCC ACTGGT	SEQ ID 1392	CAGTATGGTAGCTCGTTC
SEQ ID 1254	GCCAGTCAGACTATTGGTCCCAAGTCC TTCGGCTGG	SEQ ID 1328	TTGGGTTCTAATCGGGCC TCCGGG	SEQ ID 1393	CAGTATAATTTCTGGCCTT CGATCACCTTC
SEQ ID 1255	TCTAGTCAGAGCCTCCTGCATAGTGAT GGAAAGACCTATTTGTATTGG	SEQ ID 1329	GGTGCATCCTACAGGGCC ACTGGC	SEQ ID 1394	CACTATGGTAGTTCACCTC CAATCACCTTC
SEQ ID 1256	GCCAGTCAGAGTGTTAGTAGCAGCTTA GCCTGG	SEQ ID 1330	AGTGCAACCTCTAGGGCC ACTGGA	SEQ ID 1395	CAAGGTACACAATTTCCTC AAACGTTC
SEQ ID 1257	GCCAGTGAAGGTCTTACCACCAACTTA GCCTGG	SEQ ID 1331	AAGGTTTCTACCCGGTTC TCTGGG	SEQ ID 1396	CAAGGGACACACTGGCCG TACACTTTT
SEQ ID 1258	GCCAGTCAGAGTGTTAGCACCCTCTTA GCCTGG	SEQ ID 1332	GCTGCATCCAGTTTGCAA AGTGGG	SEQ ID 1397	CAATATTACAATCTTCCTC GATCTTTT
SEQ ID 1259	GCCAGTCAGAGTGTTTTCAACAACTAC TTAGCCTGG	SEQ ID 1333	GCTGCCTCCAATCTGCAC AGTGGC	SEQ ID 1398	CAGCATGGTGAATGGCCC ACCTTC
SEQ ID 1260	TCTAGTCAAAGCCTCGTATACAGTGAT GGAAACACCTACTTGAATTGG	SEQ ID 1334	GATGTATCCACCAGGGCC ACTGAT	SEQ ID 1399	CAAGGTAGACACTGGCCG TACACTCTT
SEQ ID 1261	TCTAGTCAGAGCCTCCTACATAGTAGT GGATACAACTATTTGGATTGG	SEQ ID 1335	AAGGCGTCTACTATAAAA AGTGGG	SEQ ID 1400	CAGTTTAATAATTGGCCTT ACACTTTT
SEQ ID 1262	TCTAGTCAGAGCCTCCTGAATAGTAAT GGATACAACTATTTGGAGTGG	SEQ ID 1336	GCTGCGTCCAATTTGCAA AGTGGG	SEQ ID 1401	CAGCGTAGCAGGTGGCCT CTCACTTTC

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SEQ ID 1263	GCCAGTCAGAGTGTTACCAGCAACTAC TTAGCCTGG	SEQ ID 1337	TGGGCATCTACCCGGGAA TCCGGG	SEQ ID 1402	CAAAGTATACAGCTTCCG CTCACTTTC
SEQ ID 1264	GCCAGTCAGAGTGTTAGCAGCAGCTCC TTAGCCTGG	SEQ ID 1338	GGTGCATCCACCAGGGCC ACTGGC	SEQ ID 1403	CAGTATGGTAGCTCACCC CCGGGCACTTTC
SEQ ID 1265	GCCAGTCAGAGTATTGGCAGCAACTTA GTCTGG	SEQ ID 1339	AAGGCGTCTACTTTAGCA AATGGG	SEQ ID 1404	CGCTATGATAACTGGCCTC CCCTTTTT
SEQ ID 1266	TCTAGTCAAAGCCTCGAACACACTGAT GGAAACACCTACTTAAGTTGG	SEQ ID 1340	GGTGCATCCACCAGGGCC AGTGGC	SEQ ID 1405	CAGTATAATCACTGGCCTC TCTACACTTTT
SEQ ID 1267	GCAAGTCAGAGCATTAGCAACTATTTA AATTGG	SEQ ID 1341	GATTCATCCAGCAGGGCC ACTGGC	SEQ ID 1406	CAGGGTAGCAACTGGCCG CTCACTTTC
SEQ ID 1268	CCAAGTCAGGACATAGGCACTTATTTA AATTGG	SEQ ID 1342	GGTGCATCCAACAGGGCC ACTGGT	SEQ ID 1407	CAAGGTACACACTGGCCT CGAACGTTC
SEQ ID 1269	GCCAGTCAAAGTGTTAACAGCAACGTA GCCTGG	SEQ ID 1343	GATGCATCCAGCAGGGCC ACTGGC	SEQ ID 1408	CACCGTTACGTGTGGCCGT TCACTTTC
SEQ ID 1270	GCCAGTCAGAGTGTTGGTACCAATTTA GCCTGG	SEQ ID 1344	GATTCATCGAATAGGGCC ACTGGC	SEQ ID 1409	CAGTATGGTAGTTCACCG ATCACCTTC
SEQ ID 1271	GCCAGTCAGAGTATTAGTAGGTGGTTG GCCTGG	SEQ ID 1345	GGTGCATCCAGCAGGGCC TCTGGC	SEQ ID 1410	CAAGGTACACATTGGCCT CGGACTTTC
SEQ ID 1272	GCGAGTCAGAACATTCGCCACTGGTTA GTCTGG	SEQ ID 1346	TGGGCGTCTACCCGGGGG TCCGGG	SEQ ID 1411	CAAGGTCTACAAATTCCG CTCACTTTC
SEQ ID 1273	TCCAGCCGGAATATTTTATACAGCGGC AACAATAAAAACTTCTTGGCTTGG	SEQ ID 1347	AAGGTTTCTAACCGGGAC TCTGGG	SEQ ID 1412	CAGTCTCTACAAACTCCTC TCACTTTC
SEQ ID 1274	GCCAGTCAGAGTATTAGCAGCACCTAC TTAGCCTGG	SEQ ID 1348	GGTGCATCCAGCAGGGCC ACTGAC	SEQ ID 1413	CAGTATGCTAGCTCAGTC ACCTTC
SEQ ID 1275	GCCAGGCAGAGCATCAGTAACCGGTTG GCCTGG	SEQ ID 1349	TATGCTTCCCAGTCCTTCT CAGGG	SEQ ID 1414	CAGTATAATAACTGGCCT CCCTTCACCTTC
SEQ ID 1276	GCCAGTGAGAGTGTTAGCAAGAGCTAC TTACTCTGG	SEQ ID 1350	TGGGCATCTGCCCGGGAA TCCGGG	SEQ ID 1415	CAGTATGGTAGCTCACAG ACCTTC
SEQ ID 1277	GCCAGTCAGAGTGTTAGCAGCAGCGCC TTAGCCTGG	SEQ ID 1351	GGTGCCTCCACCAGGGCC ACTGGT	SEQ ID 1416	CAGTATGGTAGTTCACCTC CGACCACCTTC
SEQ ID 1278	GCCAGTCAAAGTGTTACCAGCAACTTA GCCTGG	SEQ ID 1352	GAGGTTTCTAAGCGGGAC TCTGGG	SEQ ID 1417	CAGCGTAGCAACTGGCCG TGGACGTTC
SEQ ID 1279	GCCAGTCAGAGTATTGGCACTTACGTC GCCTGG	SEQ ID 1353	GAAGTTTCCAACCGATTC TCTGGA	SEQ ID 1418	CAGGCTACACACTATCCTC GGACGTTC
SEQ ID 1280	GCCAGTCAGAGTGTTAGCAGCAACTCC TTAGCCTGG	SEQ ID 1354	GCTTCATCTACTTTGCAA TCAGGG	SEQ ID 1419	CAGAGTTACATTACCCCGT GGACGTTC
SEQ ID 1281	TCCAGCCAGAGTGTTTTATATGATTCC AACAGTAAGAACTACTTAAGTTGG	SEQ ID 1355	AAGGCCTCTAGTTTAACA AGTGGG	SEQ ID 1420	CAGAGTTACGGTCCTCGG ACATTC

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SEQ ID 1282	GCCAGTCAGAGTGTTAGTAGCTACTTAGCCTGG	SEQ ID 1356	AAGGCGTCTAGTTTAGAAAGTGGG	SEQ ID 1421	CAGTGTGCTAGCTCACCTCCTGTCACTTTC
SEQ ID 1283	TCTTGTCAAAGCCTCGTATACAGTGATGGCAACACCTACTTGAATTGC	SEQ ID 1357	TTGGGTTCTACTCGGGCCTCCGGG	SEQ ID 1422	CAGTATAATAACTGGCCTCCGATAACTTTC
SEQ ID 1284	GCCAGTCAGAGTGTTAGCAGCAGCTACTTAGGCTGG	SEQ ID 1358	GGTGTTTCCACCAGGGCCACTGGC	SEQ ID 1423	CACTATAAAAGTGATTCCCGGACGTTC
SEQ ID 1285	GCCAGTCAGAGCATTGGTGGTAGCTTACACTGG	SEQ ID 1359	ACTGCATCCAAAAGGGCCACTGGC	SEQ ID 1424	CAGCATAACAGTTACCCGTGGACGTTC
SEQ ID 1286	TCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCTTGG	SEQ ID 1360	ATGGGTTCTAGTCGGGCCTCCGGG	SEQ ID 1425	CAATATTATAGTACTCCGCTCACTTTC
SEQ ID 1287	GCCAGTCAGAGTATTAGCAGCAACTTAGCCTGG	SEQ ID 1361	GGTGCATCCAGCAGGGCCACTGGC	SEQ ID 1426	CAGTATGGTAGCTCACTCCTCTTC
SEQ ID 1288	TCTAGTCATAGCCTCACAACTACTGATGGACGTACTTACGTGGCTTGG	SEQ ID 1362	GGTGCATCCACCAGGGCCACTGGT	SEQ ID 1427	CAGAGTAGTAGTTTACCTCACACTTTC
SEQ ID 1289	TCTAGTCAGAGCCTCCTGGGTGGTGATGGAAAGACCTATTTGTATTGG	SEQ ID 1363	GAGGTTTCTAACCGGGACTCTGGT	SEQ ID 1428	CAGTATGGTAACTCACCTCCGGGAGCCACCTTC
SEQ ID 1290	GCGAGTCAGGGCATTGCCAATTATTTAGCCTGG	SEQ ID 1364	GGCGCATCCAACAGGGCCACAGGC	SEQ ID 1429	CAGTATCAAAGTTACTGGACGTTC
SEQ ID 1291	GCCAGTCAGAGTATTACTACCTGGTTGGCCTGG	SEQ ID 1365	GATGCGTCCAGCAGGGCCGAAGGC	SEQ ID 1430	CACTATGGCAGCTCTCGCACCTTC
SEQ ID 1292	GCCAGTCAGAGTATTAGTAGCTGGTTGGCCTGG	SEQ ID 1366	CGTGCATCCAGCAGGGCCACTGGC	SEQ ID 1431	CAGTTTAATACCTACCCCAACACTTTT
SEQ ID 1293	GCCAGTCAGAGTGTTAATAGCGGCTACTTAGCCTGG	SEQ ID 1367	TCTACATCGACTTTACAAAGTGGA	SEQ ID 1432	CAGTATGGTAGCTCACCTGCGCTCACTTTC
SEQ ID 1294	GCCAGTCACAGTGTTGGCGCCAACTACATAGCCTGG	SEQ ID 1368	TGGGCATCTACCCGGGACTCCGGG	SEQ ID 1433	CAGTATGGTAGTCCACCTCCGACCACCTTC
SEQ ID 1295	TCTAGTCAGAGCCTCCTGCATAGTAATGGATACAACTATTTGGATTGG	SEQ ID 1369	GATGCATCCAACAGGGCCACTGGC	SEQ ID 1434	CAGTATGGTAGCTCACCTCGGGTCACTTTC
SEQ ID 1296	GCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGG	SEQ ID 1370	CGTGCATCCACCAGGGCCGCTGGT	SEQ ID 1435	CAGCGTGCCGAGTGGCCTCTCACCTTC
SEQ ID 1297	GCCAGTCAGAGTGTAATAAGCAGGTACTTAGCCTGG	SEQ ID 1371	GATGCATCCAATTTGGAAACAGGG	SEQ ID 1436	CAGTATGGTAGCTCACGTCGGACGTTC
SEQ ID 1298	TCTAGTCAAAGCCTCGTACACAGTAATGGACACACCTACTTGAGTTGG	SEQ ID 1372	TTGGGTTCTAATCGGGCCCCCGGG	SEQ ID 1437	CAGTATGGTAGCTCAGGGTACACTTTT
SEQ ID 1299	GCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCCTGG			SEQ ID 1438	CAGTATGGTAACTCACAGACCTTC
SEQ ID 1300	GCCAGTCAGAGTTTAAGTACCAACTTAGCCTGG			SEQ ID 1439	CAATTTTATGGTATTCCCCACTTC

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SEQ ID 1301	GCCAGTCAGAGTATTAGCGGCAGTTAC TTAGCCTGG			SEQ ID 1440	AAGTATAACAGTCCCCCT CGGACGTTC
SEQ ID 1302	GCCAGTCAGAGTCTTACCAGCAGCTAC TTAGCCTGG			SEQ ID 1441	CAAGGTCTACAAACTCCA TTCACTTTC
SEQ ID 1303	TCCAGCCAGGCCCTGCGAAATGTTGTC GGCCTTGGCGATGATTTAGCCTGG			SEQ ID 1442	CAGCGTAGCAACTGGCCT TTCTTC
SEQ ID 1304	TCCAACCGGAGTGTTTTATACAGCCCC AACAATCAGAACTACTTAGGTTGG			SEQ ID 1443	CAGTATGGTATCTCACCTC TCGCGTTC
SEQ ID 1305	GCCAGTCAGAGTGTTAGCAGCTACTTA GCCTGG			SEQ ID 1444	CAGAGTATCAGTTTACCG CTCACTTTC
SEQ ID 1306	GCCAGTCAGAGTGTTGGCAGCGACTTA GCCTGG			SEQ ID 1445	CAATTTTATAGTCCTCCTC GGACGTTC
SEQ ID 1307	GCCAGTCAGAGTATTAGTAGCTGCTTG GCCTGG			SEQ ID 1446	CAGTATAATAACTGGCCT AGAACGTTC
				SEQ ID 1447	CAAGGAACACATGGGCCT CACACGTTC
				SEQ ID 1448	CAATCTACACAATTTCCGT GGACGTTC
				SEQ ID 1449	AAGTATAACAGTGTCCCT CTCACTTTC
				SEQ ID 1450	CATTATAATGGTGCTTCTC GTATGTTC
				SEQ ID 1451	CAGTATAATAGTTATTGG ACGTTC
				SEQ ID 1452	CAAGCTCTACACACTCCGT GGACGTTC
				SEQ ID 1453	CAGTATAATAGTTATTCAA GGACGTTC
				SEQ ID 1454	CAGTATGGTAGCTCACTC AGGTACACTTTT
				SEQ ID 1455	CAGTATAATAACTGGCCT CGGTTC
				SEQ ID 1456	GAGTATGGTAACTCAGCT ATGTACAATTTT
				SEQ ID 1457	CAGTATAATAACTGGCCT CTCACTTTC
				SEQ ID 1458	CAGTATGCTGCCGCACCG ATTACCTTC

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				SEQ ID 1459	CAAACTTTACACACTGTCACTTTC
				SEQ ID 1460	CAGTATGGTAGCTCACCCCGGATCACCTTC
				SEQ ID 1461	CAGTATAATAACTGGCCCCGGACGTTC
				SEQ ID 1462	CAGTATAATAACTGGCCTCCTATGTACACTTTT
				SEQ ID 1463	CAGTATGGTAGCTCACCTCCGTACACTTTT
				SEQ ID 1464	CAAACTCTTCAAACTCCGCTCACTTTC
				SEQ ID 1465	CAAGGAACACACTGGCCCCCCCTCACTGTC
				SEQ ID 1466	CAGTATGGAAGCTCACCGGGAACGTTC
				SEQ ID 1467	CAGTATCATAACTGGCCTCCGTACACTTTT
				SEQ ID 1468	CAATATTATAGTAGTACTCCGTACACTTTT
				SEQ ID 1469	CAGTATGGTAGCTCACCAATATTCACTTTC
				SEQ ID 1470	CAGTATGGTAGTTCACCTAACACCTTC
				SEQ ID 1471	CAGCACCATGATTTCCCTTTCACTTTC
				SEQ ID 1472	CAGCGTTACAACTGGCCTATCACCTTC
				SEQ ID 1473	CAATATGCAAGTACTCCATACACTTTT
				SEQ ID 1474	CAGCGTAGCAACTGGCCTCGGACGTTC
				SEQ ID 1475	CAGTATGGTAGATCACCGTACACTTCT
				SEQ ID 1476	CAGTTTGATAATGTCCCAGTCACTTTC
				SEQ ID 1477	CAGCTTAATAGTTACCCTCAGACGTTC

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				SEQ ID 1478	CAAGCTCTACAAACTCCG TACACTTTT
				SEQ ID 1479	CAGTATAATAACTGGCCT CCGATCACCTTC
				SEQ ID 1480	CAAGCTCTACAAACTCGG ACATTC

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[170] In some embodiments, a nucleotide sequence encoding an antibody, antibody fragment, VH domain, VL domain or CDR of the disclosure is a wild type sequence. In some embodiments, the nucleotide sequence is codon optimized for expression in mammalian cells. In some embodiments, the nucleotide sequence is codon optimized for expression in human cells.

[171] In some embodiments, the invention relates to an antibody that is capable of binding to CLEC2D and that blocks the interaction between CLEC2D and CD161 (FIG. 1). In some embodiments, the anti-CLEC2D antibody as disclosed herein, is a monoclonal antibody. In some embodiments, the anti-CLEC2D antibody as disclosed herein, is a polyclonal antibody.

[172] In some embodiments, the invention relates to an antibody that is capable of binding to CLEC2D and that blocks the interaction between CLEC2D and CD161, which is capable of removing CLEC2D-expressing cells by means of antibody-dependent cell-mediated cytotoxicity (ADCC) and/or by complement-dependent cytotoxicity (CDC). In some embodiments, the invention relates to an antibody that is capable of binding to CLEC2D and that blocks the interaction between CLEC2D and CD161, that is capable of stimulating the cytokine production and the cytotoxicity mediated by NK cells.

[173] In some embodiments, the anti-CLEC2D antibody as disclosed herein, is a humanized antibody. In some embodiments, the anti-CLEC2D antibody as disclosed herein, is of human IgG1, IgG1 N296A, IgG2, IgG3 or IgG4 isotype. In some embodiments, the anti-CLEC2D antibody is a mouse IgG1, IgG2a, IgG2b or IgG3 isotype.

[174] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a variable heavy chain (VH) comprising an amino acid sequence having at least 50% identity, at least 55% identity, at least 60% identity, at least 65% identity, at least 70% identity, at least 75% identity, at least 80% identity, at least 85% identity, at least 90% identity, at least 91% identity, at least 92% identity, at least 93% identity, at least 94% identity, at least 95% identity, at least 96% identity, at least 97% identity, at least 98% identity, at least 99% identity, at least 99.5% identity, at least 99.8% identity, at least 99.9% identity or 100 % identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-108.

[175] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a variable light chain (VL) comprising an amino acid sequence having at least 50% identity, at least 55% identity, at least 60% identity, at least 65% identity, at least 70% identity, at least 75% identity, at least 80% identity, at least 85% identity, at least 90% identity, at least 91% identity,

at least 92% identity, at least 93% identity, at least 94% identity, at least 95% identity, at least 96% identity, at least 97% identity, at least 98% identity, at least 99% identity, at least 99.5% identity, at least 99.8% identity, at least 99.9% identity or 100 % identity to an amino acid sequence selected from the group consisting of SEQ ID NOs. 217-324.

[176] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a variable heavy chain (VH) comprising an amino acid sequence having at least 50% identity, at least 55% identity, at least 60% identity, at least 65% identity, at least 70% identity, at least 75% identity, at least 80% identity, at least 85% identity, at least 90% identity, at least 91% identity, at least 92% identity, at least 93% identity, at least 94% identity, at least 95% identity, at least 96% identity, at least 97% identity, at least 98% identity, at least 99% identity, at least 99.5% identity, at least 99.8% identity, at least 99.9% identity or 100 % identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-108; and a variable light chain (VL) comprising an amino acid sequence having at least 50% identity, at least 55% identity, at least 60% identity, at least 65% identity, at least 70% identity, at least 75% identity, at least 80% identity, at least 85% identity, at least 90% identity, at least 91% identity, at least 92% identity, at least 93% identity, at least 94% identity, at least 95% identity, at least 96% identity, at least 97% identity, at least 98% identity, at least 99% identity, at least 99.5% identity, at least 99.8% identity, at least 99.9% identity or 100 % identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 217-324.

[177] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a variable heavy chain (VH) comprising an amino acid sequence encoded by a nucleic acid selected from the group consisting of SEQ ID NOs: 109-216.

[178] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a variable light chain (VL) comprising an amino acid sequence encoded by a nucleic acid selected from the group consisting of SEQ ID NOs: 325-432.

[179] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a variable heavy chain (VH) comprising an amino acid sequence encoded by a nucleic acid selected from the group consisting of SEQ ID NOs: 109-216; and a variable light chain (VL) comprising an amino acid sequence encoded by a nucleic acid selected from the group consisting of SEQ ID NOs: 325-432.

[180] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a variable heavy chain (VH) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-108.

[181] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a variable light chain (VL) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 217-324.

[182] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a variable heavy chain (VH) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs:1-108, and a variable light chain (VL) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 217-324.

[183] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a VH comprising an amino acid sequence according to SEQ ID NO 44 and a VL comprising an amino acid sequence according to SEQ ID NO: 260.

[184] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a VH comprising an amino acid sequence according to SEQ ID NO:45, and a VL comprising an amino acid sequence according to SEQ ID NO:261.

[185] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a VH comprising an amino acid sequence according to SEQ ID NO:42, and a VL comprising an amino acid sequence according to SEQ ID NO: 258.

[186] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a VH comprising an amino acid sequence according to SEQ ID NO:1, and a VL comprising an amino acid sequence according to SEQ ID NO: 217.

[187] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a VH comprising an amino acid sequence according to SEQ ID NO:73, and a VL comprising an amino acid sequence according to SEQ ID NO:289.

[188] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a VH comprising an amino acid sequence according to SEQ ID NO:21, and a VL comprising an amino acid sequence according to SEQ ID NO:237.

[189] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a VH comprising an amino acid sequence according to SEQ ID NO:35, and a VL comprising an amino acid sequence according to SEQ ID NO:251.

[190] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a VH comprising an amino acid sequence according to SEQ ID NO:58, and a VL comprising an amino acid sequence according to SEQ ID NO: 274.

[191] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a VH comprising an amino acid sequence according to SEQ ID NO:7, and a VL comprising an amino acid sequence according to SEQ ID NO:223.

[192] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a Variable heavy chain (VH) complementarity determining region 1 (CDR1) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 433-485.

[193] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a Variable heavy chain (VH) complementarity determining region 2 (CDR2) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 486-546.

[194] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a Variable heavy chain (VH) complementarity determining region 3 (CDR3) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 547-653.

[195] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a variable light chain (VL) complementarity determining region 1 (CDR1) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 654-726.

[196] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a variable light chain (VL) complementarity determining region 2 (CDR2) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 727-783.

[197] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a variable light chain (VL) complementarity determining region 3 (CDR3) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 784-885.

[198] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a Variable heavy chain (VH) complementarity determining region 1 (CDR1) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 433-485, a VH complementarity determining region 2 (CDR2) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 486-546, and a VH complementarity determining region 3 (CDR3) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 547-653.

[199] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a Variable Light chain (VL) complementarity determining region 1 (CDR1) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 654-726, a VL complementarity determining region 2 (CDR2) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 727-783, and a VL complementarity determining region 3 (CDR3) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 784-885.

[200] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a variable heavy chain (VH) complementarity determining region 1 (CDR1) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 433-485, a VH complementarity determining region 2 (CDR2) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 486-546, and a VH complementarity determining region 3 (CDR3) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 547-653; and a variable light chain (VL) complementarity determining region 1 (CDR1) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 654-726, a VL complementarity determining region 2 (CDR2) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 727-783, and a VL complementarity determining region 3 (CDR3) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 784-885.

[201] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a VH CDR1 comprising an amino acid sequence according to the SEQ ID NO: 439, a VH CDR2 comprising an amino acid according to the SEQ ID NO:492 , and a VH CDR3 comprising an amino acid sequence according to the SEQ ID NOs: 589; and a VL CDR1 comprising an amino acid sequence according to SEQ ID NO: 687, a VL CDR2 comprising an amino acid sequence according to SEQ ID NOs: 729, and a VL CDR3 comprising an amino acid sequence according to SEQ ID NOs: 827.

[202] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a VH CDR1 comprising an amino acid sequence according to the SEQ ID NO: 439, a VH CDR2 comprising an amino acid according to the SEQ ID NO: 492 , and a VH CDR3 comprising an amino acid sequence according to the SEQ ID NOs: 590; and a VL CDR1 comprising an amino acid sequence according to SEQ ID 688, a VL CDR2 comprising an amino acid sequence

according to SEQ ID 755, and a VL CDR3 comprising an amino acid sequence according to SEQ ID 828.

[203] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a VH CDR1 comprising an amino acid sequence according to the SEQ ID 473, a VH CDR2 comprising an amino acid according to the SEQ ID 495, and a VH CDR3 comprising an amino acid sequence according to the SEQ ID 587; and a VL CDR1 comprising an amino acid sequence according to SEQ ID 655, a VL CDR2 comprising an amino acid sequence according to SEQ ID 732:, and a VL CDR3 comprising an amino acid sequence according to SEQ ID 825.

[204] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a VH CDR1 comprising an amino acid sequence according to the SEQ ID 433, a VH CDR2 comprising an amino acid according to the SEQ ID 486, and a VH CDR3 comprising an amino acid sequence according to the SEQ ID 547; and a VL CDR1 comprising an amino acid sequence according to SEQ ID 654, a VL CDR2 comprising an amino acid sequence according to SEQ ID 727, and a VL CDR3 comprising an amino acid sequence according to SEQ ID 784.

[205] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a VH CDR1 comprising an amino acid sequence according to the SEQ ID 439, a VH CDR2 comprising an amino acid according to the SEQ ID 492 , and a VH CDR3 comprising an amino acid sequence according to the SEQ ID 618; and a VL CDR1 comprising an amino acid sequence according to SEQ ID 678, a VL CDR2 comprising an amino acid sequence according to SEQ ID 730, and a VL CDR3 comprising an amino acid sequence according to SEQ ID 852.

[206] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a VH CDR1 comprising an amino acid sequence according to the SEQ ID 446, a VH CDR2 comprising an amino acid according to the SEQ ID 501, and a VH CDR3 comprising an amino acid sequence according to the SEQ ID 567; and a VL CDR1 comprising an amino acid sequence according to SEQ ID 655, a VL CDR2 comprising an amino acid sequence according to SEQ ID 735, and a VL CDR3 comprising an amino acid sequence according to SEQ ID 804.

[207] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a VH CDR1 comprising an amino acid sequence according to the SEQ ID 435, a VH CDR2 comprising an amino acid according to the SEQ ID 488 , and a VH CDR3 comprising an amino acid sequence according to the SEQ ID 581; and a VL CDR1 comprising an amino acid

sequence according to SEQ ID 680, a VL CDR2 comprising an amino acid sequence according to SEQ ID 782, and a VL CDR3 comprising an amino acid sequence according to SEQ ID 818.

[208] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a VH CDR1 comprising an amino acid sequence according to the SEQ ID 466, a VH CDR2 comprising an amino acid according to SEQ ID 521, and a VH CDR3 comprising an amino acid sequence according to the SEQ ID 603; and a VL CDR1 comprising an amino acid sequence according to the SEQ ID 662, a VL CDR2 comprising an amino acid sequence according to the SEQ ID 732, and a VL CDR3 comprising an amino acid sequence according to the SEQ ID 814.

[209] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a VH CDR1 comprising an amino acid sequence according to the SEQ ID 439, a VH CDR2 comprising an amino acid according to the SEQ ID 492, and a VH CDR3 comprising an amino acid sequence according to the SEQ ID 553; and a VL CDR1 comprising an amino acid sequence according to the SEQ ID 660, a VL CDR2 comprising an amino acid sequence according to the SEQ ID 733, and a VL CDR3 comprising an amino acid sequence according to the SEQ ID 790.

[210] The disclosure provides an antibody library comprising at least about 108 unique monoclonal antibody clones, wherein at least about 80% of the antibody clones detectably and specifically bind a CLEC2D antigen. Various anti-CLEC2D antibodies with specific combinations of heavy chain, light chain, heavy chain CDRs1-3 (*i.e.*, CDRH1, CDRH2, and CDRH3) and Light clain CDRs 1-3 (*i.e.*, CDRL1, CDRL2, and CDRL3), are described in Table 9A.

Table 9A

Anti-CLEC2D antibody No.	SEQ ID code HC AA	SEQ ID HC DNA	SEQ ID LC AA SEQ ID	SEQ ID LC DNA	SEQ ID CDRH1	SEQ ID CDRH2	SEQ ID CDRH3	SEQ ID CDRL1	SEQ ID CDRL2	SEQ ID CDRL3
A1	SEQ ID 44	SEQ ID 152	SEQ ID 260	SEQ ID 368	SEQ ID 439	SEQ ID 492	SEQ ID 589	SEQ ID 687	SEQ ID 729	SEQ ID 827
B1	SEQ ID 45	SEQ ID 153	SEQ ID 261	SEQ ID 369	SEQ ID 439	SEQ ID 492	SEQ ID 590	SEQ ID 688	SEQ ID 755	SEQ ID 828
C1	SEQ ID 75	SEQ ID 183	SEQ ID 291	SEQ ID 399	SEQ ID 453	SEQ ID 507	SEQ ID 620	SEQ ID 700	SEQ ID 760	SEQ ID 854
D1	SEQ ID 77	SEQ ID 185	SEQ ID 293	SEQ ID 401	SEQ ID 439	SEQ ID 492	SEQ ID 622	SEQ ID 706	SEQ ID 769	SEQ ID 856
E1	SEQ ID 42	SEQ ID 150	SEQ ID 258	SEQ ID 366	SEQ ID 473	SEQ ID 495	SEQ ID 587	SEQ ID 655	SEQ ID 732	SEQ ID 825
F1	SEQ ID 56	SEQ ID 164	SEQ ID 272	SEQ ID 380	SEQ ID 433	SEQ ID 486	SEQ ID 601	SEQ ID 662	SEQ ID 754	SEQ ID 838
G1	SEQ ID 64	SEQ ID 172	SEQ ID 280	SEQ ID 388	SEQ ID 469	SEQ ID 525	SEQ ID 609	SEQ ID 655	SEQ ID 735	SEQ ID 844

H1	SEQ ID 50	SEQ ID 158	SEQ ID 266	SEQ ID 374	SEQ ID 456	SEQ ID 512	SEQ ID 595	SEQ ID 692	SEQ ID 759	SEQ ID 833
I1	SEQ ID 43	SEQ ID 151	SEQ ID 259	SEQ ID 367	SEQ ID 473	SEQ ID 495	SEQ ID 588	SEQ ID 686	SEQ ID 754	SEQ ID 826
J1	SEQ ID 80	SEQ ID 188	SEQ ID 296	SEQ ID 404	SEQ ID 437	SEQ ID 506	SEQ ID 625	SEQ ID 708	SEQ ID 771	SEQ ID 859
K1	SEQ ID 33	SEQ ID 141	SEQ ID 249	SEQ ID 357	SEQ ID 454	SEQ ID 510	SEQ ID 579	SEQ ID 655	SEQ ID 735	SEQ ID 816
L1	SEQ ID 23	SEQ ID 131	SEQ ID 239	SEQ ID 347	SEQ ID 439	SEQ ID 492	SEQ ID 569	SEQ ID 670	SEQ ID 744	SEQ ID 806
M1	SEQ ID 24	SEQ ID 132	SEQ ID 240	SEQ ID 348	SEQ ID 448	SEQ ID 504	SEQ ID 570	SEQ ID 656	SEQ ID 729	SEQ ID 807
N1	SEQ ID 59	SEQ ID 167	SEQ ID 275	SEQ ID 383	SEQ ID 461	SEQ ID 516	SEQ ID 604	SEQ ID 696	SEQ ID 742	SEQ ID 840
O1	SEQ ID 74	SEQ ID 182	SEQ ID 290	SEQ ID 398	SEQ ID 474	SEQ ID 530	SEQ ID 619	SEQ ID 705	SEQ ID 743	SEQ ID 853
P1	SEQ ID 1	SEQ ID 109	SEQ ID 217	SEQ ID 325	SEQ ID 433	SEQ ID 486	SEQ ID 547	SEQ ID 654	SEQ ID 727	SEQ ID 784
Q1	SEQ ID 25	SEQ ID 133	SEQ ID 241	SEQ ID 349	SEQ ID 449	SEQ ID 505	SEQ ID 571	SEQ ID 671	SEQ ID 745	SEQ ID 808
R1	SEQ ID 61	SEQ ID 169	SEQ ID 277	SEQ ID 385	SEQ ID 437	SEQ ID 529	SEQ ID 606	SEQ ID 698	SEQ ID 764	SEQ ID 842
S1	SEQ ID 60	SEQ ID 168	SEQ ID 276	SEQ ID 384	SEQ ID 467	SEQ ID 522	SEQ ID 605	SEQ ID 697	SEQ ID 763	SEQ ID 841
T1	SEQ ID 28	SEQ ID 136	SEQ ID 244	SEQ ID 352	SEQ ID 451	SEQ ID 507	SEQ ID 574	SEQ ID 674	SEQ ID 747	SEQ ID 811
U1	SEQ ID 73	SEQ ID 181	SEQ ID 289	SEQ ID 397	SEQ ID 439	SEQ ID 492	SEQ ID 618	SEQ ID 678	SEQ ID 730	SEQ ID 852
V1	SEQ ID 4	SEQ ID 112	SEQ ID 220	SEQ ID 328	SEQ ID 436	SEQ ID 489	SEQ ID 550	SEQ ID 657	SEQ ID 730	SEQ ID 787
W1	SEQ ID 6	SEQ ID 114	SEQ ID 222	SEQ ID 330	SEQ ID 438	SEQ ID 491	SEQ ID 552	SEQ ID 659	SEQ ID 732	SEQ ID 789
X1	SEQ ID 46	SEQ ID 154	SEQ ID 262	SEQ ID 370	SEQ ID 461	SEQ ID 516	SEQ ID 591	SEQ ID 689	SEQ ID 756	SEQ ID 829
Y1	SEQ ID 21	SEQ ID 129	SEQ ID 237	SEQ ID 345	SEQ ID 446	SEQ ID 501	SEQ ID 567	SEQ ID 655	SEQ ID 735	SEQ ID 804
Z1	SEQ ID 63	SEQ ID 171	SEQ ID 279	SEQ ID 387	SEQ ID 468	SEQ ID 524	SEQ ID 608	SEQ ID 655	SEQ ID 735	SEQ ID 843
A2	SEQ ID 57	SEQ ID 165	SEQ ID 273	SEQ ID 381	SEQ ID 461	SEQ ID 516	SEQ ID 602	SEQ ID 695	SEQ ID 762	SEQ ID 839
B2	SEQ ID 47	SEQ ID 155	SEQ ID 263	SEQ ID 371	SEQ ID 462	SEQ ID 517	SEQ ID 592	SEQ ID 656	SEQ ID 729	SEQ ID 830
C2	SEQ ID 83	SEQ ID 191	SEQ ID 299	SEQ ID 407	SEQ ID 433	SEQ ID 486	SEQ ID 628	SEQ ID 656	SEQ ID 729	SEQ ID 862
D2	SEQ ID 87	SEQ ID 137	SEQ ID 245	SEQ ID 353	SEQ ID 434	SEQ ID 508	SEQ ID 575	SEQ ID 675	SEQ ID 748	SEQ ID 812
E2	SEQ ID 35	SEQ ID 143	SEQ ID 251	SEQ ID 359	SEQ ID 435	SEQ ID 488	SEQ ID 581	SEQ ID 680	SEQ ID 782	SEQ ID 818
F2	SEQ ID 81	SEQ ID 189	SEQ ID 297	SEQ ID 405	SEQ ID 475	SEQ ID 532	SEQ ID 626	SEQ ID 655	SEQ ID 729	SEQ ID 860
G2	SEQ ID 76	SEQ ID 184	SEQ ID 292	SEQ ID 400	SEQ ID 453	SEQ ID 531	SEQ ID 621	SEQ ID 662	SEQ ID 732	SEQ ID 855
H2	SEQ ID 36	SEQ ID 144	SEQ ID 252	SEQ ID 360	SEQ ID 456	SEQ ID 512	SEQ ID 582	SEQ ID 681	SEQ ID 751	SEQ ID 819
I2	SEQ ID 58	SEQ ID 166	SEQ ID 274	SEQ ID 382	SEQ ID 466	SEQ ID 521	SEQ ID 603	SEQ ID 662	SEQ ID 732	SEQ ID 814
J2	SEQ ID 52	SEQ ID 160	SEQ ID 268	SEQ ID 376	SEQ ID 450	SEQ ID 506	SEQ ID 597	SEQ ID 667	SEQ ID 734	SEQ ID 835
K2	SEQ ID 71	SEQ ID 179	SEQ ID 287	SEQ ID 395	SEQ ID 437	SEQ ID 529	SEQ ID 616	SEQ ID 703	SEQ ID 767	SEQ ID 850
L2	SEQ ID 7	SEQ ID 115	SEQ ID 223	SEQ ID 331	SEQ ID 439	SEQ ID 492	SEQ ID 553	SEQ ID 660	SEQ ID 733	SEQ ID 790
M2	SEQ ID 72	SEQ ID 180	SEQ ID 288	SEQ ID 396	SEQ ID 473	SEQ ID 495	SEQ ID 617	SEQ ID 704	SEQ ID 768	SEQ ID 851

N2	SEQ ID 62	SEQ ID 170	SEQ ID 278	SEQ ID 386	SEQ ID 450	SEQ ID 523	SEQ ID 607	SEQ ID 662	SEQ ID 732	SEQ ID 834

Table 9B. Germline information of selected anti-CLEC2D antibodies from Table 9A

Anti-CLEC2D antibody No* (Selected Antibodies from Table 9A)	**Variable Heavy chain Framework - Germline Family Information**	**Variable Light chain Framework - Germline Family Information**
A1	IGHV4; IGHD3; IGHJ2	IGKV3; IGKJ4
B1	IGHV4; IGHD3 ;IGHJ5	IGKV1; IGKJ1
E1	IGHV3; IGHD5; IGHJ4	IGKV3; IGKJ5
P1	IGHV1; IGHD6; IGHJ4	IGKV3; IGKJ5
U1	IGHV4; IGHD1; IGHJ4	IGKV4; IGKJ4
Y1	IGHV5; IGHD5; IGHJ4	IGKV3; IGKJ4
E2	IGHV1; IGHD5; IGHJ4	IGKV1; IGKJ1
I2	IGHV6; IGHD1; IGHJ4	IGKV3; IGKJ1
L2	IGHV4; IGHD3; IGHJ4	IGKV1; IGKJ3

Table 9C. Amino acid and DNA sequence information of anti-CLEC2D antibodies formatted as IgG1, IgG4, IgG N2A and IgG2.

Anti CLEC2D No. * (Selected Antibodies from Table 9A and 9B)	**IgG1 HC**	**IgG1 LC**	**IgG1 HC DNA**	**IgG1 LC DNA**	**IgG4 HC**	**IgG4 HC DNA**	**IgG N2A**	**IgG N2A DNA**	**IgG2**	**IgG2 DNA**
A1	SEQ ID 1524	SEQ ID 1632	SEQ ID 1740	SEQ ID 1848	SEQ ID 1956	SEQ ID 2064	SEQ ID 2172	SEQ ID 2280	SEQ ID 2388	SEQ ID 2496
B1	SEQ ID 1525	SEQ ID 1633	SEQ ID 1741	SEQ ID 1849	SEQ ID 1957	SEQ ID 2065	SEQ ID 2173	SEQ ID 2281	SEQ ID 2389	SEQ ID 2497
E1	SEQ ID 1522	SEQ ID 1630	SEQ ID 1738	SEQ ID 1846	SEQ ID 1954	SEQ ID 2062	SEQ ID 2170	SEQ ID 2278	SEQ ID 2386	SEQ ID 2494
P1	SEQ ID 1481	SEQ ID 1589	SEQ ID 1697	SEQ ID 1805	SEQ ID 1913	SEQ ID 2021	SEQ ID 2129	SEQ ID 2237	SEQ ID 2345	SEQ ID 2453
U1	SEQ ID 1553	SEQ ID 1661	SEQ ID 1769	SEQ ID 1877	SEQ ID 1985	SEQ ID 2093	SEQ ID 2201	SEQ ID 2309	SEQ ID 2417	SEQ ID 2525
Y1	SEQ ID 1501	SEQ ID 1609	SEQ ID 1717	SEQ ID 1825	SEQ ID 1933	SEQ ID 2041	SEQ ID 2149	SEQ ID 2257	SEQ ID 2365	SEQ ID 2473
E2	SEQ ID 1515	SEQ ID 1623	SEQ ID 1731	SEQ ID 1839	SEQ ID 1947	SEQ ID 2055	SEQ ID 2163	SEQ ID 2271	SEQ ID 2379	SEQ ID 2487

I2	SEQ ID 1538	SEQ ID 1646	SEQ ID 1754	SEQ ID 1862	SEQ ID 1970	SEQ ID 2078	SEQ ID 2186	SEQ ID 2294	SEQ ID 2402	SEQ ID 2510
L2	SEQ ID 1487	SEQ ID 1595	SEQ ID 1703	SEQ ID 1811	SEQ ID 1919	SEQ ID 2027	SEQ ID 2135	SEQ ID 2243	SEQ ID 2351	SEQ ID 2459

[211] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of the anti-CLEC2D antibody No. A1, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of the anti-CLEC2D antibody No. A1, as disclosed in Table 9A. In some embodiments, the anti-CLEC2D antibody No. A1, as disclosed in Table 9B, comprises a variable heavy chain having a framework region sequence of the Germline gene families: IGHV4, IGHD3 and IGHJ2. In some embodiments, the anti-CLEC2D antibody No. A1, as disclosed in Table 9B, comprises a variable light chain having a framework region sequence of the Germline families: IGKV3 and IGKJ4.

[212] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. B1, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. B1, as disclosed in Table 9A. In some embodiments, the anti-CLEC2D antibody No. B1, as disclosed in Table 9B, comprises a variable heavy chain having a framework region sequence of the Germline gene families: IGHV4, IGHD3 and IGHJ5. In some embodiments, the anti-CLEC2D antibody No. B1, as disclosed in Table 9B, comprises a variable light chain having a framework region sequence of the Germline families: IGKV1 and IGKJ1.

[213] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. C1, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light

chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. C1, as disclosed in Table 9A.

[214] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. D1, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. D1, as disclosed in Table 9A.

[215] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. E1, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. E1, as disclosed in Table 9A. In some embodiments, the anti-CLEC2D antibody No. E1, as disclosed in Table 9B, comprises a variable heavy chain having a framework region sequence of the Germline gene families: IGHV3, IGHD5 and IGHJ4. In some embodiments, the anti-CLEC2D antibody No. E1, as disclosed in Table 9B, comprises a variable light chain having a framework region sequence of the Germline families: IGKV3 and IGKJ5.

[216] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. F1, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. F1, as disclosed in Table 9A.

[217] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. G1, as disclosed in Table 9A. In some embodiments, an anti-

CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. G1, as disclosed in Table 9A.

[218] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. H1, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. H1, as disclosed in Table 9A.

[219] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. I1, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. I1, as disclosed in Table 9A.

[220] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. J1, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. J1, as disclosed in Table 9A.

[221] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. K1, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. K1, as disclosed in Table 9A.

[222] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. L1, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. L1, as disclosed in Table 9A.

[223] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. M1, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. M1, as disclosed in Table 9A.

[224] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. N1, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. N1, as disclosed in Table 9A.

[225] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. O1, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. O1, as disclosed in Table 9A.

[226] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of

anti-CLEC2D antibody No. P1, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. P1, as disclosed in Table 9A. In some embodiments, the anti-CLEC2D antibody No. P1, as disclosed in Table 9B, comprises a variable heavy chain having a framework region sequence of the Germline gene families: IGHV1, IGHD6 and IGHJ4. In some embodiments, the anti-CLEC2D antibody No. P1, as disclosed in Table 9B, comprises a variable light chain having a framework region sequence of the Germline families: IGKV3 and IGKJ5.

[227] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. Q1, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. Q1, as disclosed in Table 9A.

[228] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. R1, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. R1, as disclosed in Table 9A.

[229] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. S1, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. S1, as disclosed in Table 9A.

[230] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the

amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. T1, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. T1, as disclosed in Table 9A.

[231] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. U1, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. U1, as disclosed in Table 9A. In some embodiments, the anti-CLEC2D antibody No. U1, as disclosed in Table 9B, comprises a variable heavy chain having a framework region sequence of the Germline gene families: IGHV4, IGHD1 and IGHJ4. In some embodiments, the anti-CLEC2D antibody No. U1, as disclosed in Table 9B, comprises a variable light chain having a framework region sequence of the Germline families: IGKV4 and IGKJ4.

[232] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. V1, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. V1, as disclosed in Table 9A.

[233] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. W1, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. W1, as disclosed in Table 9A.

[234] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. X1, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. X1, as disclosed in Table 9A.

[235] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. Y1, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. Y1, as disclosed in Table 9A. In some embodiments, the anti-CLEC2D antibody No. Y1, as disclosed in Table 9B, comprises a variable heavy chain having a framework region sequence of the Germline gene families: IGHV5, IGHD5 and IGHJ4. In some embodiments, the anti-CLEC2D antibody No. Y1, as disclosed in Table 9B, comprises a variable light chain having a framework region sequence of the Germline families: IGKV3 and IGKJ4.

[236] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. Z1, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. Z1, as disclosed in Table 9A.

[237] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. A2, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light

chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. A2, as disclosed in Table 9A.

[238] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. B2, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. B2, as disclosed in Table 9A.

[239] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. C2, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. C2, as disclosed in Table 9A.

[240] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. D2, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. D2, as disclosed in Table 9A.

[241] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. E2, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. E2, as disclosed in Table 9A. In some embodiments, the anti-CLEC2D antibody No. E2, as disclosed in Table 9B, comprises a variable heavy chain having a framework region

sequence of the Germline gene families: IGHV1, IGHD5 and IGHJ4. In some embodiments, the anti-CLEC2D antibody No. E2, as disclosed in Table 9B, comprises a variable light chain having a framework region sequence of the Germline families: IGKV1 and IGKJ1.

[242] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. F2, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. F2, as disclosed in Table 9A.

[243] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. G2, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. G2, as disclosed in Table 9A.

[244] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. H2, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. H2, as disclosed in Table 9A.

[245] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. I2, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. I2, as disclosed in Table 9A. In some embodiments, the anti-CLEC2D antibody

No. I2, as disclosed in Table 9B, comprises a variable heavy chain having a framework region sequence of the Germline gene families: IGHV6, IGHD1 and IGHJ4. In some embodiments, the anti-CLEC2D antibody No. I2, as disclosed in Table 9B, comprises a variable light chain having a framework region sequence of the Germline families: IGKV3 and IGKJ1.

[246] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. J2, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. J2, as disclosed in Table 9A.

[247] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. K2, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. K2, as disclosed in Table 9A.

[248] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. L2, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. L2, asdisclosed in Table 9A. In some embodiments, the anti-CLEC2D antibody No. L2, as disclosed in Table 9B, comprises a variable heavy chain having a framework region sequence of the Germline gene families: IGHV4, IGHD3 and IGHJ4. In some embodiments, the anti-CLEC2D antibody No. L2, as disclosed in Table 9B, comprises a variable light chain having a framework region sequence of the Germline families: IGKV1 and IGKJ3.

[249] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the

amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. M2, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. M2, as disclosed in Table 9A.

[250] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3, according to the amino acid sequence of the heavy chain CDRs 1, 2 and 3, and light chain CDRs 1, 2 and 3 of anti-CLEC2D antibody No. N2, as disclosed in Table 9A. In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of anti-CLEC2D antibody No. N2, as disclosed in Table 9A.

[251] In some embodiments, any one or all of the anti-CLEC2D antibodies disclosed herein (*e.g.*, including any one or all of Antibody Nos: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, as disclosed in Table 9A and B) comprise a human IgG1 Fc region or backbone. In some embodiments, any one or all of the anti-CLEC2D antibodies disclosed herein (*e.g.*, including any one or all of Antibody Nos: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, as disclosed in Table 9A and B) comprise a human IgG4 Fc region or backbone. In some embodiments, any one or all of the anti-CLEC2D antibodies disclosed herein (*e.g.*, including any one or all of Antibody Nos: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, as disclosed in Table 9A and B) comprise a human IgG1 N to A Fc region or backbone. In some embodiments, any one or all of the anti-CLEC2D antibodies disclosed herein (*e.g.*, including any one or all of Antibody Nos: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, as disclosed in Table 9A and B) comprise a human IgG2 Fc region or backbone. In some embodiments, any one or all of the anti-CLEC2D antibodies disclosed herein (*e.g.*, including any one or all of Antibody Nos: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, as disclosed in Table 9) is afucosylated. In some embodiments, any one or all of the anti-CLEC2D antibodies disclosed herein (*e.g.*, including any one or all of Antibody Nos: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, as disclosed in Table 9) comprises an afucosylated antibody region.

[252] In some embodiments, any one or all of the anti-CLEC2D antibodies selected from the group consisting of Antibody Nos: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, as disclosed in Table

9A and B, comprise a human IgG1 Fc region or backbone. In some embodiments, any one or all of the anti-CLEC2D antibodies selected from the group consisting of Antibody Nos: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, as disclosed in Table 9C, comprise a human IgG4 Fc region or backbone. In some embodiments, any one or all of the anti-CLEC2D antibodies selected from the group consisting of Antibody Nos: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, as disclosed in Table 9A and B, comprise a human IgG1 N to A Fc region or backbone. In some embodiments, any one or all of the anti-CLEC2D antibodies selected from the group consisting of Antibody Nos: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, as disclosed in Table 9C, comprise a human IgG2 Fc region or backbone.

[253] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of an IgG1 formatted anti-CLEC2D antibody No. A1, as disclosed in Table 9C.

[254] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of an IgG1 formatted anti-CLEC2D antibody No. B1, as disclosed in Table 9C.

[255] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of an IgG1 formatted anti-CLEC2D antibody No. E1, as disclosed in Table 9C.

[256] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of an IgG1 formatted anti-CLEC2D antibody No. P1, as disclosed in Table 9C.

[257] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of an IgG1 formatted anti-CLEC2D antibody No. U1, as disclosed in Table 9C.

[258] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the

heavy chain and light chain of an IgG1 formatted anti-CLEC2D antibody No. Y1, as disclosed in Table 9C.

[259] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of an IgG1 formatted anti-CLEC2D antibody No. E2, as disclosed in Table 9C.

[260] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of an IgG1 formatted anti-CLEC2D antibody No. I2, as disclosed in Table 9C.

[261] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a combination of a heavy chain and a light chain, according to the amino acid sequence of the heavy chain and light chain of an IgG1 formatted anti-CLEC2D antibody No. L2, as disclosed in Table 9C.

[262] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a heavy chain, according to the amino acid sequence of the heavy chain of an IgG4 formatted anti-CLEC2D antibody No. A1, as disclosed in Table 9C.

[263] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a heavy chain, according to the amino acid sequence of the heavy chain of an IgG4 formatted anti-CLEC2D antibody No. B1, as disclosed in Table 9C.

[264] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a heavy chain, according to the amino acid sequence of the heavy chain of an IgG4 formatted anti-CLEC2D antibody No. E1, as disclosed in Table 9C.

[265] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a heavy chain, according to the amino acid sequence of the heavy chain of an IgG4 formatted anti-CLEC2D antibody No. P1, as disclosed in Table 9C.

[266] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a heavy chain, according to the amino acid sequence of the heavy chain of an IgG4 formatted anti-CLEC2D antibody No. U1, as disclosed in Table 9C.

[267] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a heavy chain, according to the amino acid sequence of the heavy chain of an IgG4 formatted anti-CLEC2D antibody No. Y1, as disclosed in Table 9C.

[268] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a heavy chain, according to the amino acid sequence of the heavy chain of an IgG4 formatted anti-CLEC2D antibody No. E2, as disclosed in Table 9C.

[269] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a heavy chain, according to the amino acid sequence of the heavy chain of an IgG4 formatted anti-CLEC2D antibody No. I2, as disclosed in Table 9C.

[270] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a heavy chain, according to the amino acid sequence of the heavy chain of an IgG4 formatted anti-CLEC2D antibody No. L2, as disclosed in Table 9C.

[271] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises an IgG N2A sequence, according to the amino acid sequence of the heavy chain of an IgG4 formatted anti-CLEC2D antibody No. L2, as disclosed in Table 9C.

[272] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a heavy chain, according to the amino acid sequence of the heavy chain of an IgG2 formatted anti-CLEC2D antibody No. A1, as disclosed in Table 9C.

[273] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a heavy chain, according to the amino acid sequence of the heavy chain of an IgG2 formatted anti-CLEC2D antibody No. B1, as disclosed in Table 9C.

[274] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a heavy chain, according to the amino acid sequence of the heavy chain of an IgG2 formatted anti-CLEC2D antibody No. E1, as disclosed in Table 9C.

[275] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a heavy chain, according to the amino acid sequence of the heavy chain of an IgG2 formatted anti-CLEC2D antibody No. P1, as disclosed in Table 9C.

[276] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a heavy chain, according to the amino acid sequence of the heavy chain of an IgG2 formatted anti-CLEC2D antibody No. U1, as disclosed in Table 9C.

[277] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a heavy chain, according to the amino acid sequence of the heavy chain of an IgG2 formatted anti-CLEC2D antibody No. Y1, as disclosed in Table 9C.

[278] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a heavy chain, according to the amino acid sequence of the heavy chain of an IgG2 formatted anti-CLEC2D antibody No. E2, as disclosed in Table 9C.

[279] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a heavy chain, according to the amino acid sequence of the heavy chain of an IgG2 formatted anti-CLEC2D antibody No. I2, as disclosed in Table 9C.

[280] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a heavy chain, according to the amino acid sequence of the heavy chain of an IgG2 formatted anti-CLEC2D antibody No. L2, as disclosed in Table 9C.

[281] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises an IgG N2A sequence, according to the amino acid sequence of the heavy chain of an IgG2 formatted anti-CLEC2D antibody No. L2, as disclosed in Table 9C.

[282] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a heavy chain, according to the amino acid sequence of the heavy chain of an IgG N2A formatted anti-CLEC2D antibody No. A1, as disclosed in Table 9C.

[283] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a heavy chain, according to the amino acid sequence of the heavy chain of an IgG N2A formatted anti-CLEC2D antibody No. B1, as disclosed in Table 9C.

[284] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a heavy chain, according to the amino acid sequence of the heavy chain of an IgG N2A formatted anti-CLEC2D antibody No. E1, as disclosed in Table 9C.

[285] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a heavy chain, according to the amino acid sequence of the heavy chain of an IgG N2A formatted anti-CLEC2D antibody No. P1, as disclosed in Table 9C.

[286] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a heavy chain, according to the amino acid sequence of the heavy chain of an IgG N2A formatted anti-CLEC2D antibody No. U1, as disclosed in Table 9C.

[287] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a heavy chain, according to the amino acid sequence of the heavy chain of an IgG N2A formatted anti-CLEC2D antibody No. Y1, as disclosed in Table 9C.

[288] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a heavy chain, according to the amino acid sequence of the heavy chain of an IgG N2A formatted anti-CLEC2D antibody No. E2, as disclosed in Table 9C.

[289] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a heavy chain, according to the amino acid sequence of the heavy chain of an IgG N2A formatted anti-CLEC2D antibody No. I2, as disclosed in Table 9C.

[290] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises a heavy chain, according to the amino acid sequence of the heavy chain of an IgG N2A formatted anti-CLEC2D antibody No. L2, as disclosed in Table 9C.

[291] In some embodiments, an anti-CLEC2D antibody, as disclosed herein, comprises an IgG N2A sequence, according to the amino acid sequence of the heavy chain of an IgG N2A formatted anti-CLEC2D antibody No. L2, as disclosed in Table 9C.

[292] In some embodiments, any one or all of the anti-CLEC2D antibodies selected from the group consisting of Antibody Nos: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, as disclosed in Table 9A, 9B and 9C, is afucosylated. In some embodiments, any one or all of the anti-CLEC2D antibodies selected from the group consisting of Antibody Nos: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, as disclosed in Table 9A, 9B and 9C, comprises an afucosylated antibody region.

[293] In some embodiments, an anti-CLEC2D antibody selected from the group consisting of Antibody Nos: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, as disclosed in Table 9A, 9B and 9C, comprises a variable heavy chain sequence and a variable light chain sequence, that recognizes and binds to a human CLEC2D protein of amino acid sequence according to at least one of SEQ ID NOs: 886-920 and SEQ ID NOs: 930-1003.

[294] In some embodiments, an anti-CLEC2D antibody selected from the group consisting of Antibody Nos: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, as disclosed in Table 9A, 9B and 9C, comprises a variable heavy chain sequence and a variable light chain sequence, that recognizes and binds to a human CLEC2D protein of amino acid sequence according to at least one of SEQ ID NOs: 886-909. In some embodiments, an anti-CLEC2D antibody or antibody fragment thereof, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain

sequence, that recognizes and binds to a human CLEC2D protein of amino acid sequence according to at least one of SEQ ID NOs: 930-1003.

[295] In some embodiments, an anti-CLEC2D antibody selected from the group consisting of Antibody Nos: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, as disclosed in Table 9A, 9B and 9C, comprises a variable heavy chain sequence and a variable light chain sequence, that recognizes and binds to conformational epitope of CLEC2D antigen, comprises of amino acids positions either overlapping and/or non-overlapping with CD161 receptor interacting amino acid residues.

[296] In some embodiments, an anti-CLEC2D antibody selected from the group consisting of Antibody Nos: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, as disclosed in Table 9A, 9B and 9C, comprises a variable heavy chain sequence and a variable light chain sequence, that inhibits or abrogates or competes with another antibody that recognizes and binds to conformational epitope of CLEC2D antigen, comprises of amino acids positions either overlapping and/or non-overlapping with CD161 receptor interacting amino acid residues.

[297] In some embodiments, an anti-CLEC2D antibody selected from the group consisting of Antibody Nos: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, as disclosed in Table 9A, 9B and 9C, comprises a variable heavy chain sequence and a variable light chain sequence that binds to conformational epitope of CLEC2D antigen comprising of any of the amino acid positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95 or a combination thereof.

[298] In some embodiments, an anti-CLEC2D antibody selected from the group consisting of Antibody Nos: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, as disclosed in Table 9A, 9B and 9C, comprises a variable heavy chain sequence and a variable light chain sequence that inhibits or abrogates or competes for, the binding of another antibody to conformational epitope of CLEC2D antigen comprising of any of the amino acid positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95 or a combination thereof.

[299] In some embodiments, an anti-CLEC2D antibody selected from the group consisting of Antibody Nos: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, as disclosed in Table 9A, 9B and 9C, comprises a variable heavy chain sequence and a variable light chain sequence that binds to

conformational epitope of CLEC2D antigen, comprises at least one of the amino acids positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95 of SEQ ID No: 886-920 and 930-1003, constituting non-linear scaffolds for CD161 receptor interacting amino acid residues, thereby blocking the interaction between CLEC2D and CD161 receptors.

[300] In some embodiments, an anti-CLEC2D antibody selected from the group consisting of Antibody Nos: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, as disclosed in Table 9A, 9B and 9C, comprises a variable heavy chain sequence and a variable light chain sequence that binds to conformational epitope of CLEC2D antigen, comprises at least one of the amino acids positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95 of SEQ ID No: 886-909 and 930-1003, constituting non-linear scaffolds for CD161 receptor interacting amino acid residues, thereby blocking the interaction between CLEC2D and CD161 receptors.

[301] In some embodiments, an anti-CLEC2D antibody selected from the group consisting of Antibody Nos: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, as disclosed in Table 9A, 9B and 9C, comprises a variable heavy chain sequence and a variable light chain sequence that binds to conformational epitope of CLEC2D antigen, comprises at least one of the amino acids positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95 of SEQ ID No: 886-890, constituting non-linear scaffolds for CD161 receptor interacting amino acid residues, thereby blocking the interaction between CLEC2D and CD161 receptors.

[302] In some embodiments, an anti-CLEC2D antibody selected from the group consisting of Antibody Nos: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, as disclosed in Table 9A, 9B and 9C, comprises a variable heavy chain sequence and a variable light chain sequence that binds to conformational epitope of CLEC2D antigen, comprises at least one of the amino acids positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95 of SEQ ID No: 886-920 and 930-1003,

constituting allosteric and non-linear scaffolds for CD161 receptor non-interacting amino acid residues, thereby blocking the interaction between CLEC2D and CD161 receptors.

[303] In some embodiments, an anti-CLEC2D antibody selected from the group consisting of Antibody Nos: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, as disclosed in Table 9A, 9B and 9C, comprises a variable heavy chain sequence and a variable light chain sequence that binds to conformational epitope of CLEC2D antigen, comprises at least one of the amino acids positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95 of SEQ ID No: 886-909 and 930-1003, constituting allosteric and non-linear scaffolds for CD161 receptor non-interacting amino acid residues, thereby blocking the interaction between CLEC2D and CD161 receptors.

[304] In some embodiments, an anti-CLEC2D antibody selected from the group consisting of Antibody Nos: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, as disclosed in Table 9A, 9B and 9C, comprises a variable heavy chain sequence and a variable light chain sequence that binds to conformational epitope of CLEC2D antigen, comprises at least one of the amino acids positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95 of SEQ ID No: 886-890, constituting allosteric and non-linear scaffolds for CD161 receptor non-interacting amino acid residues, thereby blocking the interaction between CLEC2D and CD161 receptors.

[305] In some embodiments, an anti-CLEC2D antibody selected from the group consisting of Antibody Nos: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, as disclosed in Table 9A, 9B and 9C, comprises a variable heavy chain sequence and a variable light chain sequence that when bound to CLEC2D selected from SEQ ID Nos: 886-920 and 930-1003, binds to at least one of the amino acids positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95, either independently or in combination to induce tumour killing or cytotoxicity. In some embodiments, an antibody or antigen binding fragment thereof, as disclosed herein, induces cytotoxicity in at least 5%, at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at

least 75%, at least 80%, at least 85%, at least 90% or at least 95%, of the total number of cells treated with the antibody or antigen binding fragment thereof.

[306] In some embodiments, an anti-CLEC2D antibody selected from the group consisting of Antibody Nos: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, as disclosed in Table 9A, 9B and 9C, comprises a variable heavy chain sequence and a variable light chain sequence that when bound to CLEC2D selected from SEQ ID Nos: 886-909 and 930-1003, binds to at least one of the amino acids positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95, either independently or in combination to induce tumour killing or cytotoxicity. In some embodiments, an antibody or antigen binding fragment thereof, as disclosed herein, induces cytotoxicity in at least 5%, at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90% or at least 95%, of the total number of cells treated with the antibody or antigen binding fragment thereof.

[307] In some embodiments, an anti-CLEC2D antibody selected from the group consisting of Antibody Nos: A1, B1, E1, P1, U1, Y1, E2, I2 and L2, as disclosed in Table 9A, 9B and 9C, comprises a variable heavy chain sequence and a variable light chain sequence that when bound to CLEC2D selected from SEQ ID Nos: 886-890, binds to at least one of the amino acids positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95, either independently or in combination to induce tumour killing or cytotoxicity. In some embodiments, an antibody or antigen binding fragment thereof, as disclosed herein, induces cytotoxicity in at least 5%, at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90% or at least 95%, of the total number of cells treated with the antibody or antigen binding fragment thereof.

[308] In some embodiments, an anti-CLEC2D antibody, as disclosed herein is deglycosylated. In some embodiments, a deglycosylated anti-CLEC2D antibody, as disclosed herein exhibits increased cytotoxicity towards a host cell, as compared to a glycosylated form of the same anti-

CLEC2D antibody. In some embodiments, an anti-CLEC2D antibody, as disclosed herein comprised an N-linked glycosylation.

[309] In some embodiments, an anti-CLEC2D antibody, as disclosed herein is afucosylated. In some embodiments, an afucosylated anti-CLEC2D antibody, as disclosed herein exhibits increased cytotoxicity towards a host cell, as compared to a fucosylated form of the same anti-CLEC2D antibody.

[310] In some embodiments, an anti-CLEC2D antibody, as disclosed herein is sialylated. In some embodiments, a sialylated anti-CLEC2D antibody, as disclosed herein exhibits increased cytotoxicity towards a host cell, as compared to an unsialylated form of the same anti-CLEC2D antibody.

[311] In some embodiments, an anti-CLEC2D antibody, as disclosed herein is hyper-galactosylated. In some embodiments, a hyper-galactosylated anti-CLEC2D antibody, as disclosed herein exhibits increased cytotoxicity towards a host cell, as compared to an un-galactosylated or low galactosylated form of the same anti-CLEC2D antibody.

[312] In some embodiments, an anti-CLEC2D antibody, as disclosed herein is hyper-mannosylated. In some embodiments, a hyper-mannosylated anti-CLEC2D antibody, as disclosed herein exhibits increased cytotoxicity towards a host cell, as compared to a non-galactosylated or low mannosylated form of the same anti-CLEC2D antibody.

[313] In some embodiments, the invention as disclosed herein, relates to a nucleic acid sequence encoding the amino acid sequence of the heavy chain CDRs 1, 2 and 3 of any of the anti-CLEC2D antibodies, as disclosed herein. In some embodiments, the invention as disclosed herein, relates to a nucleic acid sequence encoding the amino acid sequence of the light chain CDRs 1, 2 and 3 of any of the anti-CLEC2D antibodies, as disclosed herein.

[314] In some embodiments, the invention as disclosed herein, relates to a nucleic acid sequence encoding the amino acid sequence of the variable heavy chain of any of the anti-CLEC2D antibodies, as disclosed herein. In some embodiments, the invention as disclosed herein, relates to a nucleic acid sequence encoding the amino acid sequence of the light chain of any of the anti-CLEC2D antibodies, as disclosed herein.

[315] In some embodiments, the invention as disclosed herein, relates to a nucleic acid sequence encoding the amino acid sequence of the variable heavy chain CDRs 1, 2 and 3 of any of the anti-CLEC2D antibodies, as disclosed in Table 9A. In some embodiments, the invention

as disclosed herein, relates to a nucleic acid sequence encoding the amino acid sequence of the variable light chain CDRs 1, 2 and 3 of any of the anti-CLEC2D antibodies, as disclosed in Table 9A.

[316] In some embodiments, the invention as disclosed herein, relates to a nucleic acid sequence encoding the amino acid sequence of the variable heavy chain any of the anti-CLEC2D antibodies, as disclosed in Table 9A. In some embodiments, the invention as disclosed herein, relates to a nucleic acid sequence encoding the amino acid sequence of the variable light chain of any of the anti-CLEC2D antibodies, as disclosed in Table 9A.

[317] In some embodiments, the invention as disclosed herein, relates to a nucleic acid sequence encoding the amino acid sequence of the variable heavy chain CDRs 1, 2 and 3 of any of the anti-CLEC2D antibodies, as disclosed in Table 9A. In some embodiments, the invention as disclosed herein, relates to a nucleic acid sequence encoding the amino acid sequence of the variable heavy chain of any of the anti-CLEC2D antibodies, as disclosed in Table 9A.

[318] In some embodiments, the invention as disclosed herein, relates to a nucleic acid sequence encoding the amino acid sequence of the variable light chain CDRs 1, 2 and 3 of any of the anti-CLEC2D antibodies, as disclosed in Table 9A. In some embodiments, the invention as disclosed herein, relates to a nucleic acid sequence encoding the amino acid sequence of the variable light chain of any of the anti-CLEC2D antibodies, as disclosed in Table 9A.

[319] In some embodiments, the invention as disclosed herein, relates to a nucleic acid sequence encoding the amino acid sequence of the heavy chain of the anti-CLEC2D antibodies, as disclosed in Table 9A, having a framework region sequence of the Germline families as disclosed herein. In some embodiments, the invention as disclosed herein, relates to a nucleic acid sequence encoding the amino acid sequence of the light chain of the anti-CLEC2D antibodies, as disclosed in Table 9A, having a framework region sequence of the Germline families as disclosed herein.

[320] In some embodiments, the anti-CLEC2D antibody or antibody fragment thereof, as disclosed herein, can comprise a framework region sequence that is derived from or is a human, a murine, a rodent, a lagomorph, an equine, a bovine, an avian, a caprine, a porcine, a piscean, a canine or a feline framework germline family. In some embodiments, the anti-CLEC2D antibody or antibody fragment thereof, as disclosed herein, can comprise a framework region sequence that is derived from or is a human framework germline family.

[321] In some embodiments, the invention as disclosed herein, relates to a vector carrying the nucleic acid encoding the amino acid sequences of an anti-CLEC2D antibody, as disclosed herein. In some embodiments, the invention as disclosed herein, relates to a vector carrying any one or all of the nucleic acid sequences encoding the amino acid sequences of an anti-CLEC2D antibody, as disclosed in Table 9A.

[322] In some embodiments, the invention as disclosed herein, relates to a host cell transfected with a vector carrying the nucleic acid encoding the amino acid sequences of an anti-CLEC2D antibody, as disclosed herein. In some embodiments, the invention as disclosed herein, relates to relates to a host cell transfected with a vector carrying the nucleic acid sequences encoding the amino acid sequences of an anti-CLEC2D antibody, as disclosed in Table 9A.

[323] In some embodiments, the anti-CLEC2D antibodies or antibody fragments thereof, as disclosed herein, can be conjugated to an agent, a chemical or a small molecule. In some embodiments, the agent is a therapeutic agent. In some mebodiments, the therapeutic agent is a chemotherapeutic drug. In some embodiments, the therapeutic agent is a cytotoxic agent or drug. In some embodiments, the therapeutic agent is a radioisotope. In some embodiments, the agent is a diagnostic agent. In some embodiments, the diagnostic agent includes but is not limited to a fluorescent, chemiluminiscent or radioisotopic dye or agent.

[324] *Epitope Recognition*

[325] Generally, the term "epitope" refers to the area or region on an antigen to which an antibody specifically binds, i.e., it is the area or region in physical contact with the antibody. A protein epitope may comprise amino acid residues in the antigen that are directly involved in binding to an antibody (also called the immunodominant component of the epitope) and other amino acid residues, which are not directly involved in the binding. In some embodiments, the term epitope herein includes both types of binding sites of any particular region of CLEC2D that specifically binds to an anti-CLEC2D antibody, or another CLEC2D-specific agent according to this disclosure, unless otherwise stated (e.g., in some contexts this disclosure relates to antibodies that bind directly to particular amino acid residues). More detailed epitope mapping of specific anti-CLEC2D antibody could be determined through an alanine scan approach.

[326] In some embodiments, an anti-CLEC2D antibody or antibody fragment thereof, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence,

that recognizes and binds to a human CLEC2D protein of amino acid sequence according to at least one of SEQ ID NOs: 886 to 920 and 930-1003.

[327] In some embodiments, an anti-CLEC2D antibody or antibody fragment thereof, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence, that recognizes and binds to a human CLEC2D protein of amino acid sequence according to at least one of SEQ ID NOs: 886 to 909. In some embodiments, an anti-CLEC2D antibody or antibody fragment thereof, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence, that recognizes and binds to a human CLEC2D protein of amino acid sequence according to at least one of SEQ ID NOs: 930 to 1003.

[328] In some embodiments, an anti-CLEC2D antibody or antibody fragment thereof, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence, that recognizes and binds to conformational epitope of CLEC2D antigen, comprises of amino acids positions either overlapping and/or non-overlapping with CD161 receptor interacting amino acid residues.

[329] In some embodiments, an anti-CLEC2D antibody or antibody fragment thereof, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence, that inhibits or abrogates or competes with another antibody that recognizes and binds to conformational epitope of CLEC2D antigen, comprises of amino acids positions either overlapping and/or non-overlapping with CD161 receptor interacting amino acid residues.

[330] In some embodiments, an antibody or antigen binding fragment thereof, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence that binds to conformational epitope of CLEC2D antigen comprising of any of the amino acid positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95 or a combination thereof.

[331] In some embodiments, an antibody or antigen binding fragment thereof, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence that inhibits or abrogates or competes for, the binding of another antibody to conformational epitope of CLEC2D antigen comprising of any of the amino acid positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105;

ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95 or a combination thereof.

[332] In some embodiments, an antibody or antigen binding fragment thereof, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence that binds to conformational epitope of CLEC2D antigen, comprises at least one of the amino acids positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95 of SEQ ID No: 886-920 and 930-1003, constituting non-linear scaffolds for CD161 receptor interacting amino acid residues, thereby blocking the interaction between CLEC2D and CD161 receptors.

[333] In some embodiments, an antibody or antigen binding fragment thereof, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence that binds to conformational epitope of CLEC2D antigen, comprises at least one of the amino acids positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95 of SEQ ID No: 886-909 and 930-1003, constituting non-linear scaffolds for CD161 receptor interacting amino acid residues, thereby blocking the interaction between CLEC2D and CD161 receptors.

[334] In some embodiments, an antibody or antigen binding fragment thereof, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence that binds to conformational epitope of CLEC2D antigen, comprises at least one of the amino acids positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95 of SEQ ID No: 886-890, constituting non-linear scaffolds for CD161 receptor interacting amino acid residues, thereby blocking the interaction between CLEC2D and CD161 receptors.

[335] In some embodiments, an antibody or antigen binding fragment thereof, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence that binds to conformational epitope of CLEC2D antigen, comprises at least one of the amino acids positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138;

CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95 of SEQ ID No: 886-920 and 930-1003, constituting allosteric and non-linear scaffolds for CD161 receptor non-interacting amino acid residues, thereby blocking the interaction between CLEC2D and CD161 receptors.

[336] In some embodiments, an antibody or antigen binding fragment thereof, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence that binds to conformational epitope of CLEC2D antigen, comprises at least one of the amino acids positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95 of SEQ ID No: 886-909 and 930-1003, constituting allosteric and non-linear scaffolds for CD161 receptor non-interacting amino acid residues, thereby blocking the interaction between CLEC2D and CD161 receptors.

[337] In some embodiments, an antibody or antigen binding fragment thereof, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence that binds to conformational epitope of CLEC2D antigen, comprises at least one of the amino acids positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95 of SEQ ID No: 886-890, constituting allosteric and non-linear scaffolds for CD161 receptor non-interacting amino acid residues, thereby blocking the interaction between CLEC2D and CD161 receptors.

[338] In some embodiments, an antibody or antigen binding fragment thereof, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence that when bound to CLEC2D selected from SEQ ID Nos: 886-920 and 930-1003 binds to at least one of the amino acids positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95, either independently or in combination to induce tumour killing or cytotoxicity. In some embodiments, an antibody or antigen binding fragment thereof, as disclosed herein, induces cytotoxicity in at least 5%, at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90% or at least 95%, of the total number of cells treated with the antibody or antigen binding fragment thereof.

[339] In some embodiments, an antibody or antigen binding fragment thereof, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence that when bound to CLEC2D selected from SEQ ID Nos: 886-909 and 930-1003 binds to at least one of the amino acids positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95, either independently or in combination to induce tumour killing or cytotoxicity. In some embodiments, an antibody or antigen binding fragment thereof, as disclosed herein, induces cytotoxicity in at least 5%, at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90% or at least 95%, of the total number of cells treated with the antibody or antigen binding fragment thereof.

[340] In some embodiments, an antibody or antigen binding fragment thereof, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence that when bound to CLEC2D selected from SEQ ID Nos: 886-890 binds to at least one of the amino acids positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95, either independently or in combination to induce tumour killing or cytotoxicity. In some embodiments, an antibody or antigen binding fragment thereof, as disclosed herein, induces cytotoxicity in at least 5%, at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90% or at least 95%, of the total number of cells treated with the antibody or antigen binding fragment thereof.

[341] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence, that recognizes and binds to the amino acid residues: THR178; ASN95; ARG137; GLU179; TYR177; SER98; GLU162; GLN139; ARG101; ALA160; TRP96; CYS176; GLU138; ARG175; GLY140; SER136; ASP104; ASP92; THR97; LYS94; GLU150; THR149; GLY148; GLN141; PRO142; LYS144; THR152; TRP151; ASN147; ARG153; TRP143; ILE157; CYS163; SER129; THR93; LYS181; ASP91; ARG180; SER187; LYS194; TYR165; ALA174; LEU110; ASN167; ASP168; ILE146;

SER172; GLY161; SER173; LEU135; ASP130; GLN100; PHE155; GLY159; PRO156; LEU158; GLN117; SER115; GLU114; GLN154; ASN120; PHE116; PHE102; GLN106; SER105; ASP107; LYS186; ASP109; GLN112; VAL191; TRP145; LYS169; GLY127; PRO128; GLN83; LYS85; GLU77; GLY170; LEU119; LEU123; TRP182; SER90; ALA108; TYR88; HIS190; ILE189; ALA73; ARG84; SER78; TRP79; PRO76; PHE82; ALA171; ASP188; CYS75 within a human CLEC2D of amino acid sequence according to SEQ ID NOs: 886, 889, 894, 899, 903, 905, 906 or 907.

[342] In some embodiments, an anti-CLEC2D antibody as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence, that recognizes and binds to the amino acid residues: ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95, within a human CLEC2D of amino acid sequence according to SEQ ID NOs: 886, 889, 894, 899, 903, 905, 906 or 907.

[343] In some embodiments, an anti-CLEC2D antibody or antibody fragment thereof, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence of SEQ ID 42 & SEQ ID 258, that recognizes and binds to a human CLEC2D protein of amino acid sequence according to at least one of SEQ ID NOs: 886 to 909. In some embodiments, an anti-CLEC2D antibody or antibody fragment thereof, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence of SEQ ID 42 & SEQ ID 258, that recognizes and binds to a human CLEC2D protein of amino acid sequence according to at least one of SEQ ID NOs: 921 to 909.

[344] In some embodiments, an anti-CLEC2D antibody or antibody fragment thereof, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence, that recognizes and binds to conformational epitope of CLEC2D antigen, comprises of amino acids positions either overlapping and/or non-overlapping with CD161 receptor interacting amino acid residues.

[345] In some embodiments, an anti-CLEC2D antibody or antibody fragment thereof, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence, that inhibits or abrogates or competes with another antibody that recognizes and binds to

conformational epitope of CLEC2D antigen, and comprises of amino acids positions either overlapping and/or non-overlapping with CD161 receptor interacting amino acid residues.

[346] In some embodiments, an antibody or antigen binding fragment thereof, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence that binds to conformational epitope of CLEC2D antigen comprising of any of the amino acid positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95 or a combination thereof.

[347] In some embodiments, an antibody or antigen binding fragment thereof, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence that inhibits or abrogates or competes with, the binding of another antibody to conformational epitope of CLEC2D antigen comprising of any of the amino acid positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95 or a combination thereof.

[348] In some embodiments, an antibody or antigen binding fragment thereof, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence that binds to conformational epitope of CLEC2D antigen, comprises at least one of the amino acids positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95 of SEQ ID No: 886-920 and 930-1003, constituting non-linear scaffolds for CD161 receptor interacting amino acid residues, thereby blocking the interaction between CLEC2D and CD161 receptors.

[349] In some embodiments, an antibody or antigen binding fragment thereof, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence that binds to conformational epitope of CLEC2D antigen, comprises at least one of the amino acids positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95 of SEQ ID No: 886-909 and 930-1003, constituting non-linear scaffolds for CD161 receptor interacting amino acid residues, thereby blocking the interaction between CLEC2D and CD161 receptors.

[350] In some embodiments, an antibody or antigen binding fragment thereof, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence that binds to conformational epitope of CLEC2D antigen, comprises at least one of the amino acids positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95 of SEQ ID No: 886-890, constituting non-linear scaffolds for CD161 receptor interacting amino acid residues, thereby blocking the interaction between CLEC2D and CD161 receptors.

[351] In some embodiments, an antibody or antigen binding fragment thereof, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence that binds to conformational epitope of CLEC2D antigen, comprises at least one of the amino acids positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95 of SEQ ID No: 886-920 and 930-1003, constituting allosteric and non-linear scaffolds for CD161 receptor non-interacting amino acid residues, thereby blocking the interaction between CLEC2D and CD161 receptors.

[352] In some embodiments, an antibody or antigen binding fragment thereof, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence that binds to conformational epitope of CLEC2D antigen, comprises at least one of the amino acids positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95 of SEQ ID No: 886-909 and 930-1003, constituting allosteric and non-linear scaffolds for CD161 receptor non-interacting amino acid residues, thereby blocking the interaction between CLEC2D and CD161 receptors.

[353] In some embodiments, an antibody or antigen binding fragment thereof, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence that binds to conformational epitope of CLEC2D antigen, comprises at least one of the amino acids positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95 of SEQ ID No: 886-890 ,

constituting allosteric and non-linear scaffolds for CD161 receptor non-interacting amino acid residues, thereby blocking the interaction between CLEC2D and CD161 receptors.

[354] In some embodiments, an antibody or antigen binding fragment thereof, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence that when bound to CLEC2D selected from SEQ ID Nos: 886-920 and 930-1003, binds to at least one of the amino acids positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95, either independently or in combination to induce tumor killing or cytotoxicity. In some embodiments, an antibody or antigen binding fragment thereof, as disclosed herein, induces cytotoxicity in at least 5%, at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90% or at least 95%, of the total number of cells treated with the antibody or antigen binding fragment thereof.

[355] In some embodiments, an antibody or antigen binding fragment thereof, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence that when bound to CLEC2D selected from SEQ ID Nos: 886-909 and 930-1003, binds to at least one of the amino acids positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95, either independently or in combination to induce tumor killing or cytotoxicity. In some embodiments, an antibody or antigen binding fragment thereof, as disclosed herein, induces cytotoxicity in at least 5%, at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90% or at least 95%, of the total number of cells treated with the antibody or antigen binding fragment thereof.

[356] In some embodiments, an antibody or antigen binding fragment thereof, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence that when bound to CLEC2D selected from SEQ ID Nos: 886-890, binds to at least one of the amino acids positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138;

CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95, either independently or in combination to induce tumor killing or cytotoxicity. In some embodiments, an antibody or antigen binding fragment thereof, as disclosed herein, induces cytotoxicity in at least 5%, at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90% or at least 95%, of the total number of cells treated with the antibody or antigen binding fragment thereof.

[357] In some embodiments, an anti-CLEC2D antibody, SEQ ID 42 & SEQ ID 258, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence, that recognizes and binds to the amino acid ARG175- XAA176- TYR177-XAA178-GLU179; ARG153; ARG84; HIS190.

[358] In some embodiments, an anti-CLEC2D antibody, SEQ ID 44 & SEQ ID 260 , as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence, that recognizes and binds to the amino acid ARG101; GLU150-XAA151- THR152- ARG153-GLN154; ARG175-XAA176-TYR177-XAA178-GLU179.

[359] In some embodiments, an anti-CLEC2D antibody, SEQ ID 45 & SEQ ID 261, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence, that recognizes and binds to the amino acid GLN141; ARG101-XAA102-XAA-103-XAA104-SER105-XAA106-ASP107; HIS190.

[360] In some embodiments, an anti-CLEC2D antibody, SEQ ID 1 & SEQ ID 217, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence, that recognizes and binds to the amino acids GLN141; ARG153; ASP92-THR93-LYS94; HIS190.

[361] In some embodiments, an anti-CLEC2D antibody SEQ ID 58 & SEQ ID 274, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence, that recognizes and binds to the amino acids GLU138-XAA139-XAA140-GLN141-XAA142-XAA143-LYS144; CYS176.

[362] In some embodiments, an anti-CLEC2D antibody, SEQ ID 35 & SEQ ID 251, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence, that recognizes and binds to the amino acids GLU138-GLN139-XAA140-GLN141; ARG175-XAA176-TYR177-XAA178-XAA179-ARG180; SER187.

[363] In some embodiments, an anti-CLEC2D antibody SEQ ID 21 & SEQ ID 237, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence that recognizes and binds to the amino acids ASP92; TYR177-XAA179-XAA180-LYS181; THR152-ARG153-GLN154.

[364] In some embodiments, an anti-CLEC2D antibody, SEQ ID 7 & SEQ ID 223, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence, that recognizes and binds to the amino acids THR93-XAA94-ASN95; ARG101; GLN139; PHE116; ARG153.

[365] In some embodiments, an anti-CLEC2D antibody, SEQ ID 73 & SEQ ID 289, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence, that recognizes and binds to the amino acids THR93- LYS94; ARG101; GLN141; TYR177-XAA178-GLU179.

[366] In some embodiments, an anti-CLEC2D antibody, SEQ ID 73 & SEQ ID 289, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence, that recognizes and binds to the amino acids according to SEQ ID NO: 2560.

[367] In some embodiments, an anti-CLEC2D antibody, SEQ ID 73 & SEQ ID 289, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence, that recognizes and binds to the amino acids according to SEQ ID NO: 2561.

[368] In some embodiments, an anti-CLEC2D antibody, SEQ ID 73 & SEQ ID 289, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence, that recognizes and binds to the amino acids according to SEQ ID NO: 2562.

[369] In some embodiments, an anti-CLEC2D antibody, SEQ ID 73 & SEQ ID 289, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence, that recognizes and binds to the amino acids according to SEQ ID NO: 2563.

[370] In some embodiments, an anti-CLEC2D antibody, SEQ ID 73 & SEQ ID 289, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence, that recognizes and binds to the amino acids according to SEQ ID NO: 2564.

[371] In some embodiments, an anti-CLEC2D antibody, SEQ ID 73 & SEQ ID 289, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence, that recognizes and binds to the amino acids according to SEQ ID NO: 2565.

[372] In some embodiments, an anti-CLEC2D antibody, SEQ ID 73 & SEQ ID 289, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence, that recognizes and binds to the amino acids according to SEQ ID NO: 2566.

[373] In some embodiments, an anti-CLEC2D antibody, SEQ ID 73 & SEQ ID 289, as disclosed herein, comprises a variable heavy chain sequence and a variable light chain sequence, that recognizes and binds to the amino acids according to SEQ ID NO: 2567.

[374] *Library Screening*

[375] Without wishing to be bound by any particular technique, antibodies which bind to the antigens of the disclosure can be identified and characterized using the methods described below.

[376] Provided herein is a naïve antibody library as a source of therapeutics for treatment of diseases comprising cancers, rheumatoid arthritis, neurological disorders, infectious diseases and metabolic disorders or any combination thereof. Antibodies identified using the methods of the disclosure can be used as diagnostic tools, as prognostic tools; for research purposes, for target discovery, for validation in functional genomics or any application where antibodies or derivatives of antibodies are employed.

[377] In one embodiment, the term "panning" refers to an affinity selection technique which selects for binders against a specific target/antigen.

[378] In some embodiments, methods of screening the naïve antibody gene expression library include sequentially exploring the expression profiles of a pool of gene clones by utilizing two separate scanning tools: 1) a phage display technology, and 2) a yeast display technology (FIG. 3). Use of yeast system for antibody gene expression is advantageous because of the eukaryotic protein translation, processing and proper folding of the antibody products on the cell surface. Further, yeast expression allows proper interaction with antigenic targets with high specificity.

[379] In some embodiments, the methods disclosed herein preserve the diversity in the library that is capable of identifying unique molecules against varied antigenic targets.

[380] In some embodiments of the methods of the disclosure, the methodology also involves a strategy wherein the diversity is translated between two platforms and explored as various engineered antibody formats including, but not limited to, chimeric antibody molecules, Fv, Fav, F(ab')2, Fab', dsFv, scFv, sc(Fv)2, scFv-CH3, scFv-Fc, ScFab, dimeric and trimeric antibody fragments, minibodies, humanized monoclonal antibody molecules, human antibodies, bispecific antibodies, fusion proteins comprising an Fc region of an antibody, and any functional fragments

arising out of these molecules wherein the derivative molecules retain the immunological functionality of the parent antibody molecule, and all other antibody formats.

[381] In some embodiments, the candidate antibody molecules obtained by the present method are further optimized through rational design guided by structure-function studies of antibody-antigen interactions. The prerequisite for success of manufacturability of monoclonal antibody drugs are dependent on a variety of biological and/or correlated properties such as solubility, aggregation, antigenicity, stability and so on. As exemplified, structure-based drug design, which is rational, evidence based and faster, has contributed tremendously to the field of cancer chemotherapy, drug resistant infections, neurological diseases, amongst others. The resulting outcome of these methods is employed in the instant disclosure to improve antibody library construction and manufacturability of selected molecules.

[382] In some embodiments, the term "isolated" relates to novel and unique molecules comprising of two protein chains or fragments thereof which are not part of a biological membrane. In particular, the isolated molecule according to the current disclosure is soluble and is linked either directly or indirectly via linker molecules through covalent or non-covalent bonds. These molecules may comprise monoclonal or polyclonal antibodies, which can be easily obtained according to methods well-known to the man skilled in the art.

[383] In some embodiments, an affinity tag may be included in an antigen or antibody disclosed herein for isolation or detection purposes. Affinity tags are well known in the art and are attached to a target and used to detect or isolate the target using a molecule that binds the affinity tag. In principal, any peptide or protein for which an antibody or other specific binding agent is available can be used as an affinity tag. Exemplary affinity tags suitable for use include, but are not limited to, a monocytic adaptor protein (MONA) binding peptide, a T7 binding peptide, a v5 tag, a streptavidin binding peptide, a polyhistidine tract, protein A (Nilsson et al., EMBO J. 4:1075 (1985); Nilsson et al., Methods Enzymol. 198:3 (1991)), glutathione S transferase (Smith and Johnson, Gene 67:31 (1988)), Glu-Glu affinity tag (Grussenmeyer et al., Proc. Natl. Acad. Sci. USA 82:7952 (1985)), substance P, FLAG peptide (Hopp et al., Biotechnology 6:1204 (1988)), or other antigenic epitope or binding domain. See, in general, Ford et al., Protein Expression and Purification 2:95 (1991). In one embodiment, a His6 tag is used in the methods disclosed herein. In another embodiment, a FLAG tag is used in the methods disclosed herein. In another embodiment, a v5 tag is used in the methods and compositions

disclosed herein. DNA molecules encoding affinity tags are available from commercial suppliers (e.g., Pharmacia Biotech, Piscataway, N.J.).

[384] Taken together, the methods of the present disclosure are centralized around identifying, validating, characterizing and developing novel monoclonal antibodies against CLEC2D antigenic target. These novel monoclonal antibodies are developed for use in therapeutics, diagnostics and prognostics products applicable in various diseases, including cancers.

[385] In some embodiments, the antibody library, which can be a naïve antibody library, allows for isolation of unique antibody molecules with the desired functional properties for a specific therapeutic target. i.e., an antigen such as the CLEC2D protein or any fragments thereof disclosed herein.

[386] The combination of a diverse library and an appropriate and compatible display platform enables the rapid selection and production of therapeutic antibodies with higher affinity and improved functionality against specific antigen molecule. Typical screening for targeted therapeutic antibody molecules comprises selecting molecules from a diverse and large antibody library against a target antigen through display platforms via smaller antibody fragments followed by constructing a full-length antibody molecule expressed in a mammalian cell line. Once expressed, the process of purification and several functional assays to validate the same are performed. Optimization of parameters such as identification of epitopes, formulation, stability studies and *in vivo* efficacy further strengthen the development of the selected lead antibodies.

[387] In an exemplary embodiment of the present disclosure, the method of screening, isolation and development of monoclonal antibodies from the human naïve antibody library against CLEC2D antigen comprises the following description. Designing and generation of various CLEC2D antigen constructs, i.e., soluble ecto-domain of wild-type and mutants; full-length CLEC2D proteins, in appropriately optimized/ customized vectors to express in mammalian system followed by purification through affinity chromatography methods to homogeneity.

[388] In some embodiments, the screening of a library of molecules is performed by about 1 to 3 rounds of phage panning with a CLEC2D antigen. During each round, specific binders are selected out from the library by removing non-binders. Selected pools of molecules screened in the phage display platform are transferred, with or without randomization of selected diversity, to a yeast surface display platform. This avoids any PCR based method steps, thereby preserving the selected pool of molecules against the CLEC2D antigen. The yeast display platform

comprises expressing a variety of antibody moieties in different formats. Displayed fragments are screened against specific antigenic targets and specific populations showing higher affinity to the target antigen are separated. These selected pools are further tested for antigen specificity. Finally, individual clones are separated and clonal populations are used for sequencing of individual antibody clones.

[389] Methods of phage panning against antigens are known in the art. For example, magnetic beads can be used. Antigen coated on magnetic dynabeads can be prepared, and a phage antibody library panned against the antigen coated beads to separate phage particles expressing the desired antibody clones.

[390] Purified DNA can then be digested and ligated into a suitable yeast expression vector to generate antibodies in the desired format, such as Fab or ScFv. Yeast cells can be transformed by standard methods and checked for antibody expression. The surface expression of antibodies can be analysed with multiple tags such as FLAG, c-Myc and $(His)_6$-tag and V5-tag for heavy chains and light chains, respectively and immunohistochemistry. Flow cytometry can be used to isolate yeast cells expressing antibody sequences showing specific antigen binding. Flow cytometry sorting of yeast cell populations can be repeated at least 1x, at least 2x, at least 3x, at least 4x or at least 5x to enrich for antibody clones with higher affinity towards labelled antigens.

[391] Individual yeast clones are sequences using methods standard in the art, and the antibody sequences are further cloned into suitable mammalian gene expression vectors.

[392] The disclosure provides methods of screening a high diversity antibody gene library for antibodies that bind to a CLEC2D antigen. In some embodiments, the methods comprise inserting a library of antibody genes into a phage protein gene in a vector, and transforming phages to produce a phage library comprising the high diversity antibody gene library. The phages in the phage library display the library of antibody genes on the surface of the phage. This phage library is then panned with a CLEC2D antigen for individual phages that bind to the CLEC2D antigen, thereby producing an enriched phage library that is enriched for antibody genes that encode antibodies that bind to the CLEC2D antigen. This panning can be accomplished, for example, by conjugating the antigen to magnetic beads, which can be used to isolated phages that bind to the antigen on the beads. The panning step can be repeated at least once, at least twice or more times to enrich for phages expressing antibodies or antibody fragments that bind to the antigen.

[393] Antibody or antibody fragment genes from the enriched phage library are then transferred to a yeast surface display library. In some embodiments, this is accomplished by cloning the antibody or antibody fragment genes into a suitable yeast transformation vector, and transforming yeast cells with methods that are standard in the art. Yeast cells that express antibody or antibody fragments that bind that bind to the CLEC2D antigen are then isolated. In some embodiments, this isolation is accomplished using flow cytometry to sort the yeast cells. In some embodiments, the method further comprises repeating the flow cytometry isolation at least 1x, at least 2x, at least 3x, at least 4x or at least 5x or more times to enrich for yeast cells expressing antibodies or antibody fragments that bind the antigen. In some embodiments, the methods further comprise analyzing the surface expression of the antibody genes with a FLAG tag, a c-Myc tag, a polyhistidine tag or a V5 tag. In some embodiments, the method further comprises cloning the antibody genes that bind to CLEC2D into a mammalian expression vector.

[394] *Optimization and Purification*

[395] In some embodiments, the methods disclosed herein comprise the design, generation and optimization of vector constructs for smooth transfer of selected antibody gene sequences to mammalian cell lines such as Chinese hamster ovary (CHO) cell lines for expression, stable cell-line generation and subsequent purification of full-length monoclonal antibody. This allows the rapid and efficient establishment of stable cell lines expressing monoclonal antibodies with excellent homogeneity in terms of conformation and posttranslational modification that are seen in downstream processes.

[396] All cell lines suitable for the expression and purification of antibodies or antibody fragments are considered to be within the scope of the disclosure. In some embodiments, the cell line is a mammalian cell line. Cell lines can be isolated or derived from any source, including human, mouse and hamster. Suitable cell lines include, but are not limited to, Chinese Hamster Ovary (CHO) cells, HEK 293 cells, HEK293T cells, BHK21 cells, NSO cells, PER.C6 cells, B cells, HEK 293-6E cells, Sp2/0-Ag14 cells and DG44 cells.

[397] In some embodiments, the CDR lengths and the amino acid composition of antibody clones is analyzed to understand the novelty of these clones. Additional careful analysis is performed to eliminate clones that have motifs with detrimental to physico-chemical properties that have a direct impact on purification strategy, stability, and charge variants present or within the antibodies.

[398] In some embodiments, the scale up of lead antibody clones is achieved through defined culture media, supplements, and specific bioreactor processes which are known in the art and described herein.

[399] Exemplary purification methods of the disclosure comprise multiple steps of chromatography techniques that utilize the exploiting physico-chemical nature of the amino acid composition in antibody molecules. In addition, higher purity can be attained by effectively removing the host cell protein/impurities, polymer (or aggregate), of the antibody and improving the antibody recovery rate. Purification of antibody molecules is concluded with appropriate formulation which will further improve the stability.

[400] Therapeutic compositions comprise of conditions that are sterile and stable under the conditions of manufacture and storage.

[401] Antibody purification processes will be known to those of skill in the art. Without wishing to be bound by any particular process, exemplary antibody purification processes comprise centrifugation of a primary cell culture expressing the antibody or antibody fragment to be purified, followed by further clarification using a filter such as a 3 µm - 30 µm filter. Subsequently, collected filtrate can be further filtered, for example through 0.22 µm filters. This sample can be loaded onto a column for further purification by liquid chromatography. Exemplary columns include, but are not limited to, XK 16/20 Protein A Columns. Liquid chromatography can include treatment with a high salt wash buffer to remove loosely bound host cell proteins and other impurities. A low pH wash buffer can remove traces of impurities. Subsequently, bound protein can be eluted using 30 mM Phosphate buffer at pH.3.0-4.0. This sample can be diluted to reduce the conductivity, and then can be further purified using anion exchange (AEX) Chromatography in a flow through mode (i.e., using negative binding). An exemplary AEX column includes, but is not limited to, a Q Sepharose XK 16/20 column, which can be pre-equilibrated in 10-100 mM Histidine and/or citrate and/or phosphate and/or MES and/or acetate buffer (pH 4.5-6.5). Weakly interacting proteins can be removed using an elution buffer as a wash, and bound proteins such as the antibodies or antibody fragments of the disclosure are eluted, for example, in a single step using elution buffer containing 1 M NaCl and/or KCl. Flow through from AEX Chromatography can be loaded onto a pre-equilibrated apto SP ImpRes C10/20 column in 10-100 mM Histidine and/or citrate and/or phosphate and/or 2-(N-morpholino)ethanesulfonic acid (MES) and/or Acetate buffer (pH 4.5-6.5). Bound proteins such

as antibodies or antibody fragments of the disclosure can be eluted through step elution followed by gradient elution using elution buffer (Equilibration buffer containing 200-1000 mM NaCl and/or KCl, pH 4.5-6.5). However, high salt buffer containing 1 to 1.5 M NaCl, pH 4.5-6.5, can be to remove strongly bound proteins, if present.

[402] Taken together, antibodies and antibody fragments of the disclosure can be purified through multiple steps of chromatography techniques in order to achieve high purity, while effectively removing the host cell protein/impurities, polymer (or aggregate), of the antibody and improving the antibody recovery rate; Exemplary chromatography methods include the use of a mixed mode resin having both an ion exchange group and a hydrophobic functional group. Amino acids can be used as an additive.

[403] *Methods of Treatment*

[404] As used herein, "treating" or "treat" describes the management and care of a patient for the purpose of combating a disease, condition, or disorder and includes the administration of an antibody or pharmaceutical composition comprising same of the disclosure to alleviate one or more symptoms or complications of a disease, condition or disorder, or to eliminate the disease, condition or disorder. The term "treat" can also include treatment of a cell in vitro or an animal model.

[405] An antibody of the present disclosure, or a pharmaceutical composition thereof, can also be used to prevent a disease, condition or disorder, or used to identify suitable candidates for such purposes. As used herein, "preventing" or "prevent" describes reducing or eliminating the onset of the symptoms or complications of the disease, condition or disorder.

[406] As used herein, the term "alleviate" is meant to describe a process by which the severity of a sign or symptom of a disorder is decreased. Importantly, a sign or symptom can be alleviated without being eliminated. In a preferred embodiment, the administration of pharmaceutical compositions of this disclosure leads to the elimination of a sign or symptom, however, elimination is not required. Effective dosages are expected to decrease the severity of a sign or symptom. For instance, a sign or symptom of a disorder such as cancer, which can occur in multiple locations, is alleviated if the severity of the cancer is decreased within at least one of multiple locations.

[407] As used herein the term "symptom" is defined as an indication of disease, illness, injury, or that something is not right in the body. Symptoms are felt or noticed by the individual

experiencing the symptom, but may not easily be noticed by others. Others are defined as non-health-care professionals.

[408] As used herein the term "sign" is also defined as an indication that something is not right in the body. But signs are defined as things that can be seen by a doctor, nurse, or other health care professional.

[409] A therapeutically effective amount of an antibody of the disclosure relates generally to the amount needed to achieve a therapeutic objective. As noted above, this may be a binding interaction between the antibody and its target antigen that, in certain cases, interferes with the functioning of the target. The amount required to be administered will furthermore depend on the binding affinity of the antibody for its specific antigen, and will also depend on the rate at which an administered antibody is depleted from the free volume other subject to which it is administered. Common ranges for therapeutically effective dosing of an antibody or antibody fragment of the disclosure may be, by way of nonlimiting example, from about 0.1 mg/kg body weight to about 50 mg/kg body weight. Common dosing frequencies may range, for example, from twice daily to once a week.

[410] Where antibody fragments are used, the smallest inhibitory fragment that specifically binds to the binding domain of the target protein is preferred. For example, based upon the variable-region sequences of an antibody, peptide molecules can be designed that retain the ability to bind the target protein sequence. Such peptides can be synthesized chemically and/or produced by recombinant DNA technology. (*See*, e.g., Marasco et al., Proc. Natl. Acad. Sci. USA, 90: 7889-7893 (1993)).

[411] In a non-limiting embodiment of the disclosure, isolated monoclonal antibodies reveal differential expression of CLEC2D on various cell surfaces, including immune cells and tumor cells, in response to various inducing conditions. This indicates the use of anti-CLEC2D antibodies as therapeutic agents for multiple disease indications.

[412] The disclosure provides methods of treating diseases by modulating or inhibiting the interaction of CLEC2D with its cognate receptor CD161 by administering the compositions, the antibodies or antigen binding fragments thereof, and/or nucleic acids encoding the antibodies or antigen binding fragments thereof of the disclosure to a subject in need thereof.

[413] In some embodiments, the diseases treated by the compositions, antibodies or antigen binding fragments thereof, and/or nucleic acids encoding the antibodies or antigen binding

fragments thereof of the disclosure is a cancer, an autoimmune disease, an inflammatory disease, an infectious disease, or other diseases in which CLEC2D plays a role (e.g., by inhibiting CD161) in the initiation and/or development of the disease.

[414] Exemplary diseases include, but are not limited to seronegative spondyloarthropathies such as psoriatic arthritis, ankylosing spondylitis, reiters syndrome and spondyloarthropathy associated with inflammatory bowel disease.

[415] Exemplary diseases include, but are not limited to prosthetic joint loosening.

[416] Exemplary diseases include, but are not limited to connective tissue diseases such as juvenile rheumatoid arthritis, rheumatoid arthritis, systemic lupus erythematosus (SLE) and lupus nephritis, scleroderma, Sjogren's syndrome, mixed connective tissue disease and polymyositis, dermatomyositis.

[417] Exemplary diseases include, but are not limited to inflammatory bowel diseases such as Crohn's disease and ulcerative colitis.

[418] Exemplary diseases include, but are not limited to Whipples disease and arthritis associated with granulomatous ileocolitis.

[419] Exemplary diseases include, but are not limited to inflammatory skin conditions such as autoimmune bullous pemphigoid, autoimmune pemphigus vulgaris, eczema and dermatitis.

[420] Exemplary diseases include, but are not limited to inflammatory lung diseases such as alveolitis, pulmonary fibrosis, sarcoidoisis, asthma, bronchitis and bronchiolitis obliterans.

[421] Exemplary diseases include, but are not limited to inflammatory renal diseases such as glomerulonethritis, renal allograft rejection and renal tubular inflammation.

[422] Exemplary diseases include, but are not limited to atherosclerosis.

[423] Exemplary diseases include, but are not limited to systemic vasculitis such as temporal arteritis/giant cell arteritis, takayasu arteritis, polyarteritis nodosa, Kawasaki disease, Wegener's granulomatosis, churg strauss syndrome, microscopic polyangiitis, necrotising glomerulonephritis, henoch schonlein purpura, essential cryoglobulinaemic vasculitis, other small vessel vasculitis and Behcets disease

[424] Exemplary diseases include, but are not limited to macrophage activation diseases such as macrophage activation syndrome (MAS), adult onset stills disease and haemophagocytic syndrome.

[425] Exemplary diseases include, but are not limited to polymyalgia rheumatica, primary biliary sclerosis, sclerosing cholangitis, autoimmune hepatitis, Type 1 Diabetes Mellitus, Hashimoto's thyroiditis, Graves' disease, multiple sclerosis (MS), Guillain-Barre syndrome, Addison's disease, and/or Raynaud's phenomenon and Goodpasture's syndrome.

[426] Exemplary diseases include, but are not limited to diseases linked with cancers and cancers, which comprise breast cancer, prostate cancer, endometrial cancer, uterine cancer, bladder cancer, kidney cancer, esophageal cancer, squamous cell carcinoma, uveal melanoma, glioma, glioblastoma, myeloma, pheochromocytoma, paraganglioma, follicular lymphoma, renal cell carcinoma, cendcal cancer, ovarian cancer, cervical cancer, lung cancer, colorectal cancer, brain cancer, pancreatic cancer, gastric cancer, intestinal cancer, testicular cancer, skin cancer, thyroid cancer, thymoma, head and neck cancer, liver cancer, pharynx cancer, adrenocortical cancer, cholangiocarcinoma, mesothelioma, sarcoma, leukemia, lymphoma, Hodgkin's disease, multiple myeloma, melanoma, astrocytoma, stomach cancer, pulmonary adenocarcinoma, adenocarcinoma, acinic cell adenocarcinoma, adrenal cortical carcinomas, alveoli cell carcinoma, anaplastic carcinoma, basaloid carcinoma, basal cell carcinoma, bronchiolar carcinoma, bronchogenic carcinoma, renaladinol carcinoma, embryonal carcinoma, anometroid carcinoma, fibrolamolar liver cell carcinoma, follicular carcinomas, giant cell carcinomas, hepatocellular carcinoma, intraepidermal carcinoma, intraepithelial carcinoma, leptomanigio carcinoma, medullary carcinoma, melanotic carcinoma, menigual carcinoma, mesometonephric carcinoma, oat cell carcinoma, squamal cell carcinoma, sweat gland carcinoma, transitional cell carcinoma, tubular cell carcinoma, ameloblastic sarcoma, angiolithic sarcoma, botryoid sarcoma, endometrial stroma sarcoma, ewing sarcoma, fascicular sarcoma, giant cell sarcoma, granulositic sarcoma, immunoblastic sarcoma, juxaccordial osteogenic sarcoma, coppices sarcoma, leukocytic sarcoma (leukemia), lymphatic sarcoma (lympho sarcoma), medullary sarcoma, myeloid sarcoma (granulocitic sarcoma), austiogenci sarcoma, periosteal sarcoma, reticulum cell sarcoma (histiocytic lymphoma), round cell sarcoma, spindle cell sarcoma, synovial sarcoma, telangiectatic audiogenic sarcoma, Burkitt's lymphoma, NPDL, NML, NH, diffuse lymphomas, Hodgkin’s lymphoma, non-Hodgkin’s lymphoma, B-cell lymphoma, T-cell lymphoma, diffuse large B-cell lymphoma, acute myeloid lymphoma, chronic lymphocytic leukemia, chronic myeoloid leukemia, mantle cell lymphoma, and follicular lymphoma.

[427] Exemplary diseases include, but are not limited to Adrenocortical Carcinoma, Bladder Urothelial Carcinoma, Breast Invasive Carcinoma, Cervical Squamous Cell Carcinoma and Endocervical Adenocarcinoma, Cholangiocarcinoma, Colon Adenocarcinoma, Lymphoid Neoplasm Diffuse Large B-cell Lymphoma, Esophageal Carcinoma, Glioblastoma Multiforme, Head and Neck Squamous Cell Carcinoma, Kidney Chromophobe, Kidney Renal Clear Cell Carcinoma, Kidney Renal Papillary Cell Carcinoma, Acute Myeloid Leukemia, Brain Lower Grade Glioma, Liver Hepatocellular Carcinoma, Lung Adenocarcinoma, Lung Squamous Cell Carcinoma, Mesothelioma, Ovarian Serous Cystadenocarcinoma, Pancreatic Adenocarcinoma, Pheochromocytoma and Paraganglioma, Prostate Adenocarcinoma, Rectum Adenocarcinoma, Sarcoma, Skin Cutaneous Melanoma, Stomach Adenocarcinoma, Testicular Germ Cell Tumors, Thyroid Carcinoma, Thymoma, Uterine Corpus Endometrial Carcinoma, Uterine Carcinosarcoma, and Uveal Melanoma.

[428] According to a preferred embodiment, the compositions and methods of this disclosure are directed to the treatment of metastatic cancer to bone, wherein the metastatic cancer is breast, lung, renal, multiple myeloma, thyroid, prostate, adenocarcinoma, blood cell malignancies, including leukemia and lymphoma; head and neck cancers; gastrointestinal cancers, including esophageal cancer, stomach cancer, colon cancer, intestinal cancer, colorectal cancer, rectal cancer, pancreatic cancer, liver cancer, pharynx cancer, cancer of the bile duct or gall bladder; malignancies of the female genital tract, including ovarian carcinoma, uterine endometrial cancers, vaginal cancer, and cervical cancer; bladder cancer; brain cancer, including neuroblastoma; sarcoma, osteosarcoma; and skin cancer, including malignant melanoma or squamous cell cancer.

[429] In some embodiments, the methods of treatment of a disease or disorder in a subject, as disclosed herein, relates to activation of an immune cell in the subject in need thereof. In some embodiments, the methods of treatment of a disease or disorder in a subject, as disclosed herein, relates to activation of an immune cell (e.g., NK cell, B-cell, or T-cell). In some embodiments, the methods of treatment of a disease or disorder in a subject, as disclosed herein, relates to treatment of a mammalian subject. In some embodiments, the methods of treatment of a disease or disorder in a subject, as disclosed herein, relates to treatment of a human subject.

[430] In some embodiments, the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies of the disclosure, are used as a therapeutic agents for treatment of a disease or disorder, in a subject in need thereof.

[431] In some embodiments, the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies of the disclosure, are used as a therapeutic agents for treatment of a disease or disorder associated with differential or aberrant expression of CLEC2D on various cell surfaces, in a subject in need thereof.

[432] In some embodiments, the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies of the disclosure, are used as a therapeutic agents for treatment of a disease or disorder associated with differential or aberrant expression of CLEC2D on various cell surfaces, in a subject in need thereof, wherein the cells are immune cells or tumor cells.

[433] In some embodiments, the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies of the disclosure, are used as a therapeutic agents for treatment of a disease or disorder associated with differential or aberrant expression of CLEC2D in various cell surfaces, in a subject in need thereof, wherein the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies are administered to the subject in an amount effective for modulating or inhibiting the interaction of CLEC2D with its cognate receptor CD161.

[434] In some embodiments, the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies of the disclosure, are used as a therapeutic agents for treatment of a disease or disorder associated with differential or aberrant expression of CLEC2D in various cell surfaces, in a subject in need thereof, wherein the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies are administered to the subject in an amount effective for binding to and activating NK cells.

[435] In some embodiments, the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies of the disclosure, are used as a therapeutic agents for treatment of a disease or disorder associated with differential or aberrant expression of CLEC2D, in a subject in need thereof, wherein the method comprises administering the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies in an amount effective for treatment or alleviating the symptoms of the disease in the subject. In some embodiments, the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies of the disclosure, used in a method of treating a disease or disorder associated with differential or aberrant expression of

CLEC2D, in a subject in need thereof, modulate or inhibit the interaction of CLEC2D with its cognate receptor CD161.

[436] In some embodiments, the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies of the disclosure, are used in a method of treating a disease or disorder including but not limited to seronegative spondyloarthropathies such as psoriatic arthritis, ankylosing spondylitis, reiters syndrome and spondyloarthropathy associated with inflammatory bowel disease, in a subject in need thereof, wherein the method comprises administering the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies in an amount effective for treatment or alleviating the symptoms of the disease in the subject.

[437] In some embodiments, the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies of the disclosure, are used in a method of treating a disease or disorder including but not limited to connective tissue diseases such as juvenile rheumatoid arthritis, rheumatoid arthritis, systemic lupus erythematosus (SLE) and lupus nephritis, scleroderma, Sjogren's syndrome, mixed connective tissue disease and polymyositis, dermatomyositis, in a subject in need thereof, wherein the method comprises administering the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies in an amount effective for treatment or alleviating the symptoms of the disease in the subject.

[438] In some embodiments, the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies of the disclosure, are used in a method of treating a disease or disorder including but not limited to connective tissue diseases such as juvenile rheumatoid arthritis, rheumatoid arthritis, systemic lupus erythematosus (SLE) and lupus nephritis, scleroderma, Sjogren's syndrome, mixed connective tissue disease and polymyositis, dermatomyositis, in a subject in need thereof, wherein the method comprises administering the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies in an amount effective for treatment or alleviating the symptoms of the disease in the subject.

[439] In some embodiments, the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies of the disclosure, are used in a method of treating a disease or disorder including but not limited to connective tissue diseases such as juvenile rheumatoid arthritis, rheumatoid arthritis, systemic lupus erythematosus (SLE) and lupus nephritis, scleroderma, Sjogren's syndrome, mixed connective tissue disease and polymyositis, dermatomyositis, in a subject in need thereof, wherein the method comprises administering the anti-CLEC2D

antibodies or a composition comprising the anti-CLEC2D antibodies in an amount effective for treatment or alleviating the symptoms of the disease in the subject.

[440] In some embodiments, the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies of the disclosure, are used in a method of treating a disease or disorder including but not limited to connective tissue diseases such as inflammatory bowel diseases such as Crohn's disease and ulcerative colitis, in a subject in need thereof, wherein the method comprises administering the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies in an amount effective for treatment or alleviating the symptoms of the disease in the subject.

[441] In some embodiments, the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies of the disclosure, are used in a method of treating a disease or disorder including but not limited to connective tissue diseases such as Whipples disease and arthritis associated with granulomatous ileocolitis, in a subject in need thereof, wherein the method comprises administering the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies in an amount effective for treatment or alleviating the symptoms of the disease in the subject.

[442] In some embodiments, the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies of the disclosure, are used in a method of treating a disease or disorder including but not limited to inflammatory skin conditions such as autoimmune bullous pemphigoid, autoimmune pemphigus vulgaris, eczema and dermatitis, in a subject in need thereof, wherein the method comprises administering the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies in an amount effective for treatment or alleviating the symptoms of the disease in the subject.

[443] In some embodiments, the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies of the disclosure, are used in a method of treating a disease or disorder including but not limited to inflammatory lung diseases such as alveolitis, pulmonary fibrosis, sarcoidoisis, asthma, bronchitis and bronchiolitis obliterans, in a subject in need thereof, wherein the method comprises administering the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies in an amount effective for treatment or alleviating the symptoms of the disease in the subject.

[444] In some embodiments, the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies of the disclosure, are used in a method of treating a disease or disorder including but not limited to atherosclerosis and coronary vascular diseases in a subject in need thereof, wherein the method comprises administering the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies in an amount effective for treatment or alleviating the symptoms of the disease in the subject.

[445] In some embodiments, the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies of the disclosure, are used in a method of treating a disease or disorder including but not limited to inflammatory renal diseases such as glomerulonethritis, renal allograft rejection and renal tubular inflammation, in a subject in need thereof, wherein the method comprises administering the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies in an amount effective for treatment or alleviating the symptoms of the disease in the subject.

[446] In some embodiments, the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies of the disclosure, are used in a method of treating a disease or disorder including but not limited to systemic vasculitis such as temporal arteritis/giant cell arteritis, takayasu arteritis, polyarteritis nodosa, Kawasaki disease, Wegener's granulomatosis, churg strauss syndrome, microscopic polyangiitis, necrotising glomerulonephritis, henoch schonlein purpura, essential cryoglobulinaemic vasculitis, other small vessel vasculitis and Behcets disease, in a subject in need thereof, wherein the method comprises administering the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies in an amount effective for treatment or alleviating the symptoms of the disease in the subject.

[447] In some embodiments, the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies of the disclosure, are used in a method of treating a disease or disorder including but not limited to systemic vasculitis such as temporal arteritis/giant cell arteritis, takayasu arteritis, polyarteritis nodosa, Kawasaki disease, Wegener's granulomatosis, churg strauss syndrome, microscopic polyangiitis, necrotising glomerulonephritis, henoch schonlein purpura, essential cryoglobulinaemic vasculitis, other small vessel vasculitis and Behcets disease, in a subject in need thereof, wherein the method comprises administering the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies in an amount effective for treatment or alleviating the symptoms of the disease in the subject.

[448] In some embodiments, the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies of the disclosure, are used in a method of treating a disease or disorder including but not limited to macrophage activation diseases such as macrophage activation syndrome (MAS), adult onset stills disease and haemophagocytic syndrome, in a subject in need thereof, wherein the method comprises administering the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies in an amount effective for treatment or alleviating the symptoms of the disease in the subject.

[449] In some embodiments, the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies of the disclosure, are used in a method of treating a disease or disorder including but not limited to polymyalgia rheumatica, primary biliary sclerosis, sclerosing cholangitis, autoimmune hepatitis, Type 1 Diabetes Mellitus, Hashimoto's thyroiditis, Graves' disease, multiple sclerosis (MS), Guillain-Barre syndrome, Addison's disease, and/or Raynaud's phenomenon and Goodpasture's syndrome, in a subject in need thereof, wherein the method comprises administering the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies in an amount effective for treatment or alleviating the symptoms of the disease in the subject.

[450] In some embodiments, the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies of the disclosure, are used in a method of treating a disease or disorder including but not limited to diseases linked with cancer and cancers, in a subject in need thereof, wherein the method comprises administering the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies in an amount effective for treatment or alleviating the symptoms of the disease in the subject.

[451] In some embodiments, the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies of the disclosure, are used in a method of treating a disease or disorder including but not limited to diseases linked with cancer and cancers, which comprise breast cancer, prostate cancer, endometrial cancer, uterine cancer, bladder cancer, kidney cancer, esophageal cancer, squamous cell carcinoma, uveal melanoma, glioma, glioblastoma, myeloma, pheochromocytoma, paraganglioma, follicular lymphoma, renal cell carcinoma, cendcal cancer, ovarian cancer, cervical cancer, lung cancer, colorectal cancer, brain cancer, pancreatic cancer, gastric cancer, intestinal cancer, testicular cancer, skin cancer, thyroid cancer, thymoma, head and neck cancer, liver cancer, pharynx cancer, adrenocortical cancer, cholangiocarcinoma,

mesothelioma, sarcoma, leukemia, lymphoma, Hodgkin's disease, multiple myeloma, melanoma, astrocytoma, stomach cancer, pulmonary adenocarcinoma, adenocarcinoma, acinic cell adenocarcinoma, adrenal cortical carcinomas, alveoli cell carcinoma, anaplastic carcinoma, basaloid carcinoma, basal cell carcinoma, bronchiolar carcinoma, bronchogenic carcinoma, renaladinol carcinoma, embryonal carcinoma, anometroid carcinoma, fibrolamolar liver cell carcinoma, follicular carcinomas, giant cell carcinomas, hepatocellular carcinoma, intraepidermal carcinoma, intraepithelial carcinoma, leptomanigio carcinoma, medullary carcinoma, melanotic carcinoma, menigual carcinoma, mesometonephric carcinoma, oat cell carcinoma, squamal cell carcinoma, sweat gland carcinoma, transitional cell carcinoma, tubular cell carcinoma, ameloblastic sarcoma, angiolithic sarcoma, botryoid sarcoma, endometrial stroma sarcoma, ewing sarcoma, fascicular sarcoma, giant cell sarcoma, granulositic sarcoma, immunoblastic sarcoma, juxaccordial osteogenic sarcoma, coppices sarcoma, leukocytic sarcoma (leukemia), lymphatic sarcoma (lympho sarcoma), medullary sarcoma, myeloid sarcoma (granulocitic sarcoma), austiogenci sarcoma, periosteal sarcoma, reticulum cell sarcoma (histiocytic lymphoma), round cell sarcoma, spindle cell sarcoma, synovial sarcoma, telangiectatic audiogenic sarcoma, Burkitt's lymphoma, NPDL, NML, NH, diffuse lymphomas, Hodgkin's lymphoma, non-Hodgkin's lymphoma, B-cell lymphoma, T-cell lymphoma, diffuse large B-cell lymphoma, acute myeloid lymphoma, chronic lymphocytic leukemia, chronic myeoloid leukemia, mantle cell lymphoma, and follicular lymphoma, in a subject in need thereof, wherein the method comprises administering the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies in an amount effective for treatment or alleviating the symptoms of the disease in the subject.

[452] In some embodiments, the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies of the disclosure, are used in a method of treating a disease or disorder including but not limited to diseases linked with a metastatic cancer or cancers, in a subject in need thereof, wherein the method comprises administering the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies in an amount effective for treatment or alleviating the symptoms of the disease in the subject.

[453] In some embodiments, the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies of the disclosure, are used in a method of treating a disease or disorder including but not limited to diseases linked with a metastatic cancer or cancers, in a subject in

need thereof, wherein the method comprises administering the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies in an amount effective for treatment or alleviating the symptoms of the disease in the subject.

[454] In some embodiments, the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies of the disclosure, are used in a method of treating a disease or disorder including but not limited to diseases linked with a metastatic cancer or cancers to bone, in a subject in need thereof, wherein the method comprises administering the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies in an amount effective for treatment or alleviating the symptoms of the disease in the subject.

[455] In some embodiments, the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies of the disclosure, are used in a method of treating a disease or disorder including but not limited to diseases linked with a metastatic cancer or cancers, wherein the metastatic cancer is breast, lung, renal, multiple myeloma, thyroid, prostate, adenocarcinoma, blood cell malignancies, including leukemia and lymphoma; head and neck cancers; gastrointestinal cancers, including esophageal cancer, stomach cancer, colon cancer, intestinal cancer, colorectal cancer, rectal cancer, pancreatic cancer, liver cancer, cancer of the bile duct or gall bladder; malignancies of the female genital tract, including ovarian carcinoma, uterine endometrial cancers, vaginal cancer, and cervical cancer; bladder cancer; brain cancer, including neuroblastoma; sarcoma, osteosarcoma; and skin cancer, including malignant melanoma or squamous cell cancerin a subject in need thereof, wherein the method comprises administering the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies in an amount effective for treatment or alleviating the symptoms of the disease in the subject.

[456] In some embodiments, the anti-CLEC2D antibody and compositions of the disclosure, are used in a method of treatment of a subject by organ transplant or adoptive immune cell transplant. In some embodiments, the anti-CLEC2D antibody and compositions of the disclosure, block CD161 and CLEC2D interaction and reduces Graft vs Host rejection, due to killing if recipient dendritic cells by alloreactive NK cells.

[457] In some embodiments, the anti-CLEC2D antibody and compositions of the disclosure, are used in a method of treatment of an infectious disease in a subject caused by microorganisms including but not limited to bacteria, fungi, protozoa, parasites, and viruses. In some embodiments, the anti-CLEC2D antibody and compositions of the disclosure, is used in a

method of treatment of a bacterial disease in a subject caused by any one or more of (or any combination of) Acinetobacter baumanii, Actinobacillus sp., Actinomycetes, Actinomyces sp. (such as Actinomyces israelii and Actinomyces naeslundii), Aeromonas sp. (such as Aeromonas hydrophila, Aeromonas veronii biovar sobria (Aeromonas sobria), and Aeromonas caviae),Anaplasma phagocytophilum, Anaplasma marginale Alcaligenes xylosoxidans, Acinetobacter baumanii, Actinobacillus actinomycetemcomitans, Bacillus sp. (such as Bacillus anthracis, Bacillus cereus, Bacillus subtilis, Bacillus thuringiensis, and Bacillus stearothermophilus), Bacteroides sp. (such as Bacteroides fragilis), Bartonella sp. (such as Bartonella bacilliformis and Bartonella henselae, Bifidobacterium sp., Bordetella sp. (such as Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica), Borrelia sp. (such as Borrelia recurrentis,and Borrelia burgdorferi), Brucella sp. (such as Brucella abortus, Brucella canis, Brucella melintensis and Brucella suis), Burkholderia sp. (such as Burkholderia pseudomallei and Burkholderia cepacia), Campylobacter sp. (such as Campylobacter jejuni, Campylobacter coli, Campylobacter lari and Campylobacter fetus), Capnocytophaga sp., Cardiobacterium hominis, Chlamydia trachomatis, Chlamydophila pneumoniae, Chlamydophila psittaci, Citrobacter sp. Coxiella burnetii, Corynebacterium sp. (such as, Corynebacterium diphtheriae, Corynebacterium jeikeum and Corynebacterium), Clostridium sp. (such as Clostridium perfringens, Clostridium difficile, Clostridium botulinum and Clostridium tetani), Eikenella corrodens, Enterobacter sp. (such as Enterobacter aerogenes, Enterobacter agglomerans, Enterobacter cloacae and Escherichia coli, including opportunistic Escherichia coli, such as enterotoxigenic E. coli, enteroinvasive E. coli, enteropathogenic E. coli, enterohemorrhagic E. coli, enteroaggregative E. coli and uropathogenic E. coli) Enterococcus sp. (such as Enterococcus faecalis and Enterococcus faecium), Ehrlichia sp. (such as Ehrlichia chafeensia and Ehrlichia canis), Epidermophyton floccosum, Erysipelothrix rhusiopathiae, Eubacterium sp., Francisella tularensis, Fusobacterium nucleatum, Gardnerella vaginalis, Gemella morbillorum, Haemophilus sp. (such as Haemophilus influenzae, Haemophilus ducreyi, Haemophilus aegyptius, Haemophilus parainfluenzae, Haemophilus haemolyticus and Haemophilus parahaemolyticus, Helicobacter sp. (such as Helicobacter pylori, Helicobacter cinaedi and Helicobacter fennelliae), Kingella kingii, Klebsiella sp. (such as Klebsiella pneumoniae, Klebsiella granulomatis and Klebsiella oxytoca), Lactobacillus sp., Listeria monocytogenes, Leptospira interrogans, Legionella pneumophila, Leptospira interrogans,

Peptostreptococcus sp., Mannheimia hemolytica, Microsporum canis, Moraxella catarrhalis, Morganella sp., Mobiluncus sp., Micrococcus sp., Mycobacterium sp. (such as Mycobacterium leprae, Mycobacterium tuberculosis, Mycobacterium paratuberculosis, Mycobacterium intracellulare, Mycobacterium avium, Mycobacterium bovis, and Mycobacterium marinum), Mycoplasm sp. (such as Mycoplasma pneumoniae, Mycoplasma hominis, and Mycoplasma genitalium), Nocardia sp. (such as Nocardia asteroides, Nocardia cyriacigeorgica and Nocardia brasiliensis), Neisseria sp. (such as Neisseria gonorrhoeae and Neisseria meningitidis), Pasteurella multocida, Pityrosporum orbiculare (Malassezia furfur), Plesiomonas shigelloides. Prevotella sp., Porphyromonas sp., Prevotella melaninogenica, Proteus sp. (such as Proteus vulgaris and Proteus mirabilis), Providencia sp. (such as Providencia alcalifaciens, Providencia rettgeri and Providencia stuartii), Pseudomonas aeruginosa, Propionib acterium acnes, Rhodococcus equi, Rickettsia sp. (such as Rickettsia rickettsii, Rickettsia akari and Rickettsia prowazekii, Orientia tsutsugamushi (formerly: Rickettsia tsutsugamushi) and Rickettsia typhi), Rhodococcus sp., Serratia marcescens, Stenotrophomonas maltophilia, Salmonella sp. (such as Salmonella enterica, Salmonella typhi, Salmonella paratyphi, Salmonella enteritidis, Salmonella cholerasuis and Salmonella typhimurium), Serratia sp. (such as Serratia marcesans and Serratia liquifaciens), Shigella sp. (such as Shigella dysenteriae, Shigella flexneri, Shigella boydii and Shigella sonnei), Staphylococcus sp. (such as Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus hemolyticus, Staphylococcus saprophyticus), Streptococcus sp. (such as Streptococcus pneumoniae (for example chloramphenicol-resistant serotype 4 Streptococcus pneumoniae, spectinomycin-resistant serotype 6B Streptococcus pneumoniae, streptomycin-resistant serotype 9V Streptococcus pneumoniae, erythromycin-resistant serotype 14 Streptococcus pneumoniae, optochin-resistant serotype 14 Streptococcus pneumoniae, rifampicin-resistant serotype 18C Streptococcus pneumoniae, tetracycline-resistant serotype 19F Streptococcus pneumoniae, penicillin-resistant serotype 19F Streptococcus pneumoniae, and trimethoprim-resistant serotype 23F Streptococcus pneumoniae, chloramphenicol-resistant serotype 4 Streptococcus pneumoniae, spectinomycin-resistant serotype 6B Streptococcus pneumoniae, streptomycin-resistant serotype, 9V Streptococcus pneumoniae, optochin-resistant serotype 14 Streptococcus pneumoniae, rifampicin-resistant serotype 18C Streptococcus pneumoniae, penicillin-resistant serotype 19F, Streptococcus pneumoniae, or trimethoprim-resistant serotype 23F Streptococcus pneumoniae), Streptococcus agalactiae, Streptococcus

mutans, Streptococcus pyogenes, Group A streptococci, Streptococcus pyogenes, Group B streptococci, Streptococcus agalactiae, Group C streptococci, Streptococcus anginosus, Streptococcus equismilis, Group D streptococci, Streptococcus bovis, Group F streptococci, and Streptococcus anginosus Group G streptococci), Spirillum minus, Streptobacillus moniliformi, Treponema sp. (such as Treponema carateum, Treponema petenue, Treponema pallidum and Treponema endemicum, Trichophyton rubrum, T. mentagrophytes, Tropheryma whippelii, Ureaplasma urealyticum, Veillonella sp., Vibrio sp. (such as Vibrio cholerae, Vibrio parahemolyticus, Vibrio vulnificus, Vibrio parahaemolyticus, Vibrio vulnificus,Vibrio alginolyticus, Vibrio mimicus, Vibrio hollisae, Vibrio fluvialis, Vibrio metchnikovii, Vibrio damsela and Vibrio furnisii), Yersinia sp. (such as Yersinia enterocolitica, Yersinia pestis, and Yersinia pseudotuberculosis) and Xanthomonas maltophilia among others.

[458] In some embodiments, the anti-CLEC2D antibody and compositions of the disclosure, is used in a method of treatment of a fungal disease in a subject caused by any one or more of (or any combination of) Aspergillus, Blastomyces, Candidiasis, Coccidiodomycosis, Cryptococcus neoformans, Cryptococcus gatti, sp. Histoplasma sp. (such as Histoplasma capsulatum), Pneumocystis sp. (such as Pneumocystis jirovecii), Stachybotrys (such as Stachybotrys chartarum), Mucroymcosis, Sporothrix, fungal eye infections ringworm, Exserohilum, Cladosporium.

[459] In some embodiments, the anti-CLEC2D antibody and compositions of the disclosure, is used in a method of treatment of a protozoan disease in a subject caused by any one or more of (or any combination of) Euglenozoa, Heterolobosea, Diplomonadida, Amoebozoa, Blastocystic, and Apicomplexa. Example Euglenoza include, but are not limited to, Trypanosoma cruzi (Chagas disease), T. brucei gambiense, T. brucei rhodesiense, Leishmania braziliensis, L. infantum, L. mexicana, L. major, L. tropica, and L. donovani. Example Heterolobosea include, but are not limited to, Naegleria fowleri. Example Diplomonadids include, but are not limited to, Giardia intestinalis (G. lamblia, G. duodenalis). Example Amoebozoa include, but are not limited to, Acanthamoeba castellanii, Balamuthia madrillaris, Entamoeba histolytica. Example Blastocysts include, but are not limited to, Blastocystic hominis. Example Apicomplexa include, but are not limited to, Babesia microti, Cryptosporidium parvum, Cyclospora cayetanensis, Plasmodium falciparum, P. vivax, P. ovale, P. malariae, and Toxoplasma gondii.

[460] In some embodiments, the anti-CLEC2D antibody and compositions of the disclosure, is used in a method of treatment of a viral disease in a subject caused by any one or more of (or any combination of) Ebolavirus , measles virus, SARS, Chikungunya virus, hepatitis viruses, Marburg virus, yellow fever virus, MERS, Dengue virus, Lassa fever virus, influenza virus, rhabdovirus or HIV. A hepatitis virus may include hepatitis A, hepatitis B, or hepatitis C.

[461] In some embodiments, the anti-CLEC2D antibody and compositions of the disclosure, is used in a method of treatment of a viral disease in a subject caused by any one or more of (or any combination of) a human respiratory syncytial virus, Sudan ebola virus, Bundibugyo virus, Tai Forest ebola virus, Reston ebola virus, Achimota, Aedes flavivirus, Aguacate virus, Akabane virus, Alethinophid reptarenavirus, Allpahuayo mammarenavirus, Amapari mmarenavirus, Andes virus, Apoi virus, Aravan virus, Aroa virus, Arumwot virus, Atlantic salmon paramyxovirus, Australian bat lyssavirus, Avian bornavirus, Avian metapneumovirus, Avian paramyxoviruses, penguin or Falkland Islandsvirus, BK polyomavirus, Bagaza virus, Banna virus, Bat herpesvirus, Bat sapovirus, Bear Canon mammarenavirus, Beilong virus, Betacoronavirus, Betapapillomavirus 1-6, Bhanja virus, Bokeloh bat lyssavirus, Borna disease virus, Bourbon virus, Bovine hepacivirus, Bovine parainfluenza virus 3, Bovine respiratory syncytial virus, Brazoran virus, Bunyamwera virus, Caliciviridae virus. California encephalitis virus, Candiru virus, Canine distemper virus, Canine pneumovirus, Cedar virus, Cell fusing agent virus, Cetacean morbillivirus, Chandipura virus, Chaoyang virus, Chapare mammarenavirus,Chikungunya virus, Colobus monkey papillomavirus, Colorado tick fever virus, Cowpox virus, Crimean-Congo hemorrhagic fever virus, Culex flavivirus, Cupixi mammarenavirus, Dengue virus, Dobrava-Belgrade virus, Donggang virus, Dugbe virus, Duvenhage virus, Eastern equine encephalitis virus, Entebbe bat virus, Enterovirus A-D, European bat lyssavirus 1-2, Eyach virus, Feline morbillivirus, Fer-de-Lance paramyxovirus, Fitzroy River virus, Flaviviridae virus, Flexal mammarenavirus, GB virus C, Gairo virus, Gemycircularvirus, Goose paramyxovirus SF02, GreatIsland virus, Guanarito mammarenavirus, Hantaan virus, Hantavirus Z10, Heartland virus, Hendra virus, Hepatitis A/B/C/E, Hepatitis delta virus, Human bocavirus, Human coronavirus, Human endogenous retrovirus K, Human enteric coronavirus, Human genital-associated circular DNA virus-1, Human herpesvirus 1-8, Human immunodeficiency virus 1/2, Human mastadenovirus AG, Human papillomavirus, Human parainfluenza virus 1-4, Human paraechovirus, Human picornavirus, Human smacovirus, Ikoma

lyssavirus, Ilheus virus, Influenza A-C, Ippy mammarenavirus, Irkut virus, J-virus, JC polyomavirus, Japanese encephalitis virus, Junin mammarenavirus, KI polyomavirus, Kadipiro virus, Kamiti River virus, Kedougou virus, Khujand virus, Kokobera virus, Kyasanur forest disease virus, Lagos bat virus, Langat virus, Lassa mammarenavirus, Latino mammarenavirus, Leopards Hill virus, Liao ning virus, Ljungan virus, Lloviu virus, Louping ill virus, Lujo mammarenavirus, Luna mammarenavirus, Lunk virus, Lymphocytic choriomeningitis mammarenavirus, Lyssavirus Ozernoe, MSSI2Y225 virus, Machupo mammarenavirus, Mamastrovirus 1, Manzanilla virus, Mapuera virus, Marburg virus, Mayaro virus, Measles virus, Menangle virus, Mercadeo virus, Merkel cell polyomavirus, Middle East respiratory syndrome coronavirus, Mobala mammarenavirus, Modoc virus, Moijang virus, Mokolo virus, Monkeypox virus, Montana myotis leukoenchalitis virus, Mopeia lassa virus reassortant 29, Mopeia mammarenavirus, Morogoro virus, Mossman virus, Mumps virus, Murine pneumonia virus, Murray Valley encephalitis virus, Nariva virus, Newcastle disease virus, Nipah virus, Norwalk virus, Norway rat hepacivirus, Ntaya virus, O'nyong-nyong virus, Oliveros mammarenavirus, Omsk hemorrhagic fever virus, Oropouche virus, Parainfluenza virus 5, Parana mammarenavirus, Parramatta River virus, Peste-des-petits-ruminants virus, Pichande mammarenavirus, Picornaviridae virus, Pirital mammarenavirus, Piscihepevirus A, Porcine parainfluenza virus 1, porcine rubulavirus, Powassan virus, Primate T-lymphotropic virus 1-2, Primate erythroparvovirus 1, Punta Toro virus, Puumala virus, Quang Binh virus, Rabies virus, Razdan virus, Reptile bornavirus 1, Rhinovirus A-B, Rift Valley fever virus, Rinderpest virus, Rio Bravo virus, Rodent Torque Teno virus, Rodent hepacivirus, Ross River virus, Rotavirus A-I, Royal Farm virus, Rubella virus, Sabia mammarenavirus, Salem virus, Sandfly fever Naples virus, Sandfly fever Sicilian virus, Sapporo virus, Sathuperi virus, Seal anellovirus, Semliki Forest virus, Sendai virus, Seoul virus, Sepik virus, Severe acute respiratory syndrome-related coronavirus, Severe fever with thrombocytopenia syndrome virus, Shamonda virus, Shimoni bat virus, Shuni virus, Simbu virus, Simian torque teno virus, Simian virus 40-41, Sin Nombre virus, Sindbis virus,Small anellovirus, Sosuga virus, Spanish goat encephalitis virus, Spondweni virus, St. Louisencephalitis virus, Sunshine virus, TTV-like mini virus, Tacaribe mammarenavirus, Taila virus, Tamana bat virus, Tamiami mammarenavirus, Tembusu virus, Thogoto virus, Thottapalayam virus, Tick-borne encephalitis virus, Tioman virus, Togaviridae virus, Torque teno canis virus, Torque teno douroucouli virus, Torque teno felis virus, Torque teno midi virus,

Torque teno sus virus, Torque teno tamarin virus, Torque teno virus, Torque teno zalophus virus, Tuhoko virus, Tula virus, Tupaia paramyxovirus, Usutu virus, Uukuniemi virus, Vaccinia virus, Variola virus, Venezuelan equine encephalitis virus, Vesicular stomatitis Indiana virus, WU Polyomavirus, Wesselsbron virus, West Caucasian bat virus, West Nile virus, Western equine encephalitis virus, Whitewater Arroyo mammarenavirus, Yellow fever virus, Yokose virus, Yug Bogdanovac virus, Zaire ebolavirus, Zika virus, or Zygosaccharomyces bailii virus Z viral sequence. Examples of diseases caused by RNA viruses that may be treated include one or more of (or any combination of) Coronaviridae virus, a Picornaviridae virus, a Caliciviridae virus, a Flaviviridae virus, a Togaviridae virus, a Bornaviridae, a Filoviridae, a Paramyxoviridae, a Pneumoviridae, a Rhabdoviridae, an Arenaviridae, a Bunyaviridae, an Orthomyxoviridae, or a Deltavirus. In certain embodiments, the virus is Coronavirus, SARS, Poliovirus, Rhinovirus, Hepatitis A, Norwalk virus, Yellow fever virus, West Nile virus, Hepatitis C virus, Dengue fever virus, Zika virus, Rubella virus, Ross River virus, Sindbis virus, Chikungunya virus, Borna disease virus, Ebola virus, Marburg virus, Measles virus, Mumps virus, Nipah virus, Hendra virus, Newcastle disease virus, Human respiratory syncytial virus, Rabies virus, Lassa virus, Hantavirus, Crimean-Congo hemorrhagic fever virus, Influenza, or Hepatitis D virus. In certain embodiments, the virus is retrovirus, including but not limited to one or more of or any combination of viruses of the Genus Alpharetrovirus, Betaretrovirus, Gammaretrovirus, Deltaretrovirus, Epsilonretrovirus, Lentivirus, Spumavirus, or the Family Metaviridae, Pseudoviridae, and Retroviridae (including HIV), Hepadnaviridae (including Hepatitis B virus), and Caulimoviridae (including Cauliflower mosaic virus).

[462] In some embodiments, the infectious diseases comprises a chronic viral infection, such as HIV. In some embodiments, the infectious disease comprises a chronic bacterial infection such as tuberculosis (TB). In some embodiments, the infectious disease comprises a chronic parasitic infection such as malaria.

[463] In some embodiments, the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies of the disclosure, are used in a method of treating a disease or disorder characterized by increased expression of CLEC2D on the surface of various cells of a subject in need thereof, comprising administering to a subject in need thereof one or more anti-CLEC2D antibodies of the disclosure as therapeutic agents in an amount sufficient to either: (i) block binding of the

CLEC2D on the various cells to CD161 on the surface of an immune cell; (ii) reduce expression of CLEC2D on the various cells; (iii) reduce expression of one or more genes induced in an immune cell by binding of the CLEC2D to the CD161 on the immune cell (iv) binding to and/or activating one or more Fc receptors on the surface of the immune cell, (v) bind to CLEC2D on the surface of an immune cells and activate the immune cell, or any combination thereof.

[464] In some embodiments, the invention relates to a method of assessing the efficacy of a therapeutic agent in a subject suffering from a cancer or tumor or both, comprising: a) detecting the number of viable and/or proliferating cancer cells in a sample from a subject; b) administering a therapeutically effective amount of one or more anti-CLEC2D antibodies of the disclosure to the subject; c) repeating step a) one or more times; and d) comparing the number of viable and/or proliferating cancer cells detected in steps a) to those detected in step c), wherein the anti-CLEC2D antibodies: (i) bind to CLEC2D on the surface of the cancer cells and inhibits the interaction between the CLEC2D on the tumor cells and CD161 on the surface of immune cells; (ii) bind to CLEC2D on the surface of the cancer cells and Fc receptors on the surface of immune cells to induce lysis of the cancer cell; (iii) bind to CLEC2D on the surface of immune cells and activate the immune cells; or a combination thereof, wherein the absence of, or decrease in number of viable and/or proliferating cancer cells detected in step c) as compared to the number of viable and/or proliferating cancer cells detected in step a) indicates that the agent is effective.

[465] In some embodiments, the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies of the disclosure, may enhance the function of mucosal associated invariant T (MAIT) cells, NK cells or T cells.

[466] In some embodiments, the invention relates to a method of treatment of a disease or disorder in a subject, wherein the method comprises administering to the subject in need thereof, a combination of a therapeutically effective amount of an anti-CLEC2D antibody of the disclosure and a therapeutically effective amount of at least a second therapeutic agent. In some embodiments, the at least one second therapeutic agent as disclosed herein, comprises a therapeutic antibody against a protein or antigen expressed on the surface of a tumor cell or immune cell.

[467] In some embodiments, the at least one second therapeutic agent as disclosed herein, comprises a therapeutic antibody against a protein or antigen expressed on the surface of a tumor

cell, that induces apoptosis of the tumor cell. In some embodiments, the at least one second therapeutic agent as disclosed herein, comprises a therapeutic antibody against a protein or antigen expressed on the surface of a tumor cell, that induces killing by the immune cell through antibody directed cellular cytotoxicity (ADCC) or complement directed cytotoxicity (CDC). In some embodiments, the at least one second therapeutic agent as disclosed herein, comprises a therapeutic antibody against a protein or antigen expressed on the surface of an immune cell, that induces activation of the immune cell. In some embodiments, the at least one second therapeutic agent as disclosed herein, comprises a therapeutic antibody against a protein or antigen expressed on the surface of an immune cell, that induces cytokine production by the immune cell. In some embodiments, the at least one second therapeutic agent as disclosed herein, comprises a therapeutic antibody against a protein or antigen expressed on the surface of an immune cell, that induces chemokine production by the immune cell. In some embodiments, the at least one second therapeutic agent as disclosed herein, comprises a therapeutic antibody against a protein or antigen expressed on the surface of an immune cell, that induces production of inflammatory cytokines of the immune cell. In some embodiments, the at least one second therapeutic agent as disclosed herein, comprises a therapeutic antibody against a protein or antigen expressed on the surface of an immune cell, that activates the immune cells to recognize and induce cytotoxicity in a cancer cell. In some embodiments, the at least one second therapeutic agent as disclosed herein, comprises a therapeutic antibody against a protein or antigen expressed on the surface of an immune cell, that activates the immune cells to recognize and induce cytotoxicity in cell infected with a pathogen, wherein the pathogen includes but is not limited to a virus or a bacteria.

[468] In some embodiments, the methods of treatment of a disease or disorder in a subject, as disclosed herein, comprises administering the anti-CLEC2D antibodies or a composition comprising the anti-CLEC2D antibodies of the disclosure and at least a second therapeutic agent, sequentially or simultaneously.

[469] Treatment of Inflammatory Diseases

[470] In some embodiments, the disease or disorder treated by the antibodies and pharmaceutical compositions comprising the same of the disclosure comprises an inflammatory or autoimmune disease or disorder.

[471] As used herein, the term "inflammatory disorders" refers to pathological states resulting in inflammation, typically caused by neutrophil chemotaxis.

[472] As used herein, autoimmune diseases or disorders are caused when the body's immune system, which normally defends the body against bacteria, viruses and other infective agents, attacks "self" tissue, cells and organs. The mobilization of the immune system against such "self" targets is termed autoimmunity. Although some autoimmunity is present in every individual, rigid control systems suppress the self-recognizing cells of the immune system to an extent that the autoimmunity is normally asymptomatic. Disease states arise when there is some interruption in the control system, allowing the autoimmune cells to escape suppression, or when there is some change in a target tissue such that it is no longer recognized as self. Autoimune disorders can be characterized by inflammatory responses.

[473] Exemplary, but non-limiting examples of inflammatory or autoimmune disorders include, but are not limited to seronegative spondyloarthropathies, connective tissue diseases, inflammatory bowel diseases, arthritis, inflammatory skin conditions, inflammatory lung diseases, inflammatory renal disease, systemic vasculitis, macrophage activation diseases, polymyalgia rheumatica, primary biliary sclerosis, sclerosing cholangitis, autoimmune hepatitis, Type 1 Diabetes Mellitus, Hashimoto's thyroiditis, Graves' disease, multiple sclerosis (MS), Guillain-Barre syndrome, Addison's disease, Raynaud's phenomenon and Goodpasture's syndrome.

[474] In some embodiments, a therapeutically effective amount of an antibody of pharmaceutical composition comprising same of the disclosure alleviates or prevents a sign or a symptom of an inflammatory or autoimmune disorder.

[475] In some embodiments, a therapeutically effective amount of an antibody of pharmaceutical composition comprising same of the disclosure reduces an amount of inflammation in one or more tissues or organs of the subject.

[476] In some embodiments, a therapeutically effective amount of an antibody of pharmaceutical composition comprising same of the disclosure transiently reduces or inhibits one or more aspects of the disease or of the immune response. Such a transient inhibition or reduction of one or more aspects of the disease or of the immune system can last for hours, days, weeks, or months. Preferably, the transient inhibition or reduction in one or more aspects of the disease or of the immune response last for a few hours (e.g., 2 hours, 4 hours, 6 hours, 8 hours,

12 hours, 14 hours, 16 hours, 18 hours, 24 hours, 36 hours, or 48 hours), a few days (e.g., 3 days, 4 days, 5 days, 6 days, 7 days, or 14 days), or a few weeks (e.g., 3 weeks, 4 weeks, 5 weeks or 6 weeks).

[477] The prophylactic, therapeutic or immunomodulatory activity of an antibody or pharmaceutical composition comprising an antibody of the disclosure can be determined in vitro and/or in vivo by any technique well-known to one skilled in the art, including, e.g., by CTL assays, proliferation assays, and immunoassays (e.g., ELISAs) for the expression of particular proteins such as co-stimulatory molecules and cytokines.

[478] Treatment of Cancer

[479] As used herein, the term "severity" is meant to describe the potential of cancer to transform from a precancerous, or benign, state into a malignant state. Alternatively, or in addition, severity is meant to describe a cancer stage, for example, according to the TNM system (accepted by the International Union Against Cancer (UICC) and the American Joint Committee on Cancer (AJCC)) or by other art-recognized methods. Cancer stage refers to the extent or severity of the cancer, based on factors such as the location of the primary tumor, tumor size, number of tumors, and lymph node involvement (spread of cancer into lymph nodes). Alternatively, or in addition, severity is meant to describe the tumor grade by art-recognized methods (see, National Cancer Institute, www.cancer.gov). Tumor grade is a system used to classify cancer cells in terms of how abnormal they look under a microscope and how quickly the tumor is likely to grow and spread. Many factors are considered when determining tumor grade, including the structure and growth pattern of the cells. The specific factors used to determine tumor grade vary with each type of cancer. Severity also describes a histologic grade, also called differentiation, which refers to how much the tumor cells resemble normal cells of the same tissue type (see, National Cancer Institute, www.cancer.gov). Furthermore, severity describes a nuclear grade, which refers to the size and shape of the nucleus in tumor cells and the percentage of tumor cells that are dividing (see, National Cancer Institute, www.cancer.gov).

[480] In another aspect of this disclosure, severity describes the degree to which a tumor has secreted growth factors, degraded the extracellular matrix, become vascularized, lost adhesion to juxtaposed tissues, or metastasized. Moreover, severity describes the number of locations to which a primary tumor has metastasized. Finally, severity includes the difficulty of treating tumors of varying types and locations. For example, inoperable tumors, those cancers which

have greater access to multiple body systems (hematological and immunological tumors), and those which are the most resistant to traditional treatments are considered most severe. In these situations, prolonging the life expectancy of the subject and/or reducing pain, decreasing the proportion of cancerous cells or restricting cells to one system, and improving cancer stage/tumor grade/histological grade/nuclear grade are considered alleviating a sign or symptom of the cancer.

[481] Cancer is a group of diseases that may cause almost any sign or symptom. The signs and symptoms will depend on where the cancer is, the size of the cancer, and how much it affects the nearby organs or structures. If a cancer spreads (metastasizes), then symptoms may appear in different parts of the body.

[482] Treating cancer can result in a reduction in size of a tumor. A reduction in size of a tumor may also be referred to as "tumor regression". Preferably, after treatment, tumor size is reduced by 5% or greater relative to its size prior to treatment; more preferably, tumor size is reduced by 10% or greater; more preferably, reduced by 20% or greater; more preferably, reduced by 30% or greater; more preferably, reduced by 40% or greater; even more preferably, reduced by 50% or greater; and most preferably, reduced by greater than 75% or greater. Size of a tumor may be measured by any reproducible means of measurement. The size of a tumor may be measured as a diameter of the tumor.

[483] Treating cancer can result in a reduction in tumor volume. Preferably, after treatment, tumor volume is reduced by 5% or greater relative to its size prior to treatment; more preferably, tumor volume is reduced by 10% or greater; more preferably, reduced by 20% or greater; more preferably, reduced by 30% or greater; more preferably, reduced by 40% or greater; even more preferably, reduced by 50% or greater; and most preferably, reduced by greater than 75% or greater. Tumor volume may be measured by any reproducible means of measurement.

[484] Treating cancer results in a decrease in number of tumors. Preferably, after treatment, tumor number is reduced by 5% or greater relative to number prior to treatment; more preferably, tumor number is reduced by 10% or greater; more preferably, reduced by 20% or greater; more preferably, reduced by 30% or greater; more preferably, reduced by 40% or greater; even more preferably, reduced by 50% or greater; and most preferably, reduced by greater than 75%. Number of tumors may be measured by any reproducible means of measurement. The number of

tumors may be measured by counting tumors visible to the naked eye or at a specified magnification. Preferably, the specified magnification is 2x, 3x, 4x, 5x, 10x, or 50x.

[485] Treating cancer can result in a decrease in number of metastatic lesions in other tissues or organs distant from the primary tumor site. Preferably, after treatment, the number of metastatic lesions is reduced by 5% or greater relative to number prior to treatment; more preferably, the number of metastatic lesions is reduced by 10% or greater; more preferably, reduced by 20% or greater; more preferably, reduced by 30% or greater; more preferably, reduced by 40% or greater; even more preferably, reduced by 50% or greater; and most preferably, reduced by greater than 75%. The number of metastatic lesions may be measured by any reproducible means of measurement. The number of metastatic lesions may be measured by counting metastatic lesions visible to the naked eye or at a specified magnification. Preferably, the specified magnification is 2x, 3x, 4x, 5x, 10x, or 50x.

[486] Treating cancer can result in an increase in average survival time of a population of treated subjects in comparison to a population receiving carrier alone. Preferably, the average survival time is increased by more than 30 days; more preferably, by more than 60 days; more preferably, by more than 90 days; and most preferably, by more than 120 days. An increase in average survival time of a population may be measured by any reproducible means. An increase in average survival time of a population may be measured, for example, by calculating for a population the average length of survival following initiation of treatment with an antibody or pharmaceutical composition comprising same. An increase in average survival time of a population may also be measured, for example, by calculating for a population the average length of survival following completion of a first round of treatment with an antibody or pharmaceutical composition comprising same.

[487] Treating cancer can result in an increase in average survival time of a population of treated subjects in comparison to a population of untreated subjects. Preferably, the average survival time is increased by more than 30 days; more preferably, by more than 60 days; more preferably, by more than 90 days; and most preferably, by more than 120 days. An increase in average survival time of a population may be measured by any reproducible means. An increase in average survival time of a population may be measured, for example, by calculating for a population the average length of survival following initiation of treatment with an antibody or pharmaceutical composition comprising same. An increase in average survival time of a

population may also be measured, for example, by calculating for a population the average length of survival following completion of a first round of treatment with an antibody or pharmaceutical composition comprising same of the present disclosure.

[488] Treating cancer can result in increase in average survival time of a population of treated subjects in comparison to a population receiving monotherapy with a drug that is not an antibody of the present disclosure. Preferably, the average survival time is increased by more than 30 days; more preferably, by more than 60 days; more preferably, by more than 90 days; and most preferably, by more than 120 days. An increase in average survival time of a population may be measured by any reproducible means. An increase in average survival time of a population may be measured, for example, by calculating for a population the average length of survival following initiation of treatment with an antibody or pharmaceutical composition comprising same of the present disclosure. An increase in average survival time of a population may also be measured, for example, by calculating for a population the average length of survival following completion of a first round of treatment with an antibody or pharmaceutical composition comprising same of the present disclosure.

[489] Treating cancer can result in a decrease in the mortality rate of a population of treated subjects in comparison to a population receiving carrier alone. Treating cancer can result in a decrease in the mortality rate of a population of treated subjects in comparison to an untreated population. Treating cancer can result in a decrease in the mortality rate of a population of treated subjects in comparison to a population receiving monotherapy with a drug that is not an antibody or a pharmaceutical composition comprising same of the present disclosure. Preferably, the mortality rate is decreased by more than 2%; more preferably, by more than 5%; more preferably, by more than 10%; and most preferably, by more than 25%. A decrease in the mortality rate of a population of treated subjects may be measured by any reproducible means. A decrease in the mortality rate of a population may be measured, for example, by calculating for a population the average number of disease-related deaths per unit time following initiation of treatment with an antibody. A decrease in the mortality rate of a population may also be measured, for example, by calculating for a population the average number of disease-related deaths per unit time following completion of a first round of treatment with an antibody.

[490] Treating cancer can result in a decrease in tumor growth rate. Preferably, after treatment, tumor growth rate is reduced by at least 5% relative to number prior to treatment; more

preferably, tumor growth rate is reduced by at least 10%; more preferably, reduced by at least 20%; more preferably, reduced by at least 30%; more preferably, reduced by at least 40%; more preferably, reduced by at least 50%; even more preferably, reduced by at least 50%, and most preferably, reduced by at least 75%. Tumor growth rate may be measured by any reproducible means of measurement. Tumor growth rate can be measured according to a change in tumor diameter per unit time.

[491] Treating cancer can result in a decrease in tumor regrowth. Preferably, after treatment, tumor regrowth is less than 5%; more preferably, tumor regrowth is less than 10%; more preferably, less than 20%; more preferably, less than 30%; more preferably, less than 40%; more preferably, less than 50%; even more preferably, less than 50%; and most preferably, less than 75%. Tumor regrowth may be measured by any reproducible means of measurement. Tumor regrowth is measured, for example, by measuring an increase in the diameter of a tumor after a prior tumor shrinkage that followed treatment. A decrease in tumor regrowth is indicated by failure of tumors to reoccur after treatment has stopped.

[492] Treating cancer can result in a reduction in the rate of cellular proliferation. Preferably, after treatment, the rate of cellular proliferation is reduced by at least 5%; more preferably, by at least 10%; more preferably, by at least 20%; more preferably, by at least 30%; more preferably, by at least 40%; more preferably, by at least 50%; even more preferably, by at least 50%; and most preferably, by at least 75%. The rate of cellular proliferation may be measured by any reproducible means of measurement. The rate of cellular proliferation is measured, for example, by measuring the number of dividing cells in a tissue sample per unit time.

[493] Treating cancer can result in a reduction in the proportion of proliferating cells. Preferably, after treatment, the proportion of proliferating cells is reduced by at least 5%; more preferably, by at least 10%; more preferably, by at least 20%; more preferably, by at least 30%; more preferably, by at least 40%; more preferably, by at least 50%; even more preferably, by at least 50%; and most preferably, by at least 75%. The proportion of proliferating cells may be measured by any reproducible means of measurement. Preferably, the proportion of proliferating cells is measured, for example, by quantifying the number of dividing cells relative to the number of nondividing cells in a tissue sample. The proportion of proliferating cells can be equivalent to the mitotic index.

[494] Treating cancer can result in a decrease in size of an area or zone of cellular proliferation. Preferably, after treatment, size of an area or zone of cellular proliferation is reduced by at least 5% relative to its size prior to treatment, more preferably, reduced by at least 10%; more preferably, reduced by at least 20%; more preferably, reduced by at least 30%; more preferably, reduced by at least 40%; more preferably, reduced by at least 50%; even more preferably, reduced by at least 50%; and most preferably, reduced by at least 75%. Size of an area or zone of cellular proliferation may be measured by any reproducible means of measurement. The size of an area or zone of cellular proliferation may be measured as a diameter or width of an area or zone of cellular proliferation. Treating cancer can result in a decrease in the number or proportion of cells having an abnormal appearance or morphology. Preferably, after treatment, the number of cells having an abnormal morphology is reduced by at least 5% relative to its size prior to treatment; more preferably, reduced by at least 10%, more preferably, reduced by at least 20%; more preferably, reduced by at least 30%; more preferably, reduced by at least 40%; more preferably, reduced by at least 50%; even more preferably, reduced by at least 50%; and most preferably, reduced by at least 75%. An abnormal cellular appearance or morphology may be measured by any reproducible means of measurement. An abnormal cellular morphology can be measured by microscopy, e.g., using an inverted tissue culture microscope. An abnormal cellular morphology can take the form of nuclear pleiomorphism.

[495] Treating cancer can result in cell death, and preferably, cell death results in a decrease of at least 10% in number of cells in a population. More preferably, cell death means a decrease of at least 20%; more preferably, a decrease of at least 30%; more preferably, a decrease of at least 40%; more preferably, a decrease of at least 50%; most preferably, a decrease of at least 75%. Number of cells in a population may be measured by any reproducible means. A number of cells in a population can be measured by fluorescence activated cell sorting (FACS), immunofluorescence microscopy and light microscopy. Methods of measuring cell death are as shown in Li et al., Proc Natl Acad Sci U S A. 100(5): 2674-8, 2003. In an aspect, cell death occurs by apoptosis.

[496] Monotherapies

[497] In the some embodiments of the disclosure, the antibodies and compositions of the disclosure are administered as monotherapies for the treatment of a disease.

[498] As used herein, "monotherapy" refers to the administration of a single active or therapeutic compound to a subject in need thereof. Preferably, monotherapy will involve administration of a therapeutically effective amount of an active compound. For example, cancer monotherapy with one of the antibodies of the present disclosure, or a pharmaceutical composition thereof, to a subject in need of treatment of cancer. Monotherapy may be contrasted with combination therapy, in which a combination of multiple active compounds is administered, preferably with each component of the combination present in a therapeutically effective amount. In one aspect, monotherapy with an antibody or pharmaceutical composition of the present disclosure is more effective than combination therapy in inducing a desired biological effect.

[499] An antibody according to the disclosure can also be used as an agent for detecting the presence of CLEC2D (or a protein or a protein fragment thereof) in a sample. Preferably, the antibody contains a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (e.g., F_{ab}, scFv, or $F_{(ab)2}$) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (i.e., physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently-labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently-labeled streptavidin. The term "biological sample" is intended to include tissues, cells and biological fluids isolated from a subject, as well as tissues, cells and fluids present within a subject. Included within the usage of the term "biological sample", therefore, is blood and a fraction or component of blood including blood serum, blood plasma, or lymph. That is, the detection method of the disclosure can be used to detect an analyte mRNA, protein, or genomic DNA in a biological sample *in vitro* as well as *in vivo*. For example, *in vitro* techniques for detection of an analyte mRNA includes Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of an analyte protein include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations, and immunofluorescence. *In vitro* techniques for detection of an analyte genomic DNA include Southern hybridizations. Procedures for conducting immunoassays are described, for example in "ELISA: Theory and Practice: Methods in Molecular Biology", Vol. 42, J. R. Crowther (Ed.)

Human Press, Totowa, NJ, 1995; "Immunoassay", E. Diamandis and T. Christopoulus, Academic Press, Inc., San Diego, CA, 1996; and "Practice and Theory of Enzyme Immunoassays", P. Tijssen, Elsevier Science Publishers, Amsterdam, 1985. Furthermore, *in vivo* techniques for detection of an analyte protein include introducing into a subject a labeled anti-analyte protein antibody. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

[500] Antibodies directed against a CLEC2D protein (or a fragment thereof) may be used in methods known within the art relating to the localization and/or quantitation of a CLEC2D protein *(*e.g., for use in measuring levels of the CLEC2D protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies specific to a CLEC2D protein, or derivative, fragment, analog or homolog thereof, that contain the antibody derived antigen binding domain, are utilized as pharmacologically active compounds (referred to hereinafter as "Therapeutics").

[501] An antibody specific for a CLEC2D protein of the disclosure can be used to isolate a CLEC2D polypeptide by standard techniques, such as immunoaffinity, chromatography or immunoprecipitation. Antibodies directed against a CLEC2D protein (or a fragment thereof) can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, e.g., to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (i.e., physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I, ^{131}I, ^{35}S or ^{3}H.

[502] Combination therapies

[503] In the some embodiments of the disclosure, the antibodies and compositions of the disclosure are administered as part of a combination therapy for the treatment of a disease.

[504] For example, anti-CLEC2D antibodies have been tested in xenograft studies alone and in combination with a check point monoclonal antibody (anti PDL1). The combinatorial treatment with anti-CLEC2D and anti-PDL1 had revealed significant tumor growth reduction. Therefore, Anti-CLEC2D antibody can be used in combination with other therapies for therapeutic purposes.

[505] These therapies include, but are not restricted to, T cell targeted immunomodulatory mechanisms, other immunomodulatory mechanisms, cancer vaccines, adoptive cell therapies, oncolytic viruses, additional antibody therapies including bispecific and other combinations of antibody fragments, radiotherapy, antibody drug conjugates, small interfering RNAs, chemotherapy, immunotherapy, immune checkpoint inhibitors, mitotic inhibitors or a combination thereof.

[506] Chemotherapies, small molecules and biologics that can be administered in combination with an anti-CLEC2D antibodies or compositions of the disclosure include, but are not restricted to hormonal therapies, PARP inhibitors, Androgen receptor inhibitors, tyrosine kinase inhibitors, Abiraterone acetate, Enzalutamide, Apalutamide, Darolutamide, Phosphoinositide 3 Kinase Beta-Selective Inhibitors, Radium 223 Dichloride and other variants, androgen receptor antagonist, CYP17A1 inhibitors, LHRH antagonist, LHRH analogs, Cyclophosphamide, cabazitaxel, Docetaxel, PULP vaccines like Sipuleucel-T , Prostvac, Provange, PSCA, whole cell vaccines and others, therapeutics against PULP surface antigens, Cisplatin, Bispecific antibody-CD3 and ADAM17, pTVG-HP Plasmid DNA Vaccine and other similar vaccines, Tisotumab Vedotin , DCVAC/ PCa, GX301, GVAX-PCa and Denosumab.

[507] Chemotherapeutic drugs and anti-cancer agents that can be administered in combination with an anti-CLEC2D antibodies or compositions of the disclosure include, but are not restricted to alkylating agents, antimetabolites, plant alkaloids, vinca alkaloids, mitotic inhibitors, antitumor antibiotics, platinum based anti-neoplastics, topoisomerase inhibitors and protein kinase inhibitors. Exemplary alkylating agents comprise busulfan, cyclophosphamide and temozolamide. Exemplary antimetabolites comprise5-fluorouracil (5-FU), 6-mercaptopurine (6-MP), Capecitabine (Xeloda) and Gemcitabine. Exemplary anti tumor antibiotics comprise Dactinomycin, Bleomycin, Daunorubicin and Doxorubicin. Exemplary platinum based anti-neoplastics comprise Cisplatin and Carboplatin. Exemplary topoisomerase inhibitors comprise Etoposide, Irinotecan and Topotecan. Exemplary mitotic inhibitors comprise taxanes (e.g.,

Paclitaxel, Docetaxel), vinca alkaloids (Vinblastine, Vincristine, Vinorelbine) and colchicine. Additional chemotherapeutic agents comprise methotrexate.

[508] Therapeutic agents that can be administered in combination with an anti-CLEC2D antibody or composition comprising the same of the disclosure include, but are not restricted to Orteronel, Geldanamycin, Cabozantinib, Alpharadin, 177Lu-J591, Mitoxantrone, Viamet, CFG920, Galeteron, Olaparib, ADXS-PSA, Taxotere, Gonax, Decapeptyl, Lupron, Vantas, Casodex, Zoladex, Eligard, Leuplin, Firmagon, mitoxantrone, Emcyt, lanreotide, Zaltrap, custirsen sodium and Sprycel.

[509] The Anti-CLEC2D antibodies of the disclosure can be used in combination with monoclonal antibodies or fragments thereof, therapeutic biologics, small molecules or chemical agents that inhibit or modulate the following targets: Cluster of Differentiation 19 (CD19), Programmed cell death protein 1 (PD1), Programmed death-ligand 1 (PDL1), human epidermal growth factor receptor 2 (Her2), Signal transducer and activator of transcription 3 (STAT3), cluster of differentiation 152 (CTLA4), New York esophageal squamous cell carcinoma 1 (NYESO1), B-cell maturation antigen (BCMA), indoleamine 2,3-dioxygenase (IDO), Neo antigens, Colony Stimulating Factor 1 Receptor (CSF1R), B-lymphocyte surface antigen B1 (CD20), Wilms tumor protein (WT1), Cluster of Differentiation 47 (CD47), Mucin 1, cell surface associated (MUC1), TNF receptor superfamily member 9 (4-1BB), disialoganglioside GD2, Adenosine A2a Receptor (ADORA2A), nterferon-alpha/beta receptor alpha chain (IFNAR1), Toll-like receptor 7 (TLR7), Cluster of differentiation 40 (CD40), Mesothelin, epidermal growth factor receptor (EGFR), Histone deacetylase 1 (HDAC1), interleukin-2 receptor (IL2R), Telomerase reverse transcriptase (TERT), Toll-like receptor (TLR), Siglec-3 (CD33), Lymphocyte-activation gene 3 (LAG3), Tumor necrosis factor receptor superfamily, member 4 (OX40), C-X-C chemokine receptor type 4 (CXCR4), Histone deacetylase 6 (HDAC6), prostate-specific membrane antigen (PSMA), Epstein–Barr virus (EBV), granulocyte-macrophage colony-stimulating factor receptor (GMCSFR), Toll-like receptor 9 (TLR9), interleukin-3 receptor (CD123), Stimulator of interferon genes (STING), T-cell immunoreceptor with Ig and ITIM domains (TIGIT), T-cell immunoglobulin and mucin-domain containing-3 (TIM3), Toll-like receptor 4 (TLR4), human papillomavirus gene E6 (HPV-E6), 5'-nucleotidase (CD73), Carcinoembryonic Antigen Related Cell Adhesion Molecule 5 (CEACAM5), Survivin, Cluster of differentiation 3 (CD3), cyclic ADP ribose hydrolase (CD38), glucocorticoid-induced

TNFR-related protein (GITR), human papillomavirus E7 oncoprotein (HPVE7), Interleukin 21 Receptor (IL21R), CD137), cluster of differentiation-22 (CD22), tumor necrosis factor receptor superfamily member 8 (CD30), Glypican-3 (GPC3), Beta Catenin, fms-like tyrosine kinase 3 (FLT3), janus kinase 2 (JAK2), Epithelial cell adhesion molecule (EPCAM), Melanoma-Associated Antigen 3 (MAGE-A3), Toll-like receptor 3 (TLR3), human papillomavirus (HPV), K-ras (KRAS), Receptor Tyrosine Kinase Like Orphan Receptor 1 (ROR1), Ubiquitin Specific Peptidase 7 (USP7), Trophoblast glycoprotein (5T4), Interleukin-2 receptor alpha chain (CD25), Cytomegalovirus (CMV), C-X-C Motif Chemokine Ligand 12 (CXCL12), granulocyte colony-stimulating factor receptor (GCSFR), killer cell lectin like receptor K1 (NKG2D), premelanosome protein (PMEL), Preferentially Expressed Antigen In Melanoma (PRAME), V-domain Ig suppressor of T cell activation (VISTA), C-C Motif Chemokine Receptor 4 (CCR4), cluster of differentiation 46 (CD46), Macrophage Stimulating Protein Receptor (CDw136), cyclooxygenase-2 (COX2), SLAM family member 7 (CS1), C-X-C Motif Chemokine Receptor 1 (CXCR1), epidermal growth factor receptor variant III (EGFRvIII), p96, glucocorticoid receptor (GR), Inducible T-cell costimulator (ICOS), Insulin-like growth factor 1 (IGF1), interleukin-5 receptor (IL5R), janus kinase 1 (JAK1), prostate specific antigen (PSA), Signal transducer and activator of transcription 5 (STAT5), Transforming Growth Factor Beta Receptor 2 (TGFBR2), Vascular endothelial growth factor (VEGF), Anaplastic lymphoma kinase (ALK), alpha-galactosidase A (Alpha-gal), Cluster of Differentiation 276 (B7-H3), C-C Motif Chemokine Receptor 1 (CCR1), C-C chemokine receptor type 2 (CCR2), CD27 molecule (CD27), ectonucleoside triphosphate diphosphohydrolase 1 (CD39), carcinoembryonic antigen (CEA), Gelactin -3, Interleukin 13 Receptor Subunit Alpha 2 (IL13RA2), Interleukin 6 (IL6), Interleukin 6 Receptor (IL6R), Interleukin 1 Receptor Associated Kinase 4 (IRAK4), MER Proto-Oncogene, Tyrosine Kinase (MERTK), Macrophage migration inhibitory factor (MIF), Protein melan-A (MLANA), Prostaglandin E Receptor 4 (PTGER4), distal-less homeobox 3 (TDO), transforming growth factor beta 1 (TGFB, TGFB1), toll like receptor 2 (TLR2), tumor necrosis factor (TNF), ADORA2B, alpha fetoprotein (AFP), angiopoietin 1 (ANG1), BTLA, prominin 1 (CD133), neural cell adhesion molecule 1 (CD56), CD70 molecule (CD70), carcinoembryonic antigen related cell adhesion molecule 6 (CEACAM6), C-type lectin domain family 12 member A (CLEC12A), C-X-C motif chemokine receptor 2 (CXCR2), fibroblast activation protein alpha (FAP), histone deacetylases (HDAC), interferon alpha and beta receptor

subunit 1 (IFNAR), interferon gamma receptor 1 (IFNGR1), interleukin 17 receptor A (IL17R), Janus kinase (JAK), mucin 16, cell surface associated (MUC16), mitogen activated protein kinase (P38), tumor protein p53 (p53), DExD/H-box helicase 68 (RIG1), RAR related orphan receptor C (RORC), signal regulatory protein alpha (SIRPA), transforming growth factor beta receptor 1 (TGFBR1), dopachrome tautomerase (TRP2), adenosine A3 receptor (ADORA3), Brachyury, C-C motif chemokine receptor 7 (CCR7), syndecan 1 (CD138), L1 cell adhesion molecule (CD171), fucosyltransferase 3 (Lewis blood group) (CD174), Fc fragment of IgG receptor IIa (CD32), C-X3-C motif chemokine receptor 1 (CX3CR1), FPHA2, folate receptor 1 (FOLR1), beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group) (GloboH), isocitrate dehydrogenase (NADP(+)) 1, cytosolic (IDH1), interleukin 2 receptor subunit beta (IL2rB), Janus kinase 3 (JAK3), prostate stem cell antigen (PSCA), RAS, transforming growth factor beta 2 (TGFB2), toll like receptor 8 (TLR8), acid phosphatase, prostate (ACPP), dipeptidyl peptidase 4 (ADABP), ADAM metallopeptidase domain 17 (ADAM17), androgen receptor (AR), ATRT, AXL receptor tyrosine kinase (AXL), V-set domain containing T cell activation inhibitor 1 (B7-H4), CA19-9, integrin subunit alpha M (CD11b), Fc fragment of IgG receptor IIIa (CD16), CD16a, CD200 molecule (CD200), CD28 molecule (CD28), CD52 molecule (CD52), CD7 molecule (CD7), CD80 molecule (CD80), complement C5a receptor 1 (CD88), cadherin 3 (CDH3), CECAM1, cytochrome c oxidase subunit II (COX2), CCCTC-binding factor like (CTCFL), C-X-C motif chemokine receptor 5 (CXCR5), atypical chemokine receptor 3 (CXCR7), E1a, Gastrin, Graves disease, susceptibility to, X-linked (GD3), Gelactin-1, colony stimulating factor 2 (GMCSF), HBV, HLA-A2, HLA-DR, human papillomavirus (HPV) E6/7, HPV L2, interferon alpha and beta receptor subunit 2 (IFNAR2), insulin like growth factor 1 receptor (IGF1R), interleukin 12 (IL12), interleukin 1 beta (IL1B), interleukin 7 receptor (IL7R), C-X-C motif chemokine ligand 8 (IL8), killer cell immunoglobulin like receptor, two Ig domains and long cytoplasmic tail 1 (KIR2DL1), killer cell immunoglobulin like receptor, two Ig domains and long cytoplasmic tail 3 (KIR2DL3), LXR, CD244 molecule (2B4), Mage family member A (MAGE-A), MAGE family member A1 (MAGE-A1), MAGE family member A4 (MAGE-A4), X-linked inhibitor of apoptosis (MiHA), killer cell lectin like receptor C1 (NKG2A), natural cytotoxicity triggering receptor 1 (NKp46), nuclear receptor subfamily 2 group F member 6 (NR2F6), PTTG1 interacting protein (PBF), sperm adhesion molecule 1 (SPAM1), signal transducer and activator of transcription 1 (STAT1), toll like receptor 5

(TLR5), peroxiredoxin 2 (TSA), tyrosine kinase 2 (TYK2), kinase insert domain receptor (VEGFR2), 5' Nucleotidase, ATP binding cassette subfamily B member 5 (ABCB5), ADAM metallopeptidase domain 9 (ADAM9), Adenosine, ADP, metadherin (AEG1), absent in melanoma 2 (AIM2), Alpha-lactalbumin, anti-Mullerian hormone receptor type 2 (AMHR2), angiopoietin 2 (ANG2), Angiogenesis, aspartate beta-hydroxylase (ASPH), natural killer cell cytotoxicity receptor 3 ligand 1 (B7-H6), TNF receptor superfamily member 13C (BAFF-R), poly(ADP-ribose) polymerase family member 9 (Bal1), BRCA1 associated RING domain 1 (BARD1), BCL2 apoptosis regulator (BCL2), POU class 2 associating factor 1 (BOB-1), BTE6-lX-8b, BTE6-X-15-7, KIT proto-oncogene, receptor tyrosine kinase (cKIT), carbonic anhydrase 9 (CA9), Carbohydrate antigens, cannabinoid receptor 2 (CB2), Cbl proto-oncogene B (CBLB), C-C motif chemokine ligand 20 (CCL20), C-C motif chemokine ligand 3 (CCL3), cyclin B1 (CCNB1), C-C motif chemokine receptor 9 (CCR9), alanyl aminopeptidase, membrane (CD13), interleukin 6 signal transducer (CD130), basigin (Ok blood group) (CD147), poliovirus receptor (CD155), CD160 molecule (CD160), selectin P ligand (CD162), CD200 receptor 1 (CD200R1), complement C3d receptor 2 (CD21), TNF receptor superfamily member 13B (CD267), integrin subunit beta 1 (CD29), CD3e molecule (CD3E), CD4 molecule (CD4), CD44 molecule (Indian blood group) (CD44), integrin subunit alpha V (CD51), intercellular adhesion molecule 1 (CD54), CD8a molecule (CD8), CGEN-XXXX, Claudin 18, Claudin 6, MET proto-oncogene, receptor tyrosine kinase (cMet), coproporphyrinogen oxidase (COX), prostaglandin-endoperoxide synthase 1 (COX-1), cytochrome c oxidase subunit I (COX-1), CPEG4, cereblon (CRBN), cytokine receptor like factor 2 (CRLF2), colony stimulating factor 1 (CSF1), phosphate cytidylyltransferase 1, choline, alpha (CTA), C-X-C motif chemokine ligand 1 (CXCL1), C-X-C motif chemokine receptor 3 (CXCR3), deoxycytidine kinase (DCK), dickkopf WNT signaling pathway inhibitor 1 (DKK1), delta like canonical Notch ligand 3 (DLL3), TNF receptor superfamily member 10b (DR5), EBNA3C, epidermal growth factor (EGF), C-type lectin domain containing 14A (EGFR5), eukaryotic translation initiation factor 2 alpha kinase 3 (EIF2AK3), ELVAL4, EPH receptor A3 (EPHA3), epidermal growth factor receptor pathway substrate 8 (EPS8), ERG, Fc fragment of IgM receptor (FAIM-3), fibroblast growth factor 2 (FGF2), fms related tyrosine kinase 3 (FLT3), fibronectin 1 (FN1), folate receptor 1 (FOLR), forkhead box M1 (FOXM1), follicle stimulating hormone receptor (FSHR), Galectin 3, N-acetylgalactosaminyltransferase (GalNAc), leucine rich repeat containing 32 (GARP), GC

vitamin D binding protein (GC), Gelactin 9, Gelactin1/3/9, GM2, gonadotropin releasing hormone receptor (GNRHR), glutamyl aminopeptidase (GP160), golgi membrane protein 1 (GP73), glycoprotein A33 (gpA33), H3.3K27M, DEAD-box helicase 43 (HAGE), histone deacetylase 2 (HDAC2), histone deacetylase 8 (HDAC8), Hemagglutinin, erb-b2 receptor tyrosine kinase 3 (HER3), hypoxia inducible lipid droplet associated (HILPDA), chondroitin sulfate proteoglycan 4 (HMWMAA), HP59, HPV16, HPV11, heat shock protein family H (Hsp110) member 1 (HSP105), heat shock protein family D (Hsp60) member 1 (HSP65), heat shock protein family A (Hsp70) member 4 (HSP70), TNF receptor superfamily member 14 (HVEM), Hyaluronan, indoleamine 2,3-dioxygenase 1(IDO1), interferon gamma (IFNG), interferon gamma receptor 1 (IFNGR), interferon gamma receptor 2 (IFNGR2), insulin like growth factor 2 (IGF2), insulin like growth factor binding protein 2(IGFBP2), IGK2, interleukin 10 (IL10), interleukin 10 receptor subunit alpha (IL10RA), interleukin 12 receptor subunit beta 1 (IL12RB1), interleukin (IL13), interleukin 13 receptor subunit alpha 2 (IL13R), interleukin 13 receptor subunit alpha 1 (IL13RA1), interleukin 15 (IL15), interleukin 15 receptor subunit alpha (IL15RA), interleukin 17A (IL17 IL17A), interleukin 17B (IL17B), interleukin 1 receptor type 1 (IL1R1), interleukin 1 receptor accessory protein (IL1R3), interleukin 21 receptor (IL21R), interleukin 27 receptor subunit alpha (IL27R), interleukin 2 receptor subunit alpha (IL2RA), IL35, interleukin 9 receptor (IL9R), Integrin beta 7, interleukin 1 receptor associated kinase 1 (IRAK1), integrin subunit beta 5 (ITGB5), Kappa Myeloma antigen, kinesin family member 20A (KIF20A), killer cell immunoglobulin like receptor, two Ig domains and long cytoplasmic tail 2 (KIR2DL2), Kynurenine, Lambda myeloma antigen, lysosomal associated membrane protein 3 (LAMP), LLO, nuclear receptor subfamily 1 group H member 3 (LXRA), nuclear receptor subfamily 1 group H member 2 (LXRB), MAGEA10 MAGE family member A10 (MAGE-A10), MAGEA6 MAGE family member A6 (MAGE-A6), MAGEC2 MAGE family member C2 (MAGE-C2), Mammaglobin A, mitogen-activated protein kinase (MAPK), Mas receptor, interferon induced with helicase C domain 1 (MDA5), MG7, major histocompatibility complex II (MHCII), MIC, MHC class I polypeptide-related sequence A (MICA), MHC class I polypeptide-related sequence (MICB), matrix metallopeptidase 11 (MMP-11), motile sperm domain containing 2 (MOSPD2), Multidrug resistance-associated protein-1 (MRP1), MRP3765, muGNTP01, major vault protein (MVP), MYB proto-oncogene, transcription factor (MYB), MYB proto-oncogene like 2 (MYBL2), Myeloblastin, MYCN proto-oncogene, bHLH

transcription factor (N-myc), nuclear factor of activated T cells (NFAT), NLR family pyrin domain containing 3 (NLRP3), Oncofetal antigen, purinergic receptor P2X 5 (P2RX5), p38 map kinase, phosphoinositide-3-kinase regulatory subunit 3 (P55), PAM4, regenerating family member 3 alpha (PAP), PAS domain containing repressor 1 (PASD1), protocadherin 18 (PCDH18), programmed cell death 1 ligand 2 (PDL2), POTE ankyrin domain family member D (POTE), protein phosphatase 5 catalytic subunit (PPT), prostaglandin E receptor 2 (PTGER2), PVR related immunoglobulin domain containing (PVRIG), RBL001, ras homolog family member C (RhoC), receptor tyrosine kinase like orphan receptor 2 (ROR2), SEREX, SIM bHLH transcription factor 2 (SIM2), somatostatin receptor 2 (SSTR2), SSX family member 2 (SSX2), sterol O-acyltransferase 1 (STAT), eukaryotic translation elongation factor 1 alpha 2 (STn), mRNA cap guanine-N7 methyltransferase (TAG72), TAMA, TASTD2, TD02, transcription factor Dp family member 3 (TFDP3), Thymidylate synthase, DNA topoisomerase I (TOP1), T cell receptor beta constant 1 (TRBC1), T cell receptor beta constant 2 (TRBC2), Tryptophan, thyroid stimulating hormone receptor (TSHR), TNF superfamily member 12 (TWEAK), Tyrosine, lymphocyte antigen 6 family member K (URLC10), retroelement silencing factor 1 (UTA2-1), fms related tyrosine kinase 1 (VEGFR1), V-set and immunoglobulin domain containing 4 (VSIG-4), X antigen family, member 1 (XAGE1), zona pellucida glycoprotein 3 (ZP3), STEAP family member 1 (STEAP1), or TNF superfamily member 11 (RANKL).

[510] In some embodiments, the anti-CLEC2D antibodies or compositions of the disclosure are administered in combination with an immune checkpoint inhibitor, include, but are not limited to CTLA4, PPP2CA, PPP2CB, PTPN6, PTPN22, PDCD1, ICOS (CD278), PDL1, KIR, LAG3, HAVCR2, BTLA, CD160, TIGIT, CD96, CRTAM, LAIR1, SIGLEC7, SIGLEC9, CD244 (2B4), TNFRSF10B, TNFRSF10A, CASP8, CASP10, CASP3, CASP6, CASP7, FADD, FAS, TGFBRII, TGFRBRI, SMAD2, SMAD3, SMAD4, SMAD10, SKI, SKIL, TGIF1, IL10RA, IL10RB, HMOX2, IL6R, IL6ST, EIF2AK4, CSK, PAG1, SIT1, FOXP3, PRDM1, BATF, VISTA, GUCY1A2, GUCY1A3, GUCY1B2, GUCY1B3, MT1, MT2, CD40, OX40, CD137, GITR, CD27, SHP-1, TIM-3, CEACAM-1, CEACAM-3, or CEACAM-5. In some embodiments, anti-CLEC2D antibodies or compositions of the disclosure are administered in combination with an immune checkpoint inhibitor. Exemplary immune checkpoint genes and therapeutic targets include programmed cell death 1 (PD1), PD-L1, CLTA-4, T cell immunoglobulin and mucin 3 (TIM-3) and lymphocyte activating 3 (LAG-3). In some

embodiments, the immune checkpoint inhibitor is a therapeutic antibody that binds to and inhibits PD1, PD-L1 (Programmed death-ligand 1), CLTA-4 or TIM3. Exemplary PD1 inhibitors comprise Pembrolizumab, Nivolumab and Cemiplimab. Exemplary PD-L1 inhibitors comprise Atezolizumab, Avelumab and Durvalumab. Exemplary CLTA-4 inhibitors comprise Ipilimumab.

[511] In some embodiments, the anti-CLEC2D antibodies or compositions of the disclosure are administered in combination with a kinase inhibitor, wherein the kinase inhibitor inhibits BCR-Abl, B-raf, BTK, CDK family, c-Met, EGFR family, JAK family, MEK ½, PDGFR alpha/beta, RET, Src family, or VEGFR family kinases. In some embodiments, the kinase inhibitor as disclosed herein, is a small kinase molecule inhibitor. In some embodiments, the the kinase inhibitor as disclosed herein, is a therapeutic antibody or an antagonistic antibody. In some embodiments, the kinase inhibitor as disclosed herein, is a Crizotinib, Ceritinib, Alectinib, Brigatinib, Bosutinib, Dasatinib, Imatinib, Nilotinib, Ponatinib, Vemurafenib, Dabrafenib, Ibrutinib, Palbociclib, Sorafenib, Ribociclib, Crizotinib, Cabozantinib, Gefitinib, Erlotinib, Lapatinib, Vandetanib, Afatinib, Osimertinib, Ruxolitinib, Tofacitinib, Trametinib, Axitinib, Gefitinib, Imatinib, Lenvatinib, Nintedanib, Pazopanib, Regorafenib, Sorafenib, Sunitinib, Vandetanib, Bosutinib, Dasatinib, Ponatinib, Vandetanib, Axitinib, Lenvatinib, Nintedanib, Regorafenib, Pazopanib, Sorafenib, Sunitinib, or a combination thereof.

[512] In some embodiments, the anti-CLEC2D antibodies or compositions of the disclosure are administered in combination with an anti-CD20 antibody. In some embodiments, the anti-CLEC2D antibodies or compositions of the disclosure are administered in combination with an anti-CD20 antibody, a TNF-receptor antagonist, an anti-TNF-α, or a combination thereof, e.g., for treatment of rheumatoid arthritis. In some embodiments, the anti-CLEC2D antibodies or compositions of the disclosure are administered in combination with anti-CD11a, e.g., for treatment of psoriais, In some embodiments, the anti-CLEC2D antibodies or compositions of the disclosure are administered in combination with IFN-γ, e.g., for treatment of multiple sclerosis. In some embodiments, the anti-CLEC2D antibodies or compositions of the disclosure are administered in combination with TNF-α, e.g., for treatment of ulcerative colitis. In some embodiments, the anti-CLEC2D antibodies or compositions of the disclosure are administered in combination with Infliximab or Natalizumab, e.g., for treatment of Crohn's disease.

[513] In some embodiments, the anti-CLEC2D antibodies or compositions of the disclosure are administered in combination with a multispecific antibody directed against any combination of

immune check points gene product and/or target antigens associated with cancer. In some embodiments, the anti-CLEC2D antibodies or compositions of the disclosure are administered in combination with a bispecific antibody directed against any combination of immune check points gene product and/or target antigens associated with cancer.

[514] In some embodiments, the anti-CLEC2D antibodies or compositions of the disclosure are administered in combination with a bispecific antibody directed against an immune check point protein selected from the group consisting of include programmed cell death 1 (PD1), PD-L1, CLTA-4, T cell immunoglobulin and mucin 3 (TIM-3) and lymphocyte activating 3 (LAG-3). In some embodiments, the immune checkpoint inhibitor is a therapeutic antibody that binds to and inhibits PD1, PD-L1 (Programmed death-ligand 1), CLTA-4 or TIM3.

[515] In some embodiments, the anti-CLEC2D antibodies or compositions of the disclosure are administered in combination with a bispecific antibody directed against a tumor antigen selected from the group consisting of: B cell maturation antigen (BCMA); PSA (prostate-specific antigen); prostatespecific membrane antigen (PSMA); PSCA (Prostate stem cell antigen); Tyrosine-protein kinase transmembrane receptor ROR1; fibroblast activation protein (FAP); Tumor-associated glycoprotein 72 (TAG72); Carcinoembryonic antigen (CEA); Epithelial cell adhesion molecule (EPCAM); Mesothelin; Human Epidermal growth factor Receptor 2 (ERBB2 (Her2/neu)); Prostase; Prostatic acid phosphatase (PAP); elongation factor 2 mutant (ELF2M); Insulin-like growth factor 1 receptor (IGF-1R); gplOO; BCR-ABL (breakpoint cluster region-Abelson); tyrosinase; New York esophageal squamous cell carcinoma 1 (NY-ESO-1); k-light chain, LAGE (L antigen); MAGE (melanoma antigen); Melanoma-associated antigen 1 (MAGE-A1); MAGE A3; MAGE A6; legumain; Human papillomavirus (HPV) E6; HPVE7; prostein; survivin; PCTA1 (Galectin 8); Melan-A/MART-1; Ras mutant; TRP-1 (tyrosinase related protein 1, or gp75); Tyrosinase-related Protein 2 (TRP2); TRP-2/INT2 (TRP-2/intron 2); RAGE (renal antigen); receptor for advanced glycation end products 1 (RAGEl); Renal ubiquitous 1, 2 (RU1, RU2); intestinal carboxyl esterase (iCE); Heat shock protein 70-2 (HSP70-2) mutant; thyroid stimulating hormone receptor (TSHR); CD123; CD171; CD19; CD20; CD22; CD26; CD30; CD33; CD44v7/8 (cluster of differentiation 44, exons 7/8); CD53; CD92; CD100; CD148; CD150; CD200; CD261; CD262; CD362; CS-1 (CD2 subset 1, CRACC, SLAMF7, CD319, and 19A24); C-type lectin-like molecule-1 (CLL-1); ganglioside GD3 (aNeu5Ac(2-8)aNeu5Ac(2-3)bDGalp(l-4)bDGlcp(ll)Cer); Tn antigen (Tn Ag); Fms-Like Tyrosine Kinase 3 (FLT3); CD38;

CD138; CD44v6; B7H3 (CD276); KIT (CD1 17); Interleukin-13 receptor subunit alpha-2 (IL-13Ra2); Interleukin 11 receptor alpha (IL-l lRa); prostate stem cell antigen (PSCA); Protease Serine 2 1 (PRSS21); vascular endothelial growth factor receptor 2 (VEGFR2); Lewis(Y) antigen; CD24; Platelet derived growth factor receptor beta (PDGFR-beta); stage-specific embryonic antigen-4 (SSEA-4); Mucin 1, cell surface associated (MUCl); mucin 16 (MUCl 6); epidermal growth factor receptor (EGFR); epidermal growth factor receptor variant III (EGFRvIII); neural cell adhesion molecule (NCAM); carbonic anhydrase IX (CAIX); Proteasome (Prosome, Macropain) Subunit, Beta Type, 9 (LMP2); ephrin type-A receptor 2 (EphA2); Ephrin B2; Fucosyl GM1; sialyl Lewis adhesion molecule (sLe); ganglioside GM3 (aNeu5Ac(2-3)bDGalp(l-4)bDGlcp(l-l)Cer); TGS5; high molecular weight-melanoma-associated antigen (HMWMAA); o-acetyl-GD2 ganglioside (OAcGD2); Folate receptor alpha; Folate receptor beta; tumor endothelial marker 1 (TEM1/CD248); tumor endothelial marker 7-related (TEM7R); claudin 6 (CLDN6); G protein coupled receptor class C group 5, member D (GPRC5D); chromosome X open reading frame 6 1 (CXORF61); CD97; CD179a; anaplastic lymphoma kinase (ALK); Poly sialic acid; placenta specific1 (PLAC1); hexasaccharide portion of globoH glycoceramide (GloboH); mammary gland differentiation antigen (NY-BR-1); uroplakin 2 (UPK2); Hepatitis A virus cellular receptor 1 (HAVCR1); adrenoceptor beta 3 (ADRB3); pannexin 3 (PANX3); G protein-coupled receptor 20 (GPR20); lymphocyte antigen 6 complex, locus K 9 (LY6K); Olfactory receptor 51E2 (OR51E2);TCR Gamma Alternate Reading Frame Protein (TARP); Wilms tumor protein (WT1); ETS translocation-variant gene 6, located on chromosome 12p (ETV6-AML); sperm protein 17 (SPA17); X Antigen Family, Member 1A (XAGE1); angiopoietin-binding cell surface receptor 2 (Tie 2); CT (cancer/testis (antigen)); melanoma cancer testis antigen-1 (MAD-CT-1); melanoma cancer testis antigen-2 (MAD-CT-2); Fos-related antigen 1; p53; p53 mutant; human Telomerase reverse transcriptase (hTERT); sarcoma translocation breakpoints; melanoma inhibitor of apoptosis (ML-IAP); ERG (transmembrane protease, serine 2 (TMPRSS2) ETS fusion gene); NAcetyl glucosaminyl-transferase V (NA17); paired box protein Pax-3 (PAX3); Androgen receptor; Cyclin Bl; Cyclin Dl; v-myc avian myelocytomatosis viral oncogene neuroblastoma derived homolog (MYCN); Ras Homolog Family Member C (RhoC); Cytochrome P450 1B1 (CYP1B1); CCCTC-Binding Factor (Zinc Finger Protein)-Like (BORIS); Squamous Cell Carcinoma Antigen Recognized By T Cells-1 or 3 (SARTl, SART3); Paired box protein Pax-5 (PAX5); proacrosin binding protein

sp32 (OY-TES1); lymphocyte-specific protein tyrosine kinase (LCK); A kinase anchor protein 4 (AKAP-4); synovial sarcoma, X breakpoint- 1, -2, -3 or -4 (SSX1, SSX2, SSX3, SSX4); CD79a; CD79b; CD72; Leukocyte-associated immunoglobulin-like receptor 1 (LAIR1); Fc fragment of IgA receptor (FCAR); Leukocyte immunoglobulin-like receptor subfamily A member 2 (LILRA2); CD300 molecule-like family member f (CD300LF); C-type lectin domain family 12 member A (CLEC12A); bone marrow stromal cell antigen 2 (BST2); EGF-like module containing mucin-like hormone receptor-like 2 (EMR2); lymphocyte antigen 75 (LY75); Glypican-3 (GPC3); Fc receptor-like 5 (FCRL5); mouse double minute 2 homolog (MDM2); livin; alphafetoprotein (AFP); transmembrane activator and CAML Interactor (TACI); B-cell activating factor receptor (BAFF-R); V-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog (KRAS); immunoglobulin lambda-like polypeptide 1 (IGLL1); 707-AP (707 alanine proline); ART-4 (adenocarcinoma antigen recognized by T4 cells); BAGE (B antigen; b-catenin/m, bcatenin/mutated); CAMEL (CTL-recognized antigen on melanoma); CAPl (carcinoembryonic antigen peptide 1); CASP-8 (caspase-8); CDC27m (cell-division cycle 27 mutated); CDK4/m (cycline-dependent kinase 4 mutated); Cyp-B (cyclophilin B); DAM (differentiation antigen melanoma); EGP-2 (epithelial glycoprotein 2); EGP-40 (epithelial glycoprotein 40); Erbb 2, 3, 4 (erythroblastic leukemia viral oncogene homolog-2, -3, 4); FBP (folate binding protein); , fAchR (Fetal acetylcholine receptor); G250 (glycoprotein 250); GAGE (G antigen); GnT-V (Nacetylglucosaminyltransferase V); HAGE (helicose antigen); ULA-A (human leukocyte antigen-A); HST2 (human signet ring tumor 2); KIAA0205; KDR (kinase insert domain receptor); LDLR/FUT (low density lipid receptor/GDP L-fucose: b-D-galactosidase 2-a-L fucosyltransferase); LICAM (LI cell adhesion molecule); MC1R (melanocortin 1 receptor); Myosin/m (myosin mutated); MUM-1, -2, -3 (melanoma ubiquitous mutated 1, 2, 3); NA88-A (NA cDNA clone of patient M88); KG2D (Natural killer group 2, member D) ligands; oncofeta antigen (h5T4); pi 90 minor bcr-abl (protein of 190KD bcr-abl); Pml/RARa (promyelocytic leukaemia/retinoic acid receptor a); PRAME (preferentially expressed antigen of melanoma); SAGE (sarcoma antigen); TEL/AMLl (translocation Ets-family leukemia/acute myeloid leukemia 1); TPI/m (triosephosphate isomerase mutated); CD70; and any combination thereof.

[516] In some embodiments, the anti-CLEC2D antibodies or compositions of the disclosure are administered in combination with a drug or therapeutic agent including but not limited to Mycophenolate, Azathioprine, Cyclophosphamide, Pirfenidone, Nintedanib, Lansoprazole

(Prevacid 24HR), Omeprazole (Prilosec OTC) and Pantoprazole (protonix), or a combination thereof.

[517] In some embodiments, the anti-CLEC2D antibodies or compositions of the disclosure are administered in combination with a cytokine or chemokine including but not limited to interferon-γ (IFN-γ), tumor necrosis factor-α (TNF-α), granulocyte macrophage colony-stimulating factor (GM-CSF), IL-8, vascular endothelial growth factor (VEGF), stromal cell-derived factor-1, and interferon gamma-inducible protein-10 (IP-10), chemokines (CCL1, CCL2, CCL3, CCL4, CCL5, and CXCL8) or a combination thereof.

[518] In some embodiments, anti-CLEC2D antibodies or compositions of the disclosure are administered in combination with an adoptive cell therapy. In some embodiments, the adoptive cell therapy is autologous. In some embodiments, the adoptive cell therapy is allogenic. In some embodiments, the adoptive cell therapy comprises an immune cell such as a T cell or an NK cell. In some embodiments, the adoptive cell therapy comprises a chimeric antigen receptor T cell (CAR-T) or CAR-NK therapy.

[519] In some embodiments, the CLEC2D antibodies or compositions of the disclosure are administered in combination with adoptive cell therapy comprising a chimeric antigen receptor T cell (CAR-T) directed against target antigens associated with a solid tumor.

[520] In some embodiments, the CLEC2D antibodies or compositions of the disclosure are administered in combination with adoptive cell therapy comprising a chimeric antigen receptor T cell (CAR-T) directed against target antigens associated with cancer, including but not limited to acute lymphoblastic leukemia, diffuse large b-cell lymphoma, follicular lymphoma, chronic lymphocytic leukemia, multiple myeloma, and others.

[521] In some embodiments, the CLEC2D antibodies or compositions of the disclosure are administered in combination with adoptive cell therapy comprising a chimeric antigen receptor T cell (CAR-T) directed against a second antigen is a tumor antigen selected from the group consisting of: B cell maturation antigen (BCMA); PSA (prostate-specific antigen); prostatespecific membrane antigen (PSMA); PSCA (Prostate stem cell antigen); Tyrosine-protein kinase transmembrane receptor ROR1; fibroblast activation protein (FAP); Tumor-associated glycoprotein 72 (TAG72); Carcinoembryonic antigen (CEA); Epithelial cell adhesion molecule (EPCAM); Mesothelin; Human Epidermal growth factor Receptor 2 (ERBB2 (Her2/neu)); Prostase; Prostatic acid phosphatase (PAP); elongation factor 2 mutant (ELF2M);

Insulin-like growth factor 1 receptor (IGF-1R); gplOO; BCR-ABL (breakpoint cluster region-Abelson); tyrosinase; New York esophageal squamous cell carcinoma 1 (NY-ESO-1); k-light chain, LAGE (L antigen); MAGE (melanoma antigen); Melanoma-associated antigen 1 (MAGE-A1); MAGE A3; MAGE A6; legumain; Human papillomavirus (HPV) E6; HPVE7; prostein; survivin; PCTA1 (Galectin 8); Melan-A/MART-1; Ras mutant; TRP-1 (tyrosinase related protein 1, or gp75); Tyrosinase-related Protein 2 (TRP2); TRP-2/INT2 (TRP-2/intron 2); RAGE (renal antigen); receptor for advanced glycation end products 1 (RAGEl); Renal ubiquitous 1, 2 (RU1, RU2); intestinal carboxyl esterase (iCE); Heat shock protein 70-2 (HSP70-2) mutant; thyroid stimulating hormone receptor (TSHR); CD123; CD171; CD19; CD20; CD22; CD26; CD30; CD33; CD44v7/8 (cluster of differentiation 44, exons 7/8); CD53; CD92; CD100; CD148; CD150; CD200; CD261; CD262; CD362; CS-1 (CD2 subset 1, CRACC, SLAMF7, CD319, and 19A24); C-type lectin-like molecule-1 (CLL-1); ganglioside GD3 (aNeu5Ac(2-8)aNeu5Ac(2-3)bDGalp(l-4)bDGlcp(ll)Cer); Tn antigen (Tn Ag); Fms-Like Tyrosine Kinase 3 (FLT3); CD38; CD138; CD44v6; B7H3 (CD276); KIT (CD1 17); Interleukin-13 receptor subunit alpha-2 (IL-13Ra2); Interleukin 11 receptor alpha (IL-l lRa); prostate stem cell antigen (PSCA); Protease Serine 2 1 (PRSS21); vascular endothelial growth factor receptor 2 (VEGFR2); Lewis(Y) antigen; CD24; Platelet derived growth factor receptor beta (PDGFR-beta); stage-specific embryonic antigen-4 (SSEA-4); Mucin 1, cell surface associated (MUCl); mucin 16 (MUCl 6); epidermal growth factor receptor (EGFR); epidermal growth factor receptor variant III (EGFRvIII); neural cell adhesion molecule (NCAM); carbonic anhydrase IX (CAIX); Proteasome (Prosome, Macropain) Subunit, Beta Type, 9 (LMP2); ephrin type-A receptor 2 (EphA2); Ephrin B2; Fucosyl GM1; sialyl Lewis adhesion molecule (sLe); ganglioside GM3 (aNeu5Ac(2-3)bDGalp(l-4)bDGlcp(l-l)Cer); TGS5; high molecular weight-melanoma-associated antigen (HMWMAA); o-acetyl-GD2 ganglioside (OAcGD2); Folate receptor alpha; Folate receptor beta; tumor endothelial marker 1 (TEM1/CD248); tumor endothelial marker 7-related (TEM7R); claudin 6 (CLDN6); G protein coupled receptor class C group 5, member D (GPRC5D); chromosome X open reading frame 6 1 (CXORF61); CD97; CD179a; anaplastic lymphoma kinase (ALK); Poly sialic acid; placenta specific1 (PLAC1); hexasaccharide portion of globoH glycoceramide (GloboH); mammary gland differentiation antigen (NY-BR-1); uroplakin 2 (UPK2); Hepatitis A virus cellular receptor 1 (HAVCR1); adrenoceptor beta 3 (ADRB3); pannexin 3 (PANX3); G protein-coupled receptor 20 (GPR20); lymphocyte antigen 6

complex, locus K 9 (LY6K); Olfactory receptor 51E2 (OR51E2);TCR Gamma Alternate Reading Frame Protein (TARP); Wilms tumor protein (WT1); ETS translocation-variant gene 6, located on chromosome 12p (ETV6-AML); sperm protein 17 (SPA17); X Antigen Family, Member 1A (XAGE1); angiopoietin-binding cell surface receptor 2 (Tie 2); CT (cancer/testis (antigen)); melanoma cancer testis antigen-1 (MAD-CT-1); melanoma cancer testis antigen-2 (MAD-CT-2); Fos-related antigen 1; p53; p53 mutant; human Telomerase reverse transcriptase (hTERT); sarcoma translocation breakpoints; melanoma inhibitor of apoptosis (ML-IAP); ERG (transmembrane protease, serine 2 (TMPRSS2) ETS fusion gene); NAcetyl glucosaminyl-transferase V (NA17); paired box protein Pax-3 (PAX3); Androgen receptor; Cyclin Bl; Cyclin Dl; v-myc avian myelocytomatosis viral oncogene neuroblastoma derived homolog (MYCN); Ras Homolog Family Member C (RhoC); Cytochrome P450 1B1 (CYP1B1); CCCTC-Binding Factor (Zinc Finger Protein)-Like (BORIS); Squamous Cell Carcinoma Antigen Recognized By T Cells-1 or 3 (SARTl, SART3); Paired box protein Pax-5 (PAX5); proacrosin binding protein sp32 (OY-TES1); lymphocyte-specific protein tyrosine kinase (LCK); A kinase anchor protein 4 (AKAP-4); synovial sarcoma, X breakpoint- 1, -2, -3 or -4 (SSX1, SSX2, SSX3, SSX4); CD79a; CD79b; CD72; Leukocyte-associated immunoglobulin-like receptor 1 (LAIR1); Fc fragment of IgA receptor (FCAR); Leukocyte immunoglobulin-like receptor subfamily A member 2 (LILRA2); CD300 molecule-like family member f (CD300LF); C-type lectin domain family 12 member A (CLEC12A); bone marrow stromal cell antigen 2 (BST2); EGF-like module containing mucin-like hormone receptor-like 2 (EMR2); lymphocyte antigen 75 (LY75); Glypican-3 (GPC3); Fc receptor-like 5 (FCRL5); mouse double minute 2 homolog (MDM2); livin; alphafetoprotein (AFP); transmembrane activator and CAML Interactor (TACI); B-cell activating factor receptor (BAFF-R); V-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog (KRAS); immunoglobulin lambda-like polypeptide 1 (IGLL1); 707-AP (707 alanine proline); ART-4 (adenocarcinoma antigen recognized by T4 cells); BAGE (B antigen; b-catenin/m, bcatenin/mutated); CAMEL (CTL-recognized antigen on melanoma); CAPl (carcinoembryonic antigen peptide 1); CASP-8 (caspase-8); CDC27m (cell-division cycle 27 mutated); CDK4/m (cycline-dependent kinase 4 mutated); Cyp-B (cyclophilin B); DAM (differentiation antigen melanoma); EGP-2 (epithelial glycoprotein 2); EGP-40 (epithelial glycoprotein 40); Erbb 2, 3, 4 (erythroblastic leukemia viral oncogene homolog-2, -3, 4); FBP (folate binding protein); , fAchR (Fetal acetylcholine receptor); G250 (glycoprotein 250); GAGE (G antigen); GnT-V

(Nacetylglucosaminyltransferase V); HAGE (helicose antigen); ULA-A (human leukocyte antigen-A); HST2 (human signet ring tumor 2); KIAA0205; KDR (kinase insert domain receptor); LDLR/FUT (low density lipid receptor/GDP L-fucose: b-D-galactosidase 2-a-L fucosyltransferase); LICAM (LI cell adhesion molecule); MC1R (melanocortin 1 receptor); Myosin/m (myosin mutated); MUM-1, -2, -3 (melanoma ubiquitous mutated 1, 2, 3); NA88-A (NA cDNA clone of patient M88); KG2D (Natural killer group 2, member D) ligands; oncofeta antigen (h5T4); pi 90 minor bcr-abl (protein of 190KD bcr-abl); Pml/RARa (promyelocytic leukaemia/retinoic acid receptor a); PRAME (preferentially expressed antigen of melanoma); SAGE (sarcoma antigen); TEL/AMLl (translocation Ets-family leukemia/acute myeloid leukemia 1); TPI/m (triosephosphate isomerase mutated); CD70; and any combination thereof.

[522] An anti-CLEC2D antibodies of the disclosure may be utilized to form a bispecific antibody, wherein the bispecific antibody specifically binds to CLEC2D and a second antigen, wherein the second antigen is an immune checkpoint inhibitor including but not limited to CTLA4, PPP2CA, PPP2CB, PTPN6, PTPN22, PDCD1, ICOS (CD278), PDL1, KIR, LAG3, HAVCR2, BTLA, CD160, TIGIT, CD96, CRTAM, LAIR1, SIGLEC7, SIGLEC9, CD244 (2B4), TNFRSF10B, TNFRSF10A, CASP8, CASP10, CASP3, CASP6, CASP7, FADD, FAS, TGFBRII, TGFRBRI, SMAD2, SMAD3, SMAD4, SMAD10, SKI, SKIL, TGIF1, IL10RA, IL10RB, HMOX2, IL6R, IL6ST, EIF2AK4, CSK, PAG1, SIT1, FOXP3, PRDM1, BATF, VISTA, GUCY1A2, GUCY1A3, GUCY1B2, GUCY1B3, MT1, MT2, CD40, OX40, CD137, GITR, CD27, SHP-1, TIM-3, CEACAM-1, CEACAM-3, or CEACAM-5. In some embodiments, an anti-CLEC2D antibodies of the disclosure, is a bispecific antibody, wherein the bispecific antibody specifically binds to CLEC2D and a second antigen, wherein the second antigen is an immune checkpoint gene and therapeutic target including but not limited to programmed cell death 1 (PD1), PD-L1, CLTA-4, T cell immunoglobulin and mucin 3 (TIM-3) and lymphocyte activating 3 (LAG-3). In some embodiments, an anti-CLEC2D antibodies of the disclosure, is a bispecific antibody, wherein the bispecific antibody specifically binds to CLEC2D and a second antigen, wherein the second antigen is associated with a cytokine or chemokine including but not limited to interferon-γ (IFN-γ), tumor necrosis factor-α (TNF-α), granulocyte macrophage colony-stimulating factor (GM-CSF), IL-8, vascular endothelial growth factor (VEGF), stromal cell-derived factor-1, and interferon gamma-inducible protein-10 (IP-10), chemokines (CCL1, CCL2, CCL3, CCL4, CCL5, and CXCL8) or a combination thereof.

[523] In some embodiments, an anti-CLEC2D antibodies of the disclosure, is a bispecific antibody, wherein the bispecific antibody specifically binds to CLEC2D and a second antigen on the surface of a host cell. In some embodiments, an anti-CLEC2D antibodies of the disclosure, is a bispecific antibody, wherein the bispecific antibody comprises a first pair of variable light chain and variable heavy chain that specifically binds CLEC2D and a second pair of variable light chain and variable heavy chain that specifically binds to a second antigen on the surface of a host cell. In some embodiments, an anti-CLEC2D antibodies of the disclosure, is a bispecific antibody, wherein the bispecific antibody specifically binds to CLEC2D and a second antigen on the surface of a host cell, wherein the second antigen is an antigen associated with a cancer or tumor cell.

[524] A bispecific antibody, as disclosed herein, may comprise constant regions representing specific isotypes e.g., human IgG1, IgG2, IgG3 and IgG4 or variants thereof, as described in this disclosure. A bispecific antibody, as disclosed herein, may comprise constant regions representing specific isotypes e.g., mouse IgG1, IgG2a, IgG2b or IgG3 or variants thereof, as described in this disclosure. A bispecific antibody, as disclosed herein, may having isotype backbones of IgG1, IgG1N297A and IgG4. A bispecific antibody, as disclosed herein, can be bispecific antibody formats using tri-functional antibody, chemically linked Fab, scFvs or disulfide bonded Fvs include tandem scFvs (often used as bispecific T cell engagers or 'BiTEs'), tetravalent IgG-scFvs, diabodies, and many other formats. In some embodiments, a bispecific antibody, as disclosed herein, is produced as a diabody which are generated by combining sequences encoding two different scFvs into one construct in which heavy chains are expressed in a single polypeptide, and then joined with the corresponding light chains.

[525] In some embodiments, an anti-CLEC2D antibodies of the disclosure, is a bispecific antibody,wherein the bispecific antibody specifically binds to CLEC2D and a second antigen on the surface of a host cell, wherein the second antigen is an antigen associated with a cancer, including but not limited to breast cancer, prostate cancer, endometrial cancer, bladder cancer, kidney cancer, esophageal cancer, squamous cell carcinoma, uveal melanoma, follicular lymphoma, renal cell carcinoma, cendcal cancer, ovarian cancer, lung cancer, colorectal cancer, brain cancer, pancreatic cancer, head and neck cancer, liver cancer, leukemia, lymphoma, Hodgkin's disease, multiple myeloma, melanoma, astrocytoma, stomach cancer, pulmonary adenocarcinoma, adenocarcinoma, acinic cell adenocarcinoma, adrenal cortical carcinomas,

alveoli cell carcinoma, anaplastic carcinoma, basaloid carcinoma, basal cell carcinoma, bronchiolar carcinoma, bronchogenic carcinoma, renaladinol carcinoma, embryonal carcinoma, anometroid carcinoma, fibrolamolar liver cell carcinoma, follicular carcinomas, giant cell carcinomas, hepatocellular carcinoma, intraepidermal carcinoma, intraepithelial carcinoma, leptomanigio carcinoma, medullary carcinoma, melanotic carcinoma, menigual carcinoma, mesometonephric carcinoma, oat cell carcinoma, squamal cell carcinoma, sweat gland carcinoma, transitional cell carcinoma, tubular cell carcinoma, ameloblastic sarcoma, angiolithic sarcoma, botryoid sarcoma, endometrial stroma sarcoma, ewing sarcoma, fascicular sarcoma, giant cell sarcoma, granulositic sarcoma, immunoblastic sarcoma, juxaccordial osteogenic sarcoma, coppices sarcoma, leukocytic sarcoma (leukemia), lymphatic sarcoma (lympho sarcoma), medullary sarcoma, myeloid sarcoma (granulocitic sarcoma), austiogenci sarcoma, periosteal sarcoma, reticulum cell sarcoma (histiocytic lymphoma), round cell sarcoma, spindle cell sarcoma, synovial sarcoma, telangiectatic audiogenic sarcoma, Burkitt's lymphoma, NPDL, NML, NH and diffuse lymphomas.

[526] In some embodiments, an anti-CLEC2D antibodies of the disclosure, is a bispecific antibody,wherein the bispecific antibody specifically binds to CLEC2D and a second antigen on the surface of a host cell, wherein the second antigen is an antigen associated with a cancer or tumor cell selected from the group consisting of breast cancer, prostate cancer, endometrial cancer, bladder cancer, kidney cancer, esophageal cancer, squamous cell carcinoma, uveal melanoma, follicular lymphoma, renal cell carcinoma, cendcal cancer, ovarian cancer, lung cancer, colorectal cancer, brain cancer, pancreatic cancer, head and neck cancer, liver cancer, leukemia, lymphoma, Hodgkin's disease, multiple myeloma, melanoma, astrocytoma, stomach cancer, and pulmonary adenocarcinoma. In some embodiments, an anti-CLEC2D antibodies of the disclosure, is a bispecific antibody,wherein the bispecific antibody specifically binds to CLEC2D and a second antigen on the surface of a host cell, wherein the second antigen is a tumor antigen selected from the group consisting of: B cell maturation antigen (BCMA); PSA (prostate-specific antigen); prostatespecific membrane antigen (PSMA); PSCA (Prostate stem cell antigen); Tyrosine-protein kinase transmembrane receptor ROR1; fibroblast activation protein (FAP); Tumor-associated glycoprotein 72 (TAG72); Carcinoembryonic antigen (CEA); Epithelial cell adhesion molecule (EPCAM); Mesothelin; Human Epidermal growth factor Receptor 2 (ERBB2 (Her2/neu)); Prostase; Prostatic acid phosphatase (PAP); elongation factor 2

mutant (ELF2M); Insulin-like growth factor 1 receptor (IGF-1R); gplOO; BCR-ABL (breakpoint cluster region-Abelson); tyrosinase; New York esophageal squamous cell carcinoma 1 (NY-ESO-1); k-light chain, LAGE (L antigen); MAGE (melanoma antigen); Melanoma-associated antigen 1 (MAGE-A1); MAGE A3; MAGE A6; legumain; Human papillomavirus (HPV) E6; HPVE7; prostein; survivin; PCTA1 (Galectin 8); Melan-A/MART-1; Ras mutant; TRP-1 (tyrosinase related protein 1, or gp75); Tyrosinase-related Protein 2 (TRP2); TRP-2/INT2 (TRP-2/intron 2); RAGE (renal antigen); receptor for advanced glycation end products 1 (RAGEl); Renal ubiquitous 1, 2 (RU1, RU2); intestinal carboxyl esterase (iCE); Heat shock protein 70-2 (HSP70-2) mutant; thyroid stimulating hormone receptor (TSHR); CD123; CD171; CD19; CD20; CD22; CD26; CD30; CD33; CD44v7/8 (cluster of differentiation 44, exons 7/8); CD53; CD92; CD100; CD148; CD150; CD200; CD261; CD262; CD362; CS-1 (CD2 subset 1, CRACC, SLAMF7, CD319, and 19A24); C-type lectin-like molecule-1 (CLL-1); ganglioside GD3 (aNeu5Ac(2-8)aNeu5Ac(2-3)bDGalp(l-4)bDGlcp(ll)Cer); Tn antigen (Tn Ag); Fms-Like Tyrosine Kinase 3 (FLT3); CD38; CD138; CD44v6; B7H3 (CD276); KIT (CD1 17); Interleukin-13 receptor subunit alpha-2 (IL-13Ra2); Interleukin 11 receptor alpha (IL-l lRa); prostate stem cell antigen (PSCA); Protease Serine 2 1 (PRSS21); vascular endothelial growth factor receptor 2 (VEGFR2); Lewis(Y) antigen; CD24; Platelet derived growth factor receptor beta (PDGFR-beta); stage-specific embryonic antigen-4 (SSEA-4); Mucin 1, cell surface associated (MUCl); mucin 16 (MUCl 6); epidermal growth factor receptor (EGFR); epidermal growth factor receptor variant III (EGFRvIII); neural cell adhesion molecule (NCAM); carbonic anhydrase IX (CAIX); Proteasome (Prosome, Macropain) Subunit, Beta Type, 9 (LMP2); ephrin type-A receptor 2 (EphA2); Ephrin B2; Fucosyl GM1; sialyl Lewis adhesion molecule (sLe); ganglioside GM3 (aNeu5Ac(2-3)bDGalp(l-4)bDGlcp(l-l)Cer); TGS5; high molecular weight-melanoma-associated antigen (HMWMAA); o-acetyl-GD2 ganglioside (OAcGD2); Folate receptor alpha; Folate receptor beta; tumor endothelial marker 1 (TEM1/CD248); tumor endothelial marker 7-related (TEM7R); claudin 6 (CLDN6); G protein coupled receptor class C group 5, member D (GPRC5D); chromosome X open reading frame 6 1 (CXORF61); CD97; CD179a; anaplastic lymphoma kinase (ALK); Poly sialic acid; placenta specific1 (PLAC1); hexasaccharide portion of globoH glycoceramide (GloboH); mammary gland differentiation antigen (NY-BR-1); uroplakin 2 (UPK2); Hepatitis A virus cellular receptor 1 (HAVCR1); adrenoceptor beta 3 (ADRB3); pannexin 3 (PANX3); G protein-coupled receptor 20 (GPR20); lymphocyte antigen 6

complex, locus K 9 (LY6K); Olfactory receptor 51E2 (OR51E2);TCR Gamma Alternate Reading Frame Protein (TARP); Wilms tumor protein (WT1); ETS translocation-variant gene 6, located on chromosome 12p (ETV6-AML); sperm protein 17 (SPA17); X Antigen Family, Member 1A (XAGE1); angiopoietin-binding cell surface receptor 2 (Tie 2); CT (cancer/testis (antigen)); melanoma cancer testis antigen-1 (MAD-CT-1); melanoma cancer testis antigen-2 (MAD-CT-2); Fos-related antigen 1; p53; p53 mutant; human Telomerase reverse transcriptase (hTERT); sarcoma translocation breakpoints; melanoma inhibitor of apoptosis (ML-IAP); ERG (transmembrane protease, serine 2 (TMPRSS2) ETS fusion gene); NAcetyl glucosaminyl-transferase V (NA17); paired box protein Pax-3 (PAX3); Androgen receptor; Cyclin Bl; Cyclin Dl; v-myc avian myelocytomatosis viral oncogene neuroblastoma derived homolog (MYCN); Ras Homolog Family Member C (RhoC); Cytochrome P450 1B1 (CYP1B1); CCCTC-Binding Factor (Zinc Finger Protein)-Like (BORIS); Squamous Cell Carcinoma Antigen Recognized By T Cells-1 or 3 (SARTl, SART3); Paired box protein Pax-5 (PAX5); proacrosin binding protein sp32 (OY-TES1); lymphocyte-specific protein tyrosine kinase (LCK); A kinase anchor protein 4 (AKAP-4); synovial sarcoma, X breakpoint- 1, -2, -3 or -4 (SSX1, SSX2, SSX3, SSX4); CD79a; CD79b; CD72; Leukocyte-associated immunoglobulin-like receptor 1 (LAIR1); Fc fragment of IgA receptor (FCAR); Leukocyte immunoglobulin-like receptor subfamily A member 2 (LILRA2); CD300 molecule-like family member f (CD300LF); C-type lectin domain family 12 member A (CLEC12A); bone marrow stromal cell antigen 2 (BST2); EGF-like module containing mucin-like hormone receptor-like 2 (EMR2); lymphocyte antigen 75 (LY75); Glypican-3 (GPC3); Fc receptor-like 5 (FCRL5); mouse double minute 2 homolog (MDM2); livin; alphafetoprotein (AFP); transmembrane activator and CAML Interactor (TACI); B-cell activating factor receptor (BAFF-R); V-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog (KRAS); immunoglobulin lambda-like polypeptide 1 (IGLL1); 707-AP (707 alanine proline); ART-4 (adenocarcinoma antigen recognized by T4 cells); BAGE (B antigen; b-catenin/m, bcatenin/mutated); CAMEL (CTL-recognized antigen on melanoma); CAPl (carcinoembryonic antigen peptide 1); CASP-8 (caspase-8); CDC27m (cell-division cycle 27 mutated); CDK4/m (cycline-dependent kinase 4 mutated); Cyp-B (cyclophilin B); DAM (differentiation antigen melanoma); EGP-2 (epithelial glycoprotein 2); EGP-40 (epithelial glycoprotein 40); Erbb 2, 3, 4 (erythroblastic leukemia viral oncogene homolog-2, -3, 4); FBP (folate binding protein); , fAchR (Fetal acetylcholine receptor); G250 (glycoprotein 250); GAGE (G antigen); GnT-V

(Nacetylglucosaminyltransferase V); HAGE (helicose antigen); ULA-A (human leukocyte antigen-A); HST2 (human signet ring tumor 2); KIAA0205; KDR (kinase insert domain receptor); LDLR/FUT (low density lipid receptor/GDP L-fucose: b-D-galactosidase 2-a-L fucosyltransferase); LICAM (LI cell adhesion molecule); MC1R (melanocortin 1 receptor); Myosin/m (myosin mutated); MUM-1, -2, -3 (melanoma ubiquitous mutated 1, 2, 3); NA88-A (NA cDNA clone of patient M88); KG2D (Natural killer group 2, member D) ligands; oncofeta antigen (h5T4); pi 90 minor bcr-abl (protein of 190KD bcr-abl); Pml/RARa (promyelocytic leukaemia/retinoic acid receptor a); PRAME (preferentially expressed antigen of melanoma); SAGE (sarcoma antigen); TEL/AMLl (translocation Ets-family leukemia/acute myeloid leukemia 1); TPI/m (triosephosphate isomerase mutated); CD70; or a combination thereof.

[527] In some embodiments, an anti-CLEC2D antibodies of the disclosure, is a bispecific antibody, wherein the bispecific antibody specifically binds to CLEC2D and a second antigen, wherein the second antigen is an antigen associated with an infectious agent or pathogen. In some embodiments, an anti-CLEC2D antibodies of the disclosure, is a bispecific antibody, wherein the bispecific antibody specifically binds to CLEC2D and a second antigen, wherein the second antigen is an antigen associated with a microorganism. In some embodiments, an anti-CLEC2D antibodies of the disclosure, is a bispecific antibody, wherein the bispecific antibody specifically binds to CLEC2D and a second antigen, wherein the second antigen is an antigen associated with a microorganisms including but not limited to bacteria, fungi, protozoa, parasites, and viruses. In some embodiments, an anti-CLEC2D antibodies of the disclosure, is a bispecific antibody, wherein the bispecific antibody specifically binds to CLEC2D and a second antigen, wherein the second antigen is an antigen associated with a microorganisms including but not limited to a pathogenic bacteria, fungi, protozoa, parasites, and viruses. In some embodiments, an anti-CLEC2D antibodies of the disclosure, is a bispecific antibody, wherein the bispecific antibody specifically binds to CLEC2D and a second antigen, wherein the second antigen is an antigen associated with a microorganisms including but not limited to an intracellular bacteria. In some embodiments, an anti-CLEC2D antibodies of the disclosure, is a bispecific antibody, wherein the bispecific antibody specifically binds to CLEC2D and a second antigen, wherein the second antigen is an antigen that is specifically expressed on a host cell infected with a microorganisms including but not limited to a pathogenic bacteria, fungi, protozoa, parasites, and viruses.

[528] In some embodiments, an anti-CLEC2D antibodies of the disclosure, is a bispecific antibody, wherein the bispecific antibody specifically binds to CLEC2D and a second antigen, wherein the second antigen is an antigen associated with inflammatory or autoimmune disorders including but not limited to seronegative spondyloarthropathies, connective tissue diseases, inflammatory bowel diseases, arthritis, inflammatory skin conditions, inflammatory lung diseases, inflammatory renal disease, systemic vasculitis, macrophage activation diseases, polymyalgia rheumatica, primary biliary sclerosis, sclerosing cholangitis, autoimmune hepatitis, Type 1 Diabetes Mellitus, Hashimoto's thyroiditis, Graves' disease, multiple sclerosis (MS), Guillain-Barre syndrome, Addison's disease, Raynaud's phenomenon and Goodpasture's syndrome.

[529] In some embodiments, an anti-CLEC2D antibodies of the disclosure, is a bispecific antibody, wherein the bispecific antibody specifically binds to CLEC2D and a second antigen, wherein the second antigen is an antigen associated with connective tissue diseases such as juvenile rheumatoid arthritis, rheumatoid arthritis, systemic lupus erythematosus (SLE) and lupus nephritis, scleroderma, Sjogren's syndrome, mixed connective tissue disease and polymyositis, dermatomyositis.

[530] In some embodiments, an anti-CLEC2D antibodies of the disclosure, is a bispecific antibody, wherein the bispecific antibody specifically binds to CLEC2D and a second antigen, wherein the second antigen is an antigen associated with Whipples disease and arthritis associated with granulomatous ileocolitis, inflammatory skin conditions such as autoimmune bullous pemphigoid, autoimmune pemphigus vulgaris, eczema and dermatitis, inflammatory lung diseases such as alveolitis, pulmonary fibrosis, sarcoidoisis, asthma, bronchitis and bronchiolitis obliterans, inflammatory renal diseases such as glomerulonethritis, renal allograft rejection and renal tubular inflammation, atherosclerosis, systemic vasculitis such as temporal arteritis/giant cell arteritis, takayasu arteritis, polyarteritis nodosa, Kawasaki disease, Wegener's granulomatosis, churg strauss syndrome, microscopic polyangiitis, necrotising glomerulonephritis, henoch schonlein purpura, essential cryoglobulinaemic vasculitis, other small vessel vasculitis and Behcets disease, macrophage activation diseases such as macrophage activation syndrome (MAS), adult onset stills disease, haemophagocytic syndrome, polymyalgia rheumatica, primary biliary sclerosis, sclerosing cholangitis, autoimmune hepatitis, Type 1

Diabetes Mellitus, Hashimoto's thyroiditis, Graves' disease, multiple sclerosis (MS), Guillain-Barre syndrome, Addison's disease, and/or Raynaud's phenomenon and Goodpasture's syndrome.

[531] The bispecific antibodies of the invention are generated using any methods known in the art such as, by way of non-limiting example, the use of cross-linked fragments, quadromas, and/or any of a variety of recombinant formats such as, by way of non-limiting examples, linked antibody fragments, forced heterodimers, and or recombinant formats based on single domains. Examples of Bispecific formats include but are not limited to bispecific IgG based on Fab arm exchange (Gramer et al., 2013 MAbs. 5(6)); the CrossMab format (Klein C et al., 2012 MAbs 4(6)); multiple formats based on forced heterodimerization approaches such as SEED technology (Davis JH et al., 2010 Protein Eng Des Sel. 23(4):195-202), electrostatic steering (Gunasekaran K et al., J Biol Chem. 2010 285(25):19637-46.) or knob-into-hole (Ridgway JB et al., Protein Eng. 1996 9(7):617-21.) or other sets of mutations preventing homodimer formation (Von Kreudenstein TS et al., 2013 MAbs. 5(5):646-54.); fragment based bispecific formats such as tandem scFv (such asBiTEs) (Wolf E et al., 2005 Drug Discov. Today 10(18):1237-44.); bispecific tetravalent antibodies (Pörtner LM et al., 2012 Cancer Immunol Immunother. 61(10):1869-75.); dual affinity retargeting molecules (Moore PA et al., 2011 Blood.117(17):4542-51), diabodies (Kontermann RE et al., Nat Biotechnol. 1997 15(7):629-31).

[532] In some embodiments, the anti-CLEC2D antibodies and compositions and the additional therapeutic agent(s) act additively to treat a sign or a symptom of a disease.

[533] In some embodiments, the anti-CLEC2D antibodies and compositions and the additional therapeutic agent(s) act synergistically to treat a sign or a symptom of a disease.

[534] In some embodiments, the combination of anti-CLEC2D antibodies and compositions with an additional therapeutic agents leads to superior efficacy in the treatment of the disease or disorder, including increased reduction of one or more symptoms of the disease or disorder, the reduction in one or more side effects of the treatment, or a reduction in the therapeutically effective dose of the anti-CLEC2D antibodies or compositions or the additional therapeutic agent.

[535] The antibodies or antigen-binding fragments thereof can be conjugated to another therapeutic modality. The conjugation may bring the antibodies or antigen-binding fragments thereof of the present disclosure into close proximity to the target, such as a target cell, improve the target specificity, increase the overall binding affinity of the conjugate to the target, and/or

enhance the cytotoxicity of the NK cells towards the target, which increase the therapeutic efficacy and/or specificity of the antibodies or antigen-binding fragments thereof of the present disclosure. The another therapeutic modality can be any of the additional therapeutic agents described herein. Methods of making antibody conjugates are known in the art, for example, through protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). Coupling may be accomplished by any chemical reaction that will bind the two molecules so long as the antibody and the other moiety retain their respective activities. This linkage can include many chemical mechanisms, for instance covalent binding, affinity binding, intercalation, coordinate binding and complexation. The preferred binding is, however, covalent binding. Covalent binding can be achieved either by direct condensation of existing side chains or by the incorporation of external bridging molecules. Many bivalent or polyvalent linking agents are useful in coupling protein molecules, such as the antibodies of the present invention, to other molecules. For example, representative coupling agents can include organic compounds such as thioesters, carbodiimides, succinimide esters, diisocyanates, glutaraldehyde, diazobenzenes and hexamethylene diamines. This listing is not intended to be exhaustive of the various classes of coupling agents known in the art but, rather, is exemplary of the more common coupling agents. (*See* Killen and Lindstrom, Jour. Immun. 133:1335-2549 (1984); Jansen et al., Immunological Reviews 62:185-216 (1982); and Vitetta et al., Science 238:1098 (1987).

[536] The antibodies or antigen-binding fragments thereof of the present disclosure can also be used to make a bi-specific antibody. For example, the antibodies or antigen-binding fragments thereof of the present disclosure can be combined with the additional antibodies or antigen-binding fragments thereof described herein to form a bi-specific antibody. Methods of making bispecific antibodies are known in the art.

[537] Dosage regimens are adjusted to provide the optimum desired response, e.g., a therapeutic response or minimal adverse effects. For example, for administration of an anti-CLEC2D antibody, the dosage can range from about 0.0001 to about 1000 mg/kg. For example,

dosages can be at least 0.1, at least 0.3, at least 1, at least 3, at least 5, at least 10, at least 15, at least 20 or at least 25 mg/kg body weight. The dosing schedule is typically designed to achieve exposures that result in sustained receptor occupancy based on typical pharmacokinetic properties of an antibody. An exemplary treatment regime entails administration once per week, once every two weeks, once every three weeks, once every four weeks, once a month, once every 3 months or once every three to 6 months. The dosage and scheduling may change during a course of treatment. For example, dosing schedule may comprise administering the antibody: (i) every two weeks in 6-week cycles; (ii) every four weeks for six dosages, then every three months; (iii) every three weeks; (iv) with an initial high dose followed by a periodic lower maintenance dose. Intervals between single dosages can be, for example, weekly, every 2 weeks, every 3 weeks, monthly, every three months or yearly. Intervals can also be irregular as indicated by measuring blood levels of antibody to the target antigen in the patient. In some methods, dosage is adjusted to achieve a desired plasma a concentration of the antibody.

[538] In some embodiments, the Ab can be administered as a sustained release formulation, in which case less frequent administration is required. Dosage and frequency vary depending on the half-life of the antibody in the patient. In general, human antibodies show the longest half-life, followed by humanized antibodies, chimeric antibodies, and nonhuman antibodies. The dosage and frequency of administration can vary depending on whether the treatment is prophylactic or therapeutic. In prophylactic applications, a relatively low dosage is typically administered at relatively infrequent intervals over a long period of time. Some patients continue to receive treatment for the rest of their lives. In therapeutic applications, a relatively high dosage at relatively short intervals is sometimes required until progression of the disease is reduced or terminated, and preferably until the patient shows partial or complete amelioration of symptoms of disease. Thereafter, the patient can be administered a prophylactic regime.

[539] Actual dosage levels of the active ingredients in the pharmaceutical compositions of the present disclosure may be varied so as to obtain an amount of the active ingredient which is effective to achieve the desired therapeutic response for a particular patient, composition, and mode of administration, without being unduly toxic to the patient. The selected dosage level will depend upon a variety of pharmacokinetic factors including the activity of the particular compositions of the present disclosure employed, the route of administration, the time of administration, the rate of excretion of the particular compound being employed, the duration of

the treatment, other drugs, compounds and/or materials used in combination with the particular compositions employed, the age, sex, weight, condition, general health and prior medical history of the patient being treated, and like factors well known in the medical arts. A composition of the present disclosure can be administered via one or more routes of administration using one or more of a variety of methods well known in the art. As will be appreciated by the skilled artisan, the route and/or mode of administration will vary depending upon the desired results.

[540] *Diagnosis and Prognosis*

[541] The disclosure provides a method of treating a disease in a subject in need thereof, comprising: determining the level of CLEC2D protein in the subject; and administering a therapeutically effective amount of a CLEC2D antibody to the subject. In one embodiment, the level of CLEC2D protein is determined by measuring the level of CLEC2D expression in a cell from the subject. In one embodiment, the cell is a cancer cell (e.g., a cell from a cancer described herein).

[542] The disclosure provides a method of treating a disease in a subject in need thereof, comprising: obtaining a sample from the subject; determining the level of CLEC2D protein in the sample; if the level of CLEC2D protein in the sample is higher than the level of CLEC2D protein in a control sample, administering a therapeutically effective amount of a CLEC2D antibody to the subject. In one embodiment, the sample is a cell from the subject. In one embodiment, the cell is from a diseased tissue or organ. In one embodiment, the cell is a cancer cell (e.g., a cell from a cancer described herein). In one embodiment, the control sample is from a non-diseased tissue or organ of the subject. In one embodiment, the control sample is from a subject which does not have the disease.

[543] The disclosure provides a method of treating a disease in a subject in need thereof, comprising: obtaining a first sample from the subject; determining a first level of CLEC2D protein in the first sample; administering a therapeutically effective amount of a CLEC2D antibody to the subject; obtaining a second sample from the subject; determining a second level of CLEC2D protein in the second sample; comparing the second level with the first level; if the first level is greater than the second level, continuing administration of a therapeutically effective amount of the CLEC2D antibody to the subject. In one embodiment, the sample is a cell from the subject. In one embodiment, the cell is from a diseased tissue or organ. In one embodiment, the cell is a cancer cell (e.g., a cell from a cancer described herein). In one embodiment, the control

sample is from a non-diseased tissue or organ of the subject. In one embodiment, the control sample is from a subject which does not have the disease.

[544] The disclosure provides a method of treating a disease in a subject in need thereof, comprising: obtaining a first sample from the subject; determining a first level of CLEC2D protein in the first sample; administering a first therapeutically effective amount of a CLEC2D antibody to the subject; obtaining a second sample from the subject; determining a second level of CLEC2D protein in the second sample; comparing the second level with the first level; if the first level is lower than the second level, administering a second therapeutically effective amount of the CLEC2D antibody to the subject, wherein the second therapeutically effective amount is greater than the first therapeutically effective amount. In one embodiment, the sample is a cell from the subject. In one embodiment, the cell is from a diseased tissue or organ. In one embodiment, the cell is a cancer cell (e.g., a cell from a cancer described herein). In one embodiment, the control sample is from a non-diseased tissue or organ of the subject. In one embodiment, the control sample is from a subject which does not have the disease.

[545] The disclosure provides a method of treating a disease in a subject in need thereof, comprising: obtaining a first sample from the subject; determining a first level of CLEC2D protein in the first sample; administering a therapeutically effective amount of a CLEC2D antibody to the subject; obtaining a second sample from the subject; determining a second level of CLEC2D protein in the second sample; comparing the second level with the first level; if the first level is lower than the second level, terminating administration of the CLEC2D antibody to the subject. In one embodiment, the sample is a cell from the subject. In one embodiment, the cell is from a diseased tissue or organ. In one embodiment, the cell is a cancer cell (e.g., a cell from a cancer described herein). In one embodiment, the control sample is from a non-diseased tissue or organ of the subject. In one embodiment, the control sample is from a subject, which does not have the disease.

[546] The isolated, novel antibody clones can be used to determine stage and aggressiveness of disease and to treat the disease appropriately.

[547] The disclosure provides anti-CLEC2D antibodies and antibody fragments thereof, nucleic acids encoding the antibodies or antigen binding fragments thereof, or compositions comprising same, for use in the diagnosis and prognosis of diseases and disorders.

[548] In some embodiments, isolated monoclonal antibodies reveal the differential expression of CLEC2D on various tumor cell surfaces, indicating that CLEC2D is a novel biomarker for the diagnosis of various disease conditions. Further CLEC2D antigen is significantly overexpressed on various tumors, indicating the usefulness of this target molecule as a novel molecular marker for disease diagnosis. Moreover, the expression level of CLEC2D significantly increases under the influence of various inducing agents. The differential expression of CLEC2D antigen on induced tumor cells is correlated with different stages of disease, disease progression, metastasis, and so on. Therefore CLEC2D has an enormous potential of prognostic biomarker. In some embodiments, an increase in CLEC2D protein expression, for example on a cancer cell in a subject, is associated with a poorer prognostic outcome than if CLEC2D protein expression is not elevated.

[549] As detailed herein, isolated monoclonal antibodies are used to monitor CLEC2D surface expression on tumor cell lines.

[550] Anti-CLEC2D antibodies can be used to diagnose and prognose diseases including, but not limited to breast cancer, prostate cancer, endometrial cancer, bladder cancer, kidney cancer, esophageal cancer, squamous cell carcinoma, uveal melanoma, follicular lymphoma, renal cell carcinoma, cendcal cancer, ovarian cancer, lung cancer, colorectal cancer, brain cancer, pancreatic cancer, head and neck cancer, liver cancer, leukemia, lymphoma, Hodgkin's disease, multiple myeloma, melanoma, astrocytoma, stomach cancer, pulmonary adenocarcinoma, adenocarcinoma, acinic cell adenocarcinoma, adrenal cortical carcinomas, alveoli cell carcinoma, anaplastic carcinoma, basaloid carcinoma, basal cell carcinoma, bronchiolar carcinoma, bronchogenic carcinoma, renaladinol carcinoma, embryonal carcinoma, anometroid carcinoma, fibrolamolar liver cell carcinoma, follicular carcinomas, giant cell carcinomas, hepatocellular carcinoma, intraepidermal carcinoma, intraepithelial carcinoma, leptomanigio carcinoma, medullary carcinoma, melanotic carcinoma, menigual carcinoma, mesometonephric carcinoma, oat cell carcinoma, squamal cell carcinoma, sweat gland carcinoma, transitional cell carcinoma, tubular cell carcinoma, ameloblastic sarcoma, angiolithic sarcoma, botryoid sarcoma, endometrial stroma sarcoma, ewing sarcoma, fascicular sarcoma, giant cell sarcoma, granulositic sarcoma, immunoblastic sarcoma, juxaccordial osteogenic sarcoma, coppices sarcoma, leukocytic sarcoma (leukemia), lymphatic sarcoma (lympho sarcoma), medullary sarcoma, myeloid sarcoma (granulocitic sarcoma), austiogenci sarcoma, periosteal sarcoma, reticulum cell

sarcoma (histiocytic lymphoma), round cell sarcoma, spindle cell sarcoma, synovial sarcoma, telangiectatic audiogenic sarcoma, Burkitt's lymphoma, NPDL, NML, NH and diffuse lymphomas.

[551] In spite of various treatment options currently available, multiple cancers, such as breast cancer, prostate cancer, endometrial cancer, bladder cancer, kidney cancer, esophageal cancer, squamous cell carcinoma, uveal melanoma, follicular lymphoma, renal cell carcinoma, cendcal cancer, ovarian cancer, lung cancer, colorectal cancer, brain cancer, pancreatic cancer, head and neck cancer, liver cancer, leukemia, lymphoma, Hodgkin's disease, multiple myeloma, melanoma, astrocytoma, stomach cancer, and pulmonary adenocarcinoma, still remain as leading causes of death in people world-wide and lack unique therapeutic prospects. Diagnosis of these diseases at an early stage is one of the most important factors that determine survival. The present disclosure describes identification of CLEC2D as a biomarker target for these diseases and others, having profound therapeutic implications. The rapid advancement in overall antibody identification methods against CLEC2D, described in present disclosure, have made it possible to validate CLEC2D as novel biomarker against various disease indications mentioned above.

[552] The present disclosure provides anti-CLEC2D antibodies and fragments thereof, and compositions comprising the same, as for use in the identification of CLEC2D expression as a predictive biomarker to stratify patients who are likely to have better response on certain treatments.

[553] The present disclosure provides anti-CLEC2D antibodies and fragments thereof, nucleic acids encoding the antibodies or antigen binding fragments thereof, or compositions comprising the same, as for use in the identification of CLEC2D expression as a predictive biomarker and to pave the way to explore therapies aimed at enhancing NK cells cytolytic activity in metastatic cancer patients. In some embodiments, expression of these CLEC2D receptors on immune cells in the tumor microenvironment is associated with good prognosis. The expression of specific molecules on specific immune cells, such as NK cells and T cells, is involved in maintenance of particular immune function. The present disclosure describes the prognostic role of CLEC2D expression as NK receptor ligands, including in prostate cancer, and the association of CLEC2D expression with different prostate cancer disease stages, molecular subtypes and clinic-pathological features. Blocking CLEC2D expression on tumor cells with an anti-CLEC2D antibody signals in an NK cell mediated cytotoxic immune context and harnesses the positive

prognostic value of infiltrating T cells. The human anti-CLEC2D monoclonal antibodies of the disclosure expand the opportunity/scope of these antibodies not only as therapeutic, also, as prognostic and diagnostics in various cancer types either alone or in association with other ligands, cytokines or other cellular factors.

[554] *Pharmaceutical Formulations*

[555] The disclosure provides a pharmaceutical composition of any of the anti CLEC2D antibodies or antibody fragments thereof of the disclosure. Each of the anti-CLEC2D antibodies of the present disclosure can be formulated into a composition suitable for administration to the subject. In exemplary aspects, each of the anti-CLEC2D antibodies can be formulated with one or more agents which enhance the chemico-physico features of the anti-CLEC2D antibody, e.g., via stabilizing the anti-CLEC2D antibody at certain temperatures, e.g., room temperature, increasing shelf life, reducing degradation, e.g., oxidation protease mediated degradation, increasing half-life of the anti-CLEC2D antibody, etc. In exemplary aspects of the present disclosure, the anti-CLEC2D antibody may be formulated into a composition additionally comprising a pharmaceutically acceptable carrier, diluents, or excipient.

[556] "Pharmaceutical compostions" and "pharmaceutical formulations" are used interchangeably herein unless the context clearly suggests otherwise.

[557] The pharmaceutical compositions can be solid, semi-solid, or liquid. Generally the pharmaceutical composition is adapted for a particular route of administration. For example, the pharmaceutical composition can be adapted for oral administration, rectal administration, buccal administration, topical administration, etc. Preferably, the pharmaceutical composition is adapted for intravenous administration. In some embodiments the pharmaceutical composition comprising antibodies or antibody fragments of the disclosure is suitable for intravenous injection or infusion. In some embodiments, the aqueous stable monoclonal antibody formulation will be administered by parenteral routes preferably via intramuscular injection, sub-cutaneous injection, i.v. injection or, most preferably, i.v. infusion.

[558] As used herein, a "pharmaceutically acceptable carrier" includes any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like that are physiologically compatible. Preferably, the carrier is suitable for intravenous, intramuscular, subcutaneous, parenteral, spinal or epidermal administration (e.g., by injection or infusion). A pharmaceutical composition of this disclosure may include one or more

pharmaceutically acceptable salts, anti-oxidant, aqueous and nonaqueous carriers, and/or adjuvants such as preservatives, wetting agents, emulsifying agents and dispersing agents. For example, a pharmaceutically acceptable carrier includes any of the standard pharmaceutical carriers, such as a phosphate buffered saline solution, water, emulsions such as an oil/water or water/oil emulsion, and various types of wetting agents. The term also encompasses any of the agents approved by a regulatory agency of the US Federal government or listed in the US Pharmacopeia for use in animals, including humans.

[559] The pharmaceutical composition can comprise any pharmaceutically acceptable ingredients, including, for example, acidifying agents, additives, adsorbents, aerosol propellants, air displacement agents, alkalizing agents, anticaking agents, anticoagulants, antimicrobial preservatives, antioxidants, antiseptics, bases, binders, buffering agents, chelating agents, coating agents, coloring agents, desiccants, detergents, diluents, disinfectants, disintegrants, dispersing agents, dissolution enhancing agents, dyes, emollients, emulsifying agents, emulsion stabilizers, fillers, film forming agents, flavor enhancers, flavoring agents, flow enhancers, gelling agents, granulating agents, humectants, lubricants, mucoadhesives, ointment bases, ointments, oleaginous vehicles, organic bases, pastille bases, pigments, plasticizers, polishing agents, preservatives, sequestering agents, skin penetrants, solubilizing agents, solvents, stabilizing agents, suppository bases, surface active agents, surfactants, suspending agents, sweetening agents, therapeutic agents, thickening agents, tonicity agents, toxicity agents, viscosity-increasing agents, water-absorbing agents, watermiscible cosolvents, water softeners, or wetting agents. Other pharmaceutically acceptable excipients known in the art include diluents, carriers, fillers, binders, lubricants, disintegrants, glidants, colorants, pigments, taste masking agents, sweeteners, plasticizers, and any acceptable auxiliary substances such as absorption enhancers, penetration enhancers, surfactants, co-surfactants, preservatives, anti-oxidants and specialized oils. Specific to the field of biopharmaceutical proteins are excipients intended to stabilize proteins and cryo- protectants to provide protection during freeze-drying. Suitable excipient(s) are selected based in part on the dosage form, the intended mode of administration, the intended release rate, and manufacturing reliability. Non-limiting examples of commonly used excipients include polymers, waxes, calcium phosphates, sugars (e.g., trehalose, sucrose, or mannitol), buffers (such as phosphate, acetate, citrate, histidine, or glycine based buffers at pH between 5 and 7.5), salts (e.g., NaCl or NaEDTA), polysorbate 20, polysorbate 80, human albumin,

dextran, and benzyl alcohol.See, e.g., the Handbook of Pharmaceutical Excipients, Third Edition, A. H. Kibbe (Pharmaceutical Press, London, UK, 2000), which is incorporated by reference in its entirety. Remington 's Pharmaceutical Sciences, Sixteenth Edition, E.W. Martin (Mack Publishing Co., Easton, Pa., 1980), which is incorporated by reference in its entirety.

[560] In exemplary aspects, the pharmaceutical composition comprises formulation materials that are nontoxic to recipients at the dosages and concentrations employed. In specific embodiments, pharmaceutical compositions comprising an active agent and one or more pharmaceutically acceptable salts; polyols; surfactants; osmotic balancing agents; tonicity agents; anti-oxidants; antibiotics; antimycotics; bulking agents; lyoprotectants; anti-foaming agents; chelating agents; preservatives; colorants; analgesics; or additional pharmaceutical agents.

[561] In exemplary aspects, the pharmaceutical composition comprises one or more polyols and/or one or more surfactants, optionally, in addition to one or more excipients, including but not limited to, pharmaceutically acceptable salts; osmotic balancing agents (tonicity agents); anti-oxidants; antibiotics; antimycotics; bulking agents; lyoprotectants; antifoaming agents; chelating agents; preservatives; colorants; and analgesics.

[562] In certain embodiments, the pharmaceutical composition can contain formulation materials for modifying, maintaining or preserving, for example, the pH, osmolarity, viscosity, clarity, color, isotonicity, odor, sterility, stability, rate of dissolution or release, adsorption or penetration of the composition. In such embodiments, suitable formulation materials include, but are not limited to, amino acids (such as glycine, glutamine, asparagine, arginine or lysine); antimicrobials; antioxidants (such as ascorbic acid, sodium sulfite or sodium hydrogen-sulfite); buffers (such as borate, bicarbonate, Tris-HCl, citrates, phosphates or other organic acids); bulking agents (such as mannitol or glycine); chelating agents (such as ethylenediamine tetraacetic acid (EDTA)); complexing agents (such as caffeine, polyvinylpyrrolidone, beta-cyclodextrin or hydroxypropyl-beta-cyclodextrin); fillers; monosaccharides; disaccharides; and other carbohydrates (such as glucose, mannose or dextrins); proteins (such as serum albumin, gelatin or immunoglobulins); coloring, flavoring and diluting agents; emulsifying agents; hydrophilic polymers (such as polyvinylpyrrolidone); low molecular weight polypeptides; salt-forming counterions (such as sodium); preservatives (such as benzalkonium chloride, benzoic acid, salicylic acid, thimerosal, phenethyl alcohol, methylparaben, propylparaben, chlorhexidine,

sorbic acid or hydrogen peroxide); solvents (such as glycerin, propylene glycol or polyethylene glycol); sugar alcohols (such as mannitol or sorbitol); suspending agents; surfactants or wetting agents (such as pluronics, PEG, sorbitan esters, polysorbates such as polysorbate 20, polysorbatc, triton, tromethamine, lecithin, cholesterol, tyloxapal); stability enhancing agents (such as sucrose or sorbitol); tonicity enhancing agents (such as alkali metal halides, preferably sodium or potassium chloride, mannitol sorbitol); delivery vehicles; diluents; excipients and/or pharmaceutical adjuvants. See, REMINGTON'S PHARMACEUTICAL CAR-TSCIENCES, 18" Edition, (A. R. Genrmo, ed.), 1990, Mack Publishing Company.

[563] The pharmaceutical compositions can be formulated to achieve a physiologically compatible pH. In some embodiments, the pH of the pharmaceutical composition can be for example between about 4 or about 5 and about 8.0, between about 4.5 and about 7.5, or between about 5.0 to about 7.5. In exemplary embodiments, the pH of the pharmaceutical composition is between 5.5 and 7.5.

[564] Pharmaceutical compositions for administering the anti CLEC2D antibodies via parenteral administration are typically liquid. Water is commonly used as a main excipient, although other pharmaceutically-acceptable liquids such as ethanol, glycerol, ethyl oleate, Myglyol, benzyol oleate, castor oil, MCT, benzyl alcohol isopropyl myristate can be used alone or in combination with water or each other. Aqueous compositions that contain no other excipients are also contemplated, and can be prepared from lyophilized, amorphous, or crystalline compounds. Often the injectable composition, which can be for subcutaneous, IM, or IV injection, contains isotonizing agents. An injectable solution or suspension is typically sterile, as are all liquid pharmaceutical dosage forms.

[565] Pharmaceutical compositions for administering anti CLEC2D antibodies via topical administration include powders, creams, ointments, gels, lotions, solutions and suspensions (including mouth washes). The excipient carrier is often aqueous, oil, or polymer based, each optionally in the form of an emulsion or microemulsion. The term "topical administration" includes, for example, optical administration (e.g., via a cream/ointment) and administration to the skin (e.g., at an inflamed joint).

[566] Pharmaceutical compositions for administering anti CLEC2D antibodies via oral administration include solid oral dosage forms such as tablets, capsules, enteric coated forms thereof, lozenges, and films, as well as liquid dosage forms including solutions, suspensions,

liquid filled capsules, and mouth washes. Tablets can be soluble tablets, dispersible tablets, effervescent tablets, chewable tablets, lyophilized tablets, coated tablets (e.g., sugar-coated or enteric-coated), and modified release tablets. Capsules include hard gelatin capsules that can be filled with powder, pellets, granules, small tablets, or mini-tablets, or solutions or emulsions or combinations and can be coated for enteric or modified release. Soft capsules are also contemplated and are more typically filled with liquids, gels or dispersions, but are not limited thereto. Granules can be effervescent granules, coated granules (e.g., sugar-coated or enteric-coated), and modified release granules. Although the anti CLEC2D antibodies of the present disclosure can be administered orally, it should be understood that such administration may be considered to be a topical administration to the GI tract. Likewise, a suppository or rectal injection may also be used to topically to the intestines. The use of an oral dosage form to treat gastrointestinal disease(s) using the anti CLEC2D antibodies of the present disclosure is an aspect of the present disclosure.

[567] An overview of dosage forms can be found in Ansel's Pharmaceutical Dosage forms and Drug Delivery Systems. 9th ed. L.V. Allan, N.G. Popovitch, H.C. Ansel, 2010 Lippincott, ISBN: 978-0781779340; Formularium der Nederlandse Apothekers. 2004 WINAp ISBN 90-70605-75-9; Recepteerkunde, G. K. Bolhuis, Y. Bouwman-Boer, F. Kadir en J. Zuiderma, 2005 WINAp ISBN 90-70605-65-1 ; and Apothekenrezeptur und -defektur. Deutscher Apotheker Verlag Stuttgart 1986 ISBN 3-7692-1092-1. See also US 7,147,854 for a description of topical preparations for delivering IL-8 antibodies to treat skin inflammatory disease such as psoriasis.

[568] The pharmaceutical composition generally contains about 0.01 to 1000 mg of the antibody per dose, depending in part upon the dosage form employed. The dose can be, for example, fixed or variable (e.g, based on body weight).

[569] Development of a stable formulation is vital to successful clinical manufacturing of pharmaceutical compositions comprising the antibodies and antigen binding fragments of the disclosure.

[570] In some embodiments, a stable formulation is prepared by screening various buffers, stabilizers at different pH with the help of additives and the final stable formulation should contain the physical, chemical stability and biological activity upon storage. The role of excipients in the stable formulation is to prevent and/or reduce the rate of degradation in order to provide an acceptable shelf life.

[571] The current disclosure provides, in some embodiments, a stable liquid and/or lyophilized formulation of anti-CLEC2D monoclonal antibodies. In some embodiments, a formulation buffer contemplated for use in the present disclosure has a pH in the range from 4.0 to 8.0; preferably in the pH range from 4.5 to 7.5; most preferably in the pH range between 5.0 and 6.5.

[572] In some embodiments, the present disclosure comprises buffering agents that can be any of the following and combinations thereof, sodium citrate, citric acid; sodium phosphate mono basic, sodium phosphate dibasic; potassium phosphate mono basic, potassium phosphate dibasic; acetic acid, sodium acetate; histidine, histidine HCl; succinic acid, sodium succinate; tartaric acid, sodium tartrate; maleic acid, maleate; succinate2-(N-morpholino) ethane sulfonic acid (MES) and hydrochloric acid and sodium hydroxide to adjust the pH to desired range.

[573] In some embodiments, the composition comprises other buffers such as Tris buffer, (3-(N-morpholino)propanesulfonic acid) (MOPS), MOPS-SDS (MEPS), N-cyclohexyl-2-hydroxyl-3-aminopropanesulfonic acid (CAPSO), piperazine-N,N′-bis(2-ethanesulfonic acid) (PIPES) etc. some embodiments, the formulation comprises polyols, which are sugar alcohols. In some embodiments, the stabilizers in the formulation comprise any one of the following alone or in combination: α-trehalose, sucrose, mannitol, sorbitol. In other embodiments, the formulation comprises a second stabilizer that are any one of the following: methionine, lysine, arginine, glycine, glutamate etc.

[574] In some embodiments, the present antibody formulations comprise hydrophobic salts namely sodium camphor sulphate, tri methyl ammonium iodide. In another embodiment, the present disclosure of anti-CLEC2D monoclonal antibody formulation comprises surfactants, as well. In some embodiments, any one of following surfactants are included in the formulations, as exemplified by Polysorbate 20, Polysorbate 40, Polysorbate 80, and Poloxamer 188. In some embodiments, the composition comprising an anti-CLEC2D monoclonal antibody comprises anti-oxidants, for example methionine and/or glutathione. In some embodiments, the composition comprises hydrochloric acid and sodium hydroxide to adjust the pH of formulation buffer.

[575] In some embodiments, the present disclosure comprises other stabilizing and complexing agents such as disodium edetate (Na(2)EDTA) and diethylene triaminepentaacetic acid (DTPA). In some embodiments, all the excipients of the stable formulation are dissolved in water for injection (WFI).

[576] In one embodiment, the final aqueous stable formulation is filtered suitably to remove particulate matter. In some embodiments, filtration is done through either polyethersulfone (PES) filters, Polyvinylidene Fluoride (PVDF) filters or regenerated cellulose (RC) filters, suitably filters sized at either 0.22 and/or 0.45 micron pore size.

[577] In some embodiments, a drug delivery device is the second important aspect of the antibody formulation. In other embodiments, the drug delivery device is sterile. In other embodiments, the drug delivery device is a vial, ampoule, syringe, injection pen or an intravenous (i.v) bag.

[578] In a non-limiting embodiment of the present disclosure, functional characterization comprises performing experiments to understand the kinetics and dynamics of binding of an anti-CLEC2D antibody using techniques that include, but are not limited to, ELISA, BIAcore, flow cytometry, western-blot and imaging, amongst other techniques that are well known in the art. Further CLEC2D-CD161 interaction sites are mapped, and then monitored and validated through flow cytometry based binding experiments.

[579] In a non-limiting embodiment of the present disclosure, monoclonal antibodies function through various mechanisms to destroy tumor cells with an ultimate effect of priming either the innate or adaptive arm of the immune system. The effector functions include complement-dependent cytotoxicity (CDC), antibody-dependent cellular cytotoxicity (ADCC) and antibody-dependent cellular phagocytosis (ADCP). One non-limiting approach employed in the methods disclosed herein is to enhance the efficacy of therapeutic antibodies by modifying the immunoglobulin constant region. An example of such an antibody includes an anti-CLEC2D antibody which consists of a variable region (novel heavy chain and light chain regions) and may consist constant regions representing specific isotypes e.g., IgG1, IgG2, IgG4 or variants thereof, as described in this disclosure. Similarly, the unique variable region sequences could be used to develop antibody molecules with enhanced ADCC function or modified thermal stability as well as developing bispecific antibodies, ScFv molecules or any other antibody formats, as further described herein.

[580] In a non-limiting embodiment of the present disclosure, the phrase “cytokines” may include chemokines, interferons, interleukins, lymphokines and tumor necrosis factors, which may be produced as an effect of the treatment of isolated antibody used against any of the cell lines related to a mentioned disease and/or combination thereof.

[581] In a non-limiting embodiment of the present disclosure, the phrase an "inducer" is a molecule that regulates gene expression.

[582] An embodiment of the present disclosure comprises using methods and tools to understand interaction of genes associated with pathways such as NK-cell signature, IFN-γ production etc., in relation to a mode of action of selected antibody molecules. To exemplify, techniques such as western blot, flow cytometry, imaging through confocal microscopy and RT PCR are employed together to decipher the mechanistic impact of selected anti-CLEC2D antibody molecules, wherein the effect of various inhibitors against major signaling pathways are assessed in multiple cancer cells. In one embodiment, an IFN-γ release assay, CD107a+ expression, and/or cytoxicity assays are used to estimate the effectiveness of an anti-CLEC2D antibody.

[583] In a non-limiting embodiment of the present disclosure, anti-tumor activity is assessed in huNOG-EXL mice bearing subcutaneous PC3 tumor xenograft, wherein the effect of a selected anti-CLEC2D antibody is monitored either alone or in combination with monoclonal antibody against a checkpoint target. In another embodiment, antibody dosage regimens are adjusted to obtain an optimum and desired anti-tumor response. In some embodiments, the phrases "parenteral administration" or related terms as used herein means mode of administration other than enteral and topical administration, usually by injection and includes, but is not limited to the following administration means, intramuscular, intravenous, intrarterial, intrathecal, intracapsular, intraorbital, intracardiac, intradermal, intraperitoneal, subcutaneous, subcuticular, intraspinal, epidural, intraasternal injection and infusion.

[584] The following examples are presented in order to more fully illustrate the preferred embodiments of this disclosure. They should in no way be construed, however, as limiting the broad scope of this disclosure.

EXAMPLES

[585] Example 1: Expression of soluble CLEC2D antigen

[586] The antigen construct comprising an ecto-domain of CLEC2D, either wild type or mutated, was expressed in Chinese hamster ovary (CHO) cell line and purified as a soluble antigen. The CLEC2D ectodomain contains 5 cysteines with 2 putative disulphide bonds. The mutation H176C was carried out to introduce an additional disulphide bridge with the Cys163

amino acid to increase the stability and homogeneity of the expressed protein. The construct was developed with a C-term Histidine tag to facilitate the antigen purification process.

[587] The extracellular domain of the CLEC2D (Q72-V191, H176C) antigen was codon optimized for both human and CHO expression system and the construct was synthesized. A specific signal sequence was used for secretion of the CHO expressed antigen. The CLEC2D gene sequence and appropriate signal sequence was cloned into the pCDNA3.1 mammalian expression vector (FIG. 2A).

[588] CHO suspension cells at more than 90% viability were used for transfection of the expression plasmid encoding the CLEC2D gene. Cells were centrifuged at 1000-1400 rpm for 4-5 minutes. The spent media was decanted and the cells were re-suspended in 250 ml of OptiMEM I media. The CLEC2D expression plasmid was transfected using Lipofectamine LTX with Plus™ reagent. 500 µg of DNA was used with 1:3 DNA to transfection reagent ratio and 500 µl Plus™ reagent was used. DNA and Lipofectamine LTX complex was prepared in 250ml OptiMEM I and incubated at 20-25°C for 20 minutes for complex formation. The transfection mix was added slowly to the cell suspension. The cells were incubated for 5 hours at 37°C in a 5% CO_2 shaker incubator at 100-120 RPM. 500 ml of Power CHO2 CD growth media was added to the cells. The cells were incubated for 3 days at 37°C in a 5% CO_2 shaker incubator at 100-120 RPM. Day 3 post transfection 200 ml Power CHO2 CD growth media containing 2 mM Glutamax was added. The cells were incubated at 37°C in a 5% CO_2 shaker incubator at 100-120 RPM. Day 6 post transfection, cell culture supernatant was harvested by centrifugation at 1400-2000 rpm for 10-15 minutes.

[589] The cell harvest was centrifuged and filtrated to remove cell debris. The clear supernatant was loaded onto pre-equilibrated Ni Sepharose FF C10 column. Subsequently the column was washed with 50mM and 100 mM Imidazole solution sequentially followed by single-step elution of His-tagged CLEC2D protein with 500 mM imidazole. Multiple fractions were collected and buffer exchanged to 1 X phosphate buffered saline (PBS) pH 7.4.

[590] Purified CLEC2D antigen was analysed through SDS-PAGE. The human CLEC2D sequence has two putative N-glycosylation sites N95 and N147. The aberrant mobility in SDS-PAGE was speculated to be due to differential N-glycosylation pattern. Purified CLEC2D antigen was de-glycosylated using PNGase enzyme and appeared to be as single band on expected molecular weight as judged by SDS-PAGE analysis (FIGS. 2B-2F). Subsequently

purified CLEC2D antigen was analysed by western blot experiments using a commercially available anti-CLEC2D antibody. The purified CLEC2D antigen was also confirmed through ELISA with a commercially available anti-CLEC2D antibody. The oligomeric status of the protein was found to be a dimer using size exclusion chromatography experiments. Finally, N-terminal sequencing was carried out by Edman degradation method to confirm the antigen sequence.

[591] Example 2: Screening of antibody gene library using phage and yeast display platforms

[592] Screening of antibody gene libraries was carried out with by combining phage display and yeast display of the antibody libraries. Phage and yeast display platforms expressing a human antibody repertoire were used sequentially to identify novel antibody clones with higher affinity and specificity against CLEC2D antigen (FIG. 3). For phage panning experiments against antigens, the magnetic bead based approach was adopted. Antigen coated on magnetic dynabeads were prepared and the efficiency of conjugation was >90%. Phage antibody library was panned against the antigen coated beads to separate phage particles expressing anti-CLEC2D antibody clones. The selected phage particles were used to generate replicative form containing the heavy and light chain repertoire. Purified DNA was digested and ligated into yeast expression vector in two different plasmid constructs to generate antibodies in Fab format and ScFv format.

[593] For magnetic bead conjugation with purified CLEC2D antigen, at first, dyna beads were weighed at a quantity ranging from 0.5 mg to 1.5 mg corresponding to ~0.5-1.0 x 10^8 beads and dissolved into 0.1 M sodium phosphate buffer, pH 7.4. This suspension was vortexed for 30-60 seconds followed by incubation at room temperature for 10-15 minutes with continuous rotation. The suspension was washed twice with 0.1 M sodium phosphate buffer and re-suspended again into 100 µL of 0.1 M sodium phosphate buffer. 5-10 µg of purified soluble CLEC2D antigen solution, (75-150 µL) was added to the bead suspension. Further, the suspension was mixed well before adding the 100 µL of 3 M ammonium sulfate solution. The mixture was incubated for 15-20 hours at 30-37°C with slow tilt but continuous rotation. Post incubation the tube was placed on the magnet holder for 1 min for magnetic separation. The magnet holder (with the tube in place) was carefully turned upside-down twice to ensure no beads remain in the cap. The supernatant was removed and beads are washed four times with 1 mL 1X PBS containing BSA

(0.05%). Finally, the beads are re-suspended in 100 µL of 1X PBS with BSA (0.05%) and are used in panning.

[594] 1 µL (~10^6 number of beads) of bead alone and bead coated with CLEC2D antigen are mixed with commercial P4500/anti-CLEC2D antibody at amount of 0.1µg followed by volume make up to 100 µL with 1X PBS containing 0.5% BSA. The mixture was incubated for 2 hrs on ice followed by a washing with 1 X PBS containing 0.5% BSA. Anti-goat IgG conjugated with FITC at 1:400 dilution was added to the re-suspended beads in solution of 1X PBS containing 0.5% BSA to a volume of 100 µL before readings were taken. All the flow cytometry experiments were done using Accuri C6 flow cytometer while the analysis was done by using BD Accuri C6 software. Firstly, forward and side scatter data was seen to fix a gate followed by fluorescence reading through FLH1 filter. At least 5,000-10,000 data points are collected for each sample (FIG 4A).

[595] Phage panning experiment was started with inoculation of single colony from the freshly streaked TG1 bacterial plate into 3 ml LB medium followed by incubation at 37°C until OD600 ≈ 0.9 and this was used for phage infection later. A phage naïve antibody library was thawed and the phage particles are precipitated with 250 µl (~1/4 of the phage suspension volume) PEG/NaCl solutions (20% PEG 8000 and 2.5 M NaCl) and incubated on ice for 30 minutes followed by centrifugation of the precipitated phage at 10,000x g for 10 minutes. The supernatant was discarded and the phage pellet was re-suspended in 200 µl PBS solution. Phage suspension (200 µl) was added to the bead conjugated with BSA and incubated on a rotator at room temperature for 2 hrs followed by adding the supernatant to bead conjugated with CLEC2D antigen and 10 µL of supernatant was kept aside for plaques assay later on. Phage suspension with conjugated bead with antigen was incubated on a rotator at room temperature for 2 hrs. The beads were washed two times with 1 ml 0.05% PBST (0.05% Tween-20 in PBS). Finally, magnetic beads bound with phage particle are re-suspended in 100 µl PBS. 10 µL of beads suspension was kept aside for plaques assay later on. The remaining 90 µl of the suspension was added to 2 ml of grown TG1 cells prepared earlier and the mixture was incubated at 37°C for 1 h. Post incubation it was diluted into 10 ml LB medium containing ampicillin at a final concentration of 25 µg /ml. After two hours of incubation at 37°C with constant shaking at 250 rpm, concentration of ampicillin was increased to a final concentration of 100 µg/ml. M13KO7, helper phage, was mixed into the amplified TG1 cells with multiplicity of infection (MOI) of 10

and incubated at 37°C for another 30 minutes. Helper phage-infected bacteria was spun down and the pellet was re-suspended into 10 ml of LB medium supplemented with 100 µg/ml ampicillin and 25 µg/ml kanamycin followed by incubation at 30°C for 30 minutes to 100 minutes for phage amplification. The bacterial culture was pelleted down by centrifugation for 10 minutes at 10,000 g. The pellet was discarded and supernatant was used for precipitation of amplified phage molecules by adding PEG/NaCL solution to the supernatant (~1/4th volume of supernatant). The mixture was incubated for 30 min on ice, followed by spinning the precipitated phage at 10,000 g for 10 minutes. Supernatant was discarded and pellet was re-suspended in 1ml of PBS. The Plaques assay was performed from the 10 µL of amplified phage suspension to estimate the amplified phage number while the remaining of the precipitated phage are stored with 50% glycerol at -80°C freezer for long term storage.

[596] Plaque assay was performed at every step to ensure the numbers of phage particles. A single colony from the TG1 bacterial plate was inoculated in bacteria in 3 ml LB medium and was grown at 37°C until OD600 ≈ 0.9. 0.7% of agarose was prepared in purified water and stored at 50°C in aliquots of 3 ml each in a 15 ml of falcon tubes. The phage supernatant and pellet were diluted at respective steps from 10^{-1} to 10^{-5}. 100 µl of diluted phage and 100 µl TG1 cells were added in to each of agarose aliquots and mixed followed by immediately spreading on LB Agar plate. The plates were incubated in 37°C in an incubator for overnight. The plaque formation was observed and counted next day. The number of panned molecules was calculated based on number of plaques observed (Table 10).

Table 10: Estimation of phage particle number at every step of panning process against CLEC2D antigen.

Process Step	Pfu/mL
Panning with BSA conjugated beads	4×10^8
Supernatant from BSA panning	1×10^9
CLEC2D binders	4×10^6

[597] Single colony from the TG1 bacterial plate was inoculated into 20 ml LB medium at 37°C until OD600 reaches ~ 0.9. 200 µl of the precipitated panned phage suspension was inoculated into 2 ml TG1 cells (in 10 different tubes and each tube contains 2-5 ml of TG1 cells)

followed by incubating the mixture at 37°C with shaking for 1 hour. Volume in each tube was diluted into 10 ml LB medium containing 25 µg/ml Ampicillin. Following additional 2 hours of incubation at 37°C with shaking at 220 rpm, ampicillin concentration was increased to a final concentration of 100 µg/ml and incubated further for 30 minutes to 100 min. Bacterial culture was spun down at 10,000 g for 10 minutes, and the pellet was used for DNA isolation through Qiagen midi prep as per manufacturer's protocol for further use.

[598] Construction of heavy and light chain libraries in to yeast shuttle vectors in Fab format:

[599] Isolated replicative form DNA of panned molecules along with the in-house yeast expression vector pZB003 (MTCC 25127) designated for light chain incorporation are digested with HindIII and AscI followed by ligation and transformation individually into TG1, highly competent cells. Likewise, heavy chain pool (sourced from isolated replicative form) and the respective vector pZB002 (MTCC 25126) are digested with NcoI and NotI followed by ligation and transformation into TG1, highly competent cells. Transformation efficiency obtained for both heavy and light chain panned library are $>10^7$ cfu. Obtained transformed colonies for both heavy and light chain libraries are checked for insert release using NcoI/NotI for heavy chain (FIG. 4B) and HindIII/AscI for light chain (FIG. 4C) before they are scraped for glycerol stock preparation. Insert release for both the chains confirmed the presence of panned variable heavy and light chain-kappa molecules. Glycerol stocks are stored at -80°C for future use. Tables 10, 11 and 12 provide for components applicable in constructing libraries in yeast vectors.

Table 11

Components	Amount/Volume
DNA	20 ug
NcoI	4 uL
NotI	4 uL
CutSmart Buffer	10
Water	Respective Volume
Total	100 uL

Table 12

Components	Amount/Volume
DNA	20 ug
HindIII	4 uL
AscI	4 uL
CutSmart Buffer	10
Water	Respective Volume
Total	100 uL

Table 13

Components	Amount/Volume
Vector	100 ng
Insert	100 ng
T4 DNA ligase	0.5 uL
T4 DNA ligase Buffer	2 uL
Water	Respective Volume
Total	20 uL

[600] Construction of heavy and light chain libraries in to yeast shuttle vectors in ScFv format:

[601] ScFv format comprises of transfer of light chain (kappa repertoire originated from panned phage against CLEC2D antigen) into pZB004.4 vector between NdeI and AscI restriction sites followed by generation of a pool of light chain ScFv library. Subsequently the library was confirmed with restriction digestion confirmation followed by transfer of panned heavy chain pool into ScFv-light chain library between NcoI and NotI restriction enzymes. This final library was used as ScFv library of panned molecules which will be further transformed, sorted and screened in yeast expression system. Isolated replicative form DNA of panned molecules along with the in-house ScFv yeast expression vector are digested with NdeI and AscI followed by ligation and transformation individually into TG1, highly competent cells.

[602] Obtained transformed colonies for light chain libraries are checked for insert release using NdeI/AscI before they are scraped for glycerol stock preparation. Insert release confirmed the presence of panned molecules. Glycerol stocks are stored at -80°C for future use. Plasmid isolation was carried out using Qiagen midi prep kit which will be used for incorporation of heavy chain repertoire obtained from panning.

[603] Likewise, heavy chain pool from isolated replicative form and the ScFv containing light chain library are digested with NcoI and NotI (FIG. 4D) followed by ligation and transformation into TG1, highly competent cells. Transformation efficiency obtained for both heavy and light chain panned library are $>10^7$ cfu. Colonies were confirmed with insert release for both heavy with NcoI/NotI and light chains with NdeI/AscI (FIG. 4E).

[604] Tables 13, 14 and 15 provide for components applicable in constructing libraries in yeast expression vector.

Table 14

Components	Amount/Volume
DNA	20 ug
NdeI	4 uL
AscI	4 uL
CutSmart Buffer	10
Water	Respective Volume
Total	100 uL

Table 15

Components	Amount/Volume
DNA	20 ug
NcoI	4 uL
NotI	4 uL
CutSmart Buffer	10
Water	Respective Volume
Total	100 uL

Table 16

Components	Amount/Volume
Vector	100 ng
Insert	100 ng
T4 DNA ligase	0.5 uL
T4 DNA ligase Buffer	2 uL
Water	Respective Volume
Total	20 uL

[605] DNA isolated in large scale was checked for restriction digestion, before transferred for yeast transformation. Post confirmation through restriction digestion at least 10 independent clones containing variable heavy and light-kappa chains for each of formats were sent for sequencing reactions. The sequencing results have been summarized in terms of productive heavy and light-kappa chains in the following Table 17.

Table 17: summarizes the percentage productivity for variable heavy chain and light-kappa chain as estimated from sequencing reactions carried out from independent clones.

Antigen	Format	Chain Type	Productivity
CLEC2D	Fab	Variable heavy chain pool	81%
		Variable Light chain Pool	80%
	ScFv	Heavy and Light chain repertoire	85%

[606] As detailed above, phage antibody library was panned against the CLEC2D antigen coated beads in order to eliminate non-specific binders. The selected phage particles were used to generate replicative form containing the heavy and light chain repertoire. This method was devoid of any PCR based approached which might introduce unwanted biasness towards the panned pool of molecules. Purified replicative form of DNA was digested and ligated into yeast expression vector in two different plasmid constructs to generate antibody in Fab format and ScFv format, wherein the cloning efficiency was estimated to be >95% and the efficiency of TG1 cells transformation was more than 10^7 cfu. These parameters were essential to meet to ensure complete capturing of panned diversity.

[607] Subsequently, yeast DNA libraries in both formats i.e., ScFv and Fab, were transformed into yeast cells. Transformed yeast cells were checked for heavy chain, light chain and Fab molecule expression. Surface expression of antibody genes were analysed with multiple tags such as FLAG, c-Myc and $(His)_6$-tag and V5-tag for heavy chains and light chains, respectively. Flow cytometry based sorting was carried out to isolate yeast cells expressing antibody sequences showing specific antigen binding ()). Flow sorting of yeast cell populations were repeated 2-3 times to enrich antibody clones with higher affinity towards labelled CLEC2D antigen.

[608] Generation of yeast ScFv library

[609] EBY100 strain (S. cerevisiae cells) was grown for overnight in to 5 ml YPD media on a platform shaker at 220 rpm and 30°C. The next morning, an aliquot of the overnight culture was inoculated into 100 ml YPD media at OD600 ~0.3. The inoculated cells continued to grow on a platform shaker at 30°C and 220 rpm until OD600 reached to ~1.6 (usually after 5 hours - 6 hours). Yeast cells were collect by centrifugation at 3000 rpm for 3 minutes and the media was removed. The cell pellet was washed twice with 50 ml ice cold water and once by 50 ml of ice cold electroporation buffer (1 M Sorbitol / 1 mM CaCl2). The yeast cells were condition by re-suspending the cell pellet in 20 ml (0.1 M LiAc/10 mM DTT) and shaking at 220 rpm in a culture flask for 30 minutes at 30°C. The conditioned cells were collected by centrifugation, washed once with 50 ml ice-cold electroporation buffer and re-suspended the cell pellet in 100 µl to 200 µl electroporation buffer to reach a final volume of 1 ml.

[610] This corresponds to approximately 1.6×10^9 cells/ml and is sufficient for 2 electroporation reactions of 400 µl each. The cells were kept on ice until electroporation. 400 µl electro competent cells were gently mixed with required amount of plasmid DNA and transfered to a pre-chilled Bio-Rad GenePulser cuvette (0.2 cm electrode gap) and kept on ice for 5 min until electroporation. The cells were electroporated at 2.5 kV and 25 µF. Electroporated cells were transfered from each cuvette into 8 mL of 1:1 mix of 1 M sorbitol: YPD media, and incubated on a platform shaker at 220 rpm and 30°C for 1 hour. Cells were collected by centrifugation and resuspended in SDCAA media. 10-fold serially diluted cells were prepare from the cell suspension and 100 µl of 10-3 and 10-4 diluted cells were plated onto selective plates (SDCAA plates) and incubated at 30°C incubator for 3-4 days. Library size was determined from the colony counts after 3-4 days (FIG. 5A). After 3-4 days colonies were observed on SDCAA plate. Finally, 20% glycerol stock of the yeast ScFv antibody library was prepared by scrapping yeast cells and stored at -80°C.

[611] Generation of Yeast haploid antibody libraries for the development of Fab antibody library

[612] Transformation was performed according to manufacturer's (Zymo Research) protocol with minor modifications. Briefly, EBY100ura3Δ4.03 strain (*S. cerevisiae* cells) and YVH10 were grown for overnight in 5 ml YPD media on a platform shaker at 220 rpm and 30°C. The OD600 value of overnight culture was checked and the overnight culture was re-inoculated into

50 ml YPD medium with starting OD600~0.4, until OD600 reached ~1.0-1.2 at 30°C, in incubator shaker with 220 rpm. Yeast cells were collected by centrifugation at 3000 rpm for 3 minutes and the media was removed. Cell pellet was washed with 10 ml EZ1 solution followed by centrifugation at 3000 rpm for 10 min. Then, cell pellet was resuspended in to 600 µl of EZ2 solution and further incubated at RT for 5 min. 200 µl of EZ2 solution containing competent yeast cells was mixed with appropriate amount of plasmid DNA and 500 µl of EZ3 solution. Above mix of competent yeast cells and DNA was incubated at 30°C for 1 hr and 30 min. The yeast cells were centrifuged at 2400 rpm for 5 min. 200 µl of the supernatant was discarded and the cell pellet resuspended in the remaining supernatant.

[613] 10-fold serially diluted cells from the cell suspension was prepared and 100 µl of 10-3 diluted cells was plated on selective plates and incubated at 30°C incubator for 3-4 days. EBY100ura3Δ4.03 transformed with heavy chain antibody library was selected on tryptophan drop out glucose medium. However, YVH10 strain with light chain antibody library was selected on uracil drop out medium. Library size was determined from the colony counts after three days and estimated to be ~10^5. (FIG. 5A) 20% glycerol stock of the haploid yeast antibody libraries was prepared and stored at -80°C.

[614] Generation of diploid yeast Fab library through yeast mating

[615] The two haploid yeast strains with heavy and light chain libraries having different mating types were scraped with amino acid drop out glucose media. OD600 of the both haploid cell cultures was checked. About 1 OD600 of each culture was taken in 1.5 ml microfuge tube and spun at 13000 rpm for 3-5 min. Discard the supernatant then added 100 µL of purified water in each pellet and mix them together. Plated mixed yeast cultures onto YPD plate and incubated for 5-6 hrs at 30°C. Yeast cells from the YPD plate after 5-6 hrs were scraped and OD600 of the scraped yeast cells was monitored. The scraped culture were inoculated into ura trp double drop out glucose media with starting OD600 of 0.1 and incubated for at least 24 hrs at 30°C, 220rpm (for diploid enrichment).

[616] OD600 of enriched diploid culture was monitored and dilutions were prepared from enriched culture containing approximately 500 and 1000 cells. The dilutions were plated onto single and double drop out amino acid glucose agar plates and incubated at 30°C for 2-3 days. Diploid library was selected on ura trp double drop out glucose plate. 20% glycerol stock of the remaining enriched diploid culture was prepared and stored at -80°C. Percentage mating

efficiency was calculated as the number of diploid colonies grown in the double drop out media plates divided by the number of total colonies grown in the single drop out plates. Yeast fab antibody library was generated through yeast mating (FIG. 5C).

[617] Flow sorting of Yeast Fab and ScFv library

[618] The yeast samples were inoculated into 3 ml of SDCAA media and incubated yeast cell for overnight at 30°C, 220 rpm. Next day, the OD600 value of the inoculated cultures was monitored by diluting of 1:10. 0.3 OD600 cells of the yeast samples was inoculated into 20 ml 2x SGCAA media and incubated for 48 hrs in incubator shaker at 20°C, at 220 rpm. The OD600 of the induced culture was monitored by diluting 1:10 after 48 hrs. About 0.1 OD600 cells was taken from grown yeast cultures into 1.5 ml tube and spun at 13,000 rpm for 2 minutes. The supernatant was discarded and the pellet was washed by adding 100 µl of 1X PBS and 242pun at 13,000 rpm for 2 minutes. The supernatant was discarded again. 200 µl of primary antibody or biotinylated antigen with an appropriate concentration was added in yeast cell pellet and incubated for 45 min on rotation at RT. After incubation, the cells were spun at 13,000 rpm for 2 min and the supernatant was discarded. Cell pellet was washed twice by adding 200 µl of PBS containing 0.1% BSA and spun at 13,000 rpm for 2 minutes and the supernatant was discarded. 200 µl of secondary antibody with an appropriate concentration was added in to yeast cell pellet and incubated for 30 min on ice. After incubation, the cells were spun at 13,000 rpm for 2 minutes and the supernatant was discarded. The pellet was washed thrice by adding 200 µl of 1X PBS containing 0.1% BSA and spun at 13,000 rpm for 2 minutes. 300 µL of 1X PBS was added in yeast cell pellet and samples were analysed through flow sorter (FIGS. 5D and 5E). Concentrations for primary, secondary antibodies and biotinylated antigen are presented in Table 18.

Table 18

Expression of library		
Format of antibody library	Primary antibody (Concentration)	Secondary antibody (Concentration)
ScFv	Myc Tag polyclonal (5µg/ml)	Goat anti-Chicken IgY (H+L) Secondary Antibody, Alexa Fluor 488 (5µg/ml)

Fab	V5 Tag (5µg/ml)	Goat anti-Chicken IgY (H+L) Secondary Antibody, Alexa Fluor 488 (5µg/ml)
Binding of library		
Format of antibody library	Primary antibody (Concentration)	Secondary antibody (Concentration)
ScFv	Biotinylated ZM008 antigen (250 nM for flow resort-1, 100 nM for flow sort-1, 50 nM for flow resort-2,)	Streptavidin, Alexa Fluor™ 633 conjugate (5µg/ml)
Fab	Biotinylated ZM008 antigen (250 nM for flow resort-1, 100 nM for flow sort-1, 50 nM for flow resort-2,)	

[619] Individual clone screening from sorted/resorted ScFv or sorted/resorted Fab pool

[620] Similar flow staining protocol was used as discussed during flow sorting for individual clone screening. About 1000 colonies were screened through flow cytometry for expression and antigen binding (FIGS. 5F, 5G, and 5H). These clones were selected on the basis of >2% and >5% positive for both binding and expression in case of Fab and ScFv clones respectively.

[621] In addition selected pool of antibody genes as obtained from sorting against soluble CLEC2D antigen were subjected for next generation sequencing. This exercise was carried out for both ScFv and Fab format of antibody gene pools. As exemplified, Seq IDs SEQ ID 44; SEQ ID 45; SEQ ID 42; SEQ ID 1; SEQ ID 73; SEQ ID 21; SEQ ID 35; SEQ ID 58; SEQ ID 7; SEQ ID 260; SEQ ID 261; SEQ ID 258; SEQ ID 217; SEQ ID 289; SEQ ID 237; SEQ ID 251; SEQ ID 274; SEQ ID 223 were enriched at the final sorted round ranging from 2.5 fold to 7 fold, as applicable to clones screened in Fab format, while the clones screened in ScFv format were enriched to fold ranging from 2 fold to 106 fold, to an approximate. The fold enrichment estimation was carried out through number of gene copies seen at every round of sorting. This further supports the fact that antibodies against CLEC2D antigen were screened, isolated and identified via a robust platform comprising naïve antibody library screened phage and yeast display technologies.

[622] Finally, individual yeast clones were identified using flow cytometry assays. Subsequently, peer group antibody gene sequencing was carried out and novel antibody

sequences were taken for further cloning to mammalian gene expression vectors. Yeast plasmid DNA was isolated from selected yeast clones, existing in both Fab or ScFv formats, using Zymoprep Yeast Plasmid miniprep kit-The variable region of heavy and light chains in selected yeast clones with Fab format were amplified using vector specific primer followed by sequencing. While for clones in ScFv format, isolated plasmids from yeast colonies were subsequently transformed into NEB-alpha cells for larger production. The isolated plasmids from NEB-alpha cells were sent for sequencing confirmation. FIG. 5H summarizes percentage binding of monoclonal antibody clones with CLEC2D antigen, as determined by flow cytometry. The data suggest at least about 80% of the monoclonal antibody clones revealed detectably and specifically binding to CLEC2D antigen.

[623] All sequence identifiers and relevant sequence identity analysis are described in Table 19, which lists antibody clones for variable heavy chains, and Table 20, which lists antibody clones for variable kappa light chains.

Table 19. SEQ ID NOs of VH Sequences of Anti-CLEC2D

% Sequence Identity	Variable heavy chain Sequence ID NOs
35%-40%	SEQ ID NO: 33; SEQ ID NO: 34; SEQ ID NO: 87; SEQ ID NO: 82; SEQ ID NO: 104
40%-45%	SEQ ID NO: 11; SEQ ID NO: 35; SEQ ID NO: 86; SEQ ID NO: 22; SEQ ID NO: 69; SEQ ID NO: 41; SEQ ID NO: 3; SEQ ID NO: 66; SEQ ID NO: 37; SEQ ID NO: 56; SEQ ID NO: 21; SEQ ID NO: 38; SEQ ID NO: 90; SEQ ID NO: 100; SEQ ID NO: 18; SEQ ID NO: 20; SEQ ID NO: 83; SEQ ID NO: 1; SEQ ID NO: 19
45%-50%	SEQ ID NO: 105; SEQ ID NO: 101; SEQ ID NO: 4; SEQ ID NO: 72; SEQ ID NO: 28; SEQ ID NO: 64; SEQ ID NO: 25; SEQ ID NO: 60; SEQ ID NO: 55; SEQ ID NO: 52; SEQ ID NO: 27; SEQ ID NO: 43; SEQ ID NO: 70; SEQ ID NO: 71; SEQ ID NO: 14; SEQ ID NO: 85; SEQ ID NO: 13; SEQ ID NO: 61; SEQ ID NO: 42; SEQ ID NO: 39; SEQ ID NO: 10; SEQ ID NO: 49; SEQ ID NO: 24; SEQ ID NO: 40; SEQ ID NO: 63; SEQ ID NO: 78; SEQ ID NO: 2; SEQ ID NO: 94; SEQ ID NO: 5

50%-55%	SEQ ID NO: 97; SEQ ID NO: 16; SEQ ID NO: 76; SEQ ID NO: 9; SEQ ID NO: 89; SEQ ID NO: 107; SEQ ID NO: 68; SEQ ID NO: 29; SEQ ID NO: 67; SEQ ID NO: 74; SEQ ID NO: 32; SEQ ID NO: 81; SEQ ID NO: 106; SEQ ID NO: 31; SEQ ID NO: 62; SEQ ID NO: 48; SEQ ID NO: 75; SEQ ID NO: 12; SEQ ID NO: 102; SEQ ID NO: 54; SEQ ID NO: 80; SEQ ID NO: 26; SEQ ID NO: 30; SEQ ID NO: 92; SEQ ID NO: 108; SEQ ID NO: 79
55%-60%	SEQ ID NO: 45; SEQ ID NO: 15; SEQ ID NO: 51; SEQ ID NO: 44; SEQ ID NO: 73; SEQ ID NO: 36; SEQ ID NO: 77; SEQ ID NO: 50; SEQ ID NO: 6
60%-80%	SEQ ID NO: 9; SEQ ID NO: 53; SEQ ID NO: 95; SEQ ID NO: 23; SEQ ID NO: 103; SEQ ID NO: 7
80%-90%	SEQ ID NO: 57; SEQ ID NO: 91; SEQ ID NO: 98; SEQ ID NO: 84; SEQ ID NO: 58; SEQ ID NO: 88; SEQ ID NO: 96; SEQ ID NO: 47; SEQ ID NO: 17; SEQ ID NO: 8
90%-99%	SEQ ID NO: 46; SEQ ID NO: 65; SEQ ID NO: 59; SEQ ID NO: 99

Table 20. SEQ ID NOs of VL Sequences of Anti-CLEC2D

% Sequence Identity	Variable kappa light chain Sequence IDs
50%-60%	SEQ ID NO: 282; SEQ ID NO: 308; SEQ ID NO: 287; SEQ ID NO: 321; SEQ ID NO: 236; SEQ ID NO: 265; SEQ ID NO: 270; SEQ ID NO: 275; SEQ ID NO: 306; SEQ ID NO: 296; SEQ ID NO: 241; SEQ ID NO: 314; SEQ ID NO: 223
60%-65%	SEQ ID NO: 254; SEQ ID NO: 289; SEQ ID NO: 238; SEQ ID NO: 268; SEQ ID NO: 248; SEQ ID NO: 284; SEQ ID NO: 244; SEQ ID NO: 310; SEQ ID NO: 243; SEQ ID NO: 285; SEQ ID NO: 220; SEQ ID NO: 255; SEQ ID NO: 293; SEQ ID NO: 298; SEQ ID NO: 235; SEQ ID NO: 319; SEQ ID NO: 245; SEQ ID NO: 224; SEQ ID NO: 291; SEQ ID NO: 277; SEQ ID NO: 232
65%-70%	SEQ ID NO: 307; SEQ ID NO: 262; SEQ ID NO: 253; SEQ ID NO: 276; SEQ ID NO: 323; SEQ ID NO: 234; SEQ ID NO: 261; SEQ ID NO: 312; SEQ ID NO: 290

70%-75%	SEQ ID NO: 259; SEQ ID NO: 239; SEQ ID NO: 281; SEQ ID NO: 228; SEQ ID NO: 217; SEQ ID NO: 227; SEQ ID NO: 251
75%-80%	SEQ ID NO: 231; SEQ ID NO: 250; SEQ ID NO: 260; SEQ ID NO: 226; SEQ ID NO: 271; SEQ ID NO: 256; SEQ ID NO: 272; SEQ ID NO: 278; SEQ ID NO: 302; SEQ ID NO: 320; SEQ ID NO: 295; SEQ ID NO: 292; SEQ ID NO: 229; SEQ ID NO: 264; SEQ ID NO: 252; SEQ ID NO: 267; SEQ ID NO: 304; SEQ ID NO: 300; SEQ ID NO: 311; SEQ ID NO: 324
80%-85%	SEQ ID NO: 222; SEQ ID NO: 258; SEQ ID NO: 219; SEQ ID NO: 313; SEQ ID NO: 294; SEQ ID NO: 303; SEQ ID NO: 317; SEQ ID NO: 273; SEQ ID NO: 266; SEQ ID NO: 315; SEQ ID NO: 257; SEQ ID NO: 288; SEQ ID NO: 301; SEQ ID NO: 221; SEQ ID NO: 240; SEQ ID NO: 299; SEQ ID NO: 247; SEQ ID NO: 263; SEQ ID NO: 274
85%-99%	SEQ ID NO: 218; SEQ ID NO: 249; SEQ ID NO: 230; SEQ ID NO: 279; SEQ ID NO: 316; SEQ ID NO: 237; SEQ ID NO: 322; SEQ ID NO: 225; SEQ ID NO: 318; SEQ ID NO: 233; SEQ ID NO: 305; SEQ ID NO: 280; SEQ ID NO: 283; SEQ ID NO: 242; SEQ ID NO: 286; SEQ ID NO: 297; SEQ ID NO: 309; SEQ ID NO: 246

[624] Example 3: Antibody sequence analysis to identify novel antibody clones

[625] Variable regions of isolated antibodies for both heavy and light chains that specifically bind the CLEC2D antigen comprise of six hyper variable regions: 3 hyper variable regions from light chain (CDRL1, CDRL2, and CDRL3) and 3 hyper variable regions from heavy chain (CDRH1, CDRH2, and CDRH3). The length of the hypervariable regions may vary significantly, as shown for CDRH3, whose lengths have significant representation in the pool, ranging from 4-23 amino acids. The amino acid compositions were measured at every heavy chain CDRH3 length to understand the sequence variability of selected antibody genes against CLEC2D (FIGS. 6A, 6B, 6C, and 6D).The antibody sequences were analysed to determine uniqueness. Multiple sequence alignment tools were used to compare the antibody gene sequences with published antibody sequences in databases like IMGT, IgBLAST etc.

[626] Further analysis of selected sequences identified antibody genes with de-amidation motifs, isomerization motifs, proteolytic cleavage motifs, N-linked glycosylation sites, plastic

binding motifs, streptavidin binding motifs, human Fc binding motifs, mouse IgM binding motifs, bovine IgG motifs, proline rich motifs and cysteine rich motifs, etc. Such antibody genes were not deemed suitable for therapeutic monoclonal antibody development and therefore were not considered for further evaluation. Based on the extend of binding observed for antibody genes against soluble CLEC2D antigen at the level of individual yeast colony screening, top 40 binders, not limited to, were of further interest towards subsequent development. Only confirmed antibody gene sequences were taken for further cloning, expression and characterization.

[627] Example 4: Cloning of novel antibody genes

[628] Error free antibody variable heavy and variable light chain regions were subsequently cloned into mammalian expression vectors, having various isotype backbones, either wildtype or mutants, originated from human, mouse and cynomolgus monkey species. Table 21 below summarizes relevants vectors developed towards cloning of identified anti CLEC2D antibody genes and deposited to Microbial Type Culture Collection and Gene Bank (MTCC), India.

Table 21

S. No.	Taxonomic Designation	Identification Reference	MTCC Number Assigned
1	*E.coli*	pZB005	MTCC 25356
2	*E.coli*	pZB006	MTCC 25357
3	*E.coli*	pZB007	MTCC 25358
4	*E.coli*	pZB008	MTCC 25359
5	*E.coli*	pZB009	MTCC 25360
6	*E.coli*	pZB010	MTCC 25361
7	*E.coli*	pZB011	MTCC 25362
8	*E.coli*	pZB012	MTCC 25363
9	*E.coli*	pZB013	MTCC 25364
10	*E.coli*	pZB014	MTCC 25365

[629] As exemplified by, the mammalian expression vectors pZB007 (MTCC 25358) & pZB008 (MTCC 25359) were designated and used for variable heavy chain and light chain gene cloning, respectively (FIGS. 7A and 7B). The vectors were custom designed and synthesized for the expression of antibody genes under the control of suitable promoter sequences. The plasmids carry a kanamycinR / puromycinR cassette driven by strong promoter and high-copy-number ColE1/pMB1/pBR322/pUC origin of replication for propagation (FIGS. 7A and 7B).

[630] Sequence confirmed selected plasmids, as screened through phage and yeast display platform, against soluble CLEC2D antigen, using human naïve antibody library, were used as template for subsequent PCR amplification. PCR reactions were performed using sequence specific primers to amplify the selected clones having variable heavy and light chain regions. PCR reactions was carried out on an Eppendorf™ Mastercycler™ pro PCR System in 50 µL mixture volume consisting of 0.2 µM of each primer (Eurofins, India), 200 units of Phusion polymerase (NEB). Following an initial denaturation at 94 °C for 3 min, 30 cycles of 30 seconds denaturation at 94 °C, and 50 seconds annealing at 60 °C, 10 seconds primer extension at 72 °C, 10 minutes final extension at 72 °C were performed. The PCR amplified product was extracted using QIAquick Gel Extraction kit. The plasmid vector pZB007was linearized through restriction enzyme digestion by *AscI* and *XbaI* and for pZB008with *EcoRI* and *AscI*. The inserts fragment and linearized vector were gel extracted using QIAGEN kit (20021).These purified vector and insert were used for recombination using Infusion HD Cloning kit (Takara, USA). Transformation of infusion reaction mixture into bacterial cells were performed. 100 µL aliquot of competent *E.coli* cells (Stellar) were taken from –80ºC freezer, thawed on ice for 5 minutes. 50% of recombination sample were added to the competent cells and gently mixed, incubated on ice for 20 minutes. Heat shock was given at 42˚C for 50 seconds in a dry bath. The vials were quick chilled on ice for 2 minutes. 0.950 mL of LB broth pre-warmed at 37ºC was added and incubated at 37ºC, 220 rpm for 1 hour, in shaker incubator. 100 µL of the resulting culture was plated on LB agar media with kanamycin and incubated for overnight at 37 ºC.

[631] Transformants containing specific DNA plasmid were inoculated in 5 mL of LB broth with Kanamycin and were incubated at 220 rpm, at 37 ºC for overnight. Plasmid DNA was isolated from overnight grown culture using QIAGEN kit. Isolated clones were screened through restriction enzyme analysis performed using *SpeI* and *XhoI* enzymes and confirmed through sequencing and found to be error free. Sequence confirmed plasmid DNA from confirmed clones were purified at large scale using QIAprep Spin Midiprep kit (Qiagen) and in order to be used for subsequent transfection experimentation.

[632] Example 5: Preparation of anti-CLEC2D antibody and Selection of CHO expressed novel monoclonal antibodies

[633] Strategy to select novel monoclonal antibody clones

[634] Owing to riveting design and properties of therapeutic antibody, it is required to be rational towards selecting a specific monoclonal antibody for further development. Moreover, generation, manufacturing and storage of antibodies are continuing to pose challenges as molecule properties such as pharmacokinetics, solubility, expression, viscosity and long-term stability are difficult to predict and understanding inter-parameter relationship is rather limited. Moreover considering the selected/identified diverse antibody genes which funnelled through antibody display platforms needed to be arranged through the ranking protocol. A comprehensive scoring function/methods was employed/developed based on existing sequencing data, exemplified by uniqueness, presence of certain motifs which could be not beneficial for further selection/development of clones; affinity towards CLEC2D antigen either in soluble form or as membrane bound format, and functionality; titre, yield, recovery, analytical profile, amongst others, either as independent or in combination, thereof.

The clones would go through multiple rounds of checks on salient parameters in due course of development having a dynamic selection system which will effectively be employed towards selection of final clones.

[635] CHO cell transfection with full length CLEC2D gene for cell surface expression.

[636] In order to estimate the binding propensity of novel antibody genes identified against CLEC2D protein expressed on cell surface, a full length CLEC2D construct was synthesized. Native signal sequence was used for efficient surface expression on CHO cells. The full length CLEC2D gene sequence was cloned into the pCDNA3.1 mammalian expression vector (FIG. 8A). Subsequently the construct was transformed into neb-alpha and isolated in large quantity using Qiagen midi prep kit. CHO suspension cells with >90% viability were transfected with a full-length CLEC2D gene expression plasmid. As exemplified, for 10ml volume of transfection 1.25 $X10^6$ cells/ml were taken, wherein CHO cells were centrifuged at 1000-1400 rpm for 4-5 minutes. The spent media was decanted, and the cells were re-suspended in 2.5 ml of OptiMEM I media. DNA constructs were transfected using Lipofectamine LTX with Plus™ reagent. 5-10 µg of DNA was used with 1:3 to 1:6 DNA to transfection reagent ratio and 5-10 µl Plus™ reagent was used. DNA and Lipofectamine LTX complex was prepared in 2.5 ml OptiMEM I and incubated at 20-25°C for 5 minutes for complex formation. The transfection mix was added slowly to the cell suspension. The cells were incubated for 4-6 hours at 37°C in a 5% CO_2 shaker incubator at 100-120 RPM. 5 ml of Power CHO2 CD growth media was added to the cells. The

cells were incubated at 37°C in a 5% CO_2 shaker incubator at 100-120 RPM. 2-4 days post transfection 2 ml Power CHO2 CD growth media was added and Glutamax was added from 200 mM stock to achieve a final concentration of 2 mM. The cells were incubated at 37°C in a 5% CO_2 shaker incubator at 100-120 RPM. Cells were analyzed for surface antigen binding by flow-cytometry on day 3, day 4 and day 5 after transfection. Transfected CHO cells with full length constructs will be known here onwards as C4548, unless mentioned otherwise elsewhere.

[637] C4548 cells, transiently expressing full-length membrane anchored CLEC2D antigen were validated through both flow cytometry and confocal microscopy by using commercial anti CLEC2D antibody. Approximately, 50,000-100,000 cells were taken in a 96-well U bottom plate. 1-5 µg of commercial anti- CLEC2D Antibody (4C7) (Cat # H00029121-M01;Novus Biologicals) in 100 µl assay buffer was added to the both untransfected CHO and C4548 transfected with full length CLEC2D surface antigen construct and incubated for 1 hr at room temperature in DPBS with 1-2 % BSA. After 1 hr incubation, the plate was centrifuged at 1000-1400 rpm for 3-5 minutes. The cells were further washed twice with 200 µl of 0.1% BSA solution. 1 in 100 dilution of secondary antibody i.e., anti-mouse Alexa 488 (Thermo Fisher Scientific) was added. Subsequently, the plates were incubated at room temperature for 30 minutes in dark. The wells were washed twice with 0.1% BSA solution and analyzed by flow cytometry. Cell surface binding of the monoclonal antibody was estimated by comparing increase in fluorescence signal between CLEC2D expressing CHO cells and un-transfected CHO cells. Surface expression of CLEC2D antigen was optimum on day 4 to day 5 on C4548 transfected CHO cells (FIG. 8B).

[638] For confocal microscopy experimentation, 250 µl of 12 µg/ml Poly D Lysine was added per well and incubated overnight at 37°C. Chambers were washed twice with 500µl of DPBS and stored in 2 °C to 8 °C. Un-transfected and CLEC2D antigen expressing CHO cells, C4548, were used, wherein cell count and viability data was collected using vi-cell Beckman coulter. 50,000 cells were seeded in 500 µl growth media (Power CHO2 with 4mM Glutamine+1% Penstrep) with 10% FBS per well. All the cells were incubated in humidified 5% CO2 incubator at 37°C for 2 days prior to the experiment. Further, cells were washed with 1X PBS then fixed in 2% formaldehyde in PBS for 5 minutes at room temperature (RT). Cells were then rinsed twice with 1X PBS followed by blocking with 5%BSA for 1hr at RT. After 1hour incubated with diluted primary antibody i.e., anti- CLEC2D Antibody (4C7) (2µg) for 1hour at RT followed by washing

for at least three times in PBS and then incubated with the anti-mouse Alexa 488 (Thermo Fisher Scientific), secondary antibody, (2μg) for 1 hour at RT. Cell nuclei were stained using DAPI (1:1000 for 5 min at RT). Cells were then rinsed thrice in 1X PBS and remained submerged in PBS until imaging. Immunofluorescence microscopy was performed on Olympus FV3000- 4 laser scanning confocal microscope with a 60 X magnification with 1.35-NA objective. Cells were imaged at 16 hrs after treatment by using appropriate wavelengths (For DAPI, λex 405 nm and λem 430-470 nm; for Alexa 488, λex 488 nm and λem 510-530 nm. Images were analyzed with Fiji ImageJ software.

As confirmed by microscopy images, the surface expression of CLEC2D on C4548 cells, were observed as distributed on cell surface while untransfected CHO cells fails to provide any anti-CLEC2D antibody dependent signal under microscopy (FIG. 8C).

[639] CHO cell transfection to express novel anti-CLEC2D monoclonal antibody clones

Antibody heavy chain and light chain genes were expressed using mammalian gene expression vectors with appropriate signal sequences for secretion of correctly folded monoclonal antibodies into culture media. CHO suspension cells at more than 90% viability were transfected for antibody gene expression. CHO cells, at 1.25 x10^6 cells/ml, were centrifuged at 1000-1400 rpm for 4-5 minutes. The spent media was decanted. The cells were re-suspended in 25 ml of OptiMEM I media. Antibody heavy chain and light chain gene expressing plasmids were co-transfected at various stoichiometry (such as, 1:2, 1:3, 1:4 , 2:3, 3:1, 4:1 etc.) using Lipofectamine LTX with Plus™ reagent. 50-100 μg of DNA was used with 1:3 to 1:6 DNA to transfection reagent ratio and 50-100 μl Plus™ reagent. DNA and Lipofectamine LTX complex was prepared in 25 ml OptiMEM I and incubated at 20-25°C for 5 minutes for complex formation. The transfection mix was added slowly to the cell suspension. The cells were incubated for 4-6 hours at 37°C in a 5% CO_2 shaker incubator at 100-120 RPM. 50 ml of Power CHO2 CD growth media was added to the cells. The cells were incubated at 37°C in a 5% CO_2 shaker incubator at 100-120 RPM. 2-4 days post transfection 20 ml Power CHO2 CD growth media was added, and Glutamax was added from 200 mM stock to achieve final concentration of 2mM. The cells were incubated at 37°C in a 5% CO_2 shaker incubator at 100-120 RPM. Day 6 post transfection, cell culture supernatant (50 mL) was harvested by centrifugation at 1400-2000 rpm for 10-15 minutes.

[640] Screening of CHO expressed monoclonal antibodies using cell surface binding: transient

[641] Subsequently, harvested culture supernatant of 50 mL containing secreted novel anti CLEC2D antibody clones were subjected to purification by Protein A affinity chromatography using cellgravity columns containing Mabselect SuRe resin (GE Healthcare). The method starts with Protein A column sanitization step wherein 3 Column Volume (CV) of 0.5M Sodium Hydroxide (NaOH) solution was passed at RT for 5 minutes followed by 8 Column Volume of Purified water. Subsequently, Protein A column was equilibrated with 3 CV of Protein A equilibration buffer comprises of 30 mM Sodium phosphate, 120 mM NaCl pH 7.0±0.2. 50 mL culture supernatant was loaded on equilibrated Protein A column while flow through was reloaded. This procedure was repeated twice. 3 CV of Protein A equilibration buffer washing was carried out followed by 3 CV of Protein A high salt buffer (30mM Sodium phosphate, 1M NaCl pH 7.0±0.2) wash.

[642] Further 3 CV of Protein A equilibration buffer was passed through the column followed by 4 CV of Protein A low pH buffer (30mM Sodium phosphate, 50mM NaCl pH 6.0±0.2) wash. Next, 5 CV of Protein A elution buffer (30mM Sodium phosphate, 50mM NaCl pH 3.0±0.1) was employed in order to elute the bound monoclonal anti CLEC2D antibody. Further, Protein-A elute, containing antibody, was neutralized to pH ~7.0 by adding appropriate amount of 1M Tris solution.

[643] Following neutralization, Protein-A elute was concentrated and buffer exchanged into 1X PBS using Amicon 30kDa cut-off concentrator. Protein sample was recovered from concentrator and concentration was measured by A280 using Nanodrop Biophotometer. Proteins were analysed by SDS-PAGE as shown in FIG. 9A, under reducing and non-reducing condition. Subsequently, these protein samples were used for further experimentation.

[644] As judged by quantitation, clones with product yield higher than 100 µg were shortlisted for the SDS-PAGE analysis to check the product quality under reducing and non-reducing conditions. Successively, clones with prominent bands in SDS-PAGE gels, as explained by, appearance of ~150kDa under non-reducing condition and ~50kDa (representing heavy chain) and ~25kDa (representing Light chain) under reducing condition were shortlisted for further analysis (FIG. 9A). In addition, purity was also judged through number of bands appeared along with the target protein and were also considered as criteria for selecting/shortlisting the clones. Proteins with more than 3 bands under non-reducing conditions similarly proteins with more

than 1 band for heavy chain or light chain under reducing conditions were not taken into consideration.

[645] Cell surface binding assay: through Flow cytometry and Confocal Microscopy

[646] CHO suspension cells transiently expressing full-length membrane anchored CLEC2D antigen were used to screen antibody samples (cell culture supernatant and/or purified protein). 50,000-100,000 cells were taken in a 96-well U bottom plate. 100 µl of cell culture supernatant or 0.03-3 µg of purified antibody in 100 µl assay buffer was added to the CLEC2D expressing cells and incubated for 1 hr at room temperature in DPBS with 1-2 % BSA. After 1 hr incubation, the plate was centrifuged at 1000-1400 rpm for 3-5 minutes. The cells were further washed twice with 200 µl of 0.1% BSA solution. 1 in 100 dilution of secondary antibody - goat anti human IgG FITC was added. Subsequently, the plates were incubated at room temperature for 30 minutes in dark. The wells were washed twice with 0.1% BSA solution and analyzed by flow cytometry. Commercially available anti-CLEC2D monoclonal Ab (Novus Biologicals) was used as a positive control and anti-mouse Alexa 488 (Thermo Fisher Scientific) was used as the secondary antibody. Cell surface binding of the monoclonal antibody was estimated by comparing increase in fluorescence signal between CLEC2D expressing CHO cells and un-transfected CHO cells.

[647] In order to screen identified novel anti CLEC2D monoclonal antibody, validated C4548 cells and PC3 cells were subjected for monitoring CLEC2D antigen binding through both flow cytometry and confocal microscopy. Prior to experimentation, cell count was taken by Vi-cell XR automated cell counter. Method of sample preparation for flow cytometry was as described above while ~1-5 µg of purified Anti CLEC2D antibody clones and reference positive control, respectively, to estimate the membrane bound CLEC2D binding on Untransfected CHO cells and C4548 cells. Cells were centrifuged at 1400-1500 rpm for 4-5 minutes. The pellet was re-suspended in 1ml DPBS. 50,000 cells were aliquoted in each well of a 96 well plate. Both test samples and reference control was added to each well and incubated for 30-60 minutes at room temperature (25^{0}C). The plate was centrifuged at 1400-1500 rpm for 4-5 minutes, the supernatant was aspirated and cells were washed with 0.1% BSA in DPBS. 2.5 ml of 2% BSA was diluted to 50 ml with DPBS. Goat anti human IgG FITC conjugate was used as secondary antibody. 1:100 dilution of secondary antibody was prepared in DPBS and 100 µl was added to each well. The plate was incubated for 30 minutes at room temperature (25^{0}C) in dark. The cells were washed

with 0.1% BSA and re-suspended in 100 µl of 1% BSA. Samples were analyzed by flow-cytometry (FIG. 9B).

[648] Binding of test sample supernatant on un-transfected CHO cells was estimated and used for calculation of specific binding on C4548 cell surface using following formula:

$$\text{Fold change in MFI} = \frac{\text{Median FITC-A of test sample on CHO cells}}{\text{Median FITC-A of test sample on C4548 cells}}$$

[649] For microscopy experimentation, PC3 cells were seeded, wherein, 250 µl of 12 µg/ml Poly D Lysine was added per well and incubated overnight at 37°C. Chambers were washed twice with 500 µl of DPBS and stored in 2°C to 8°C. Adherent cell lines such as PC3, were trypsinized using 0.05% trypsin. Cell count and viability data was collected with hemocytometer using trypan blue staining. Cells were seeded at a density of 20000 cells/well with 500 µl growth media per well and incubated in humidified 5% CO2 incubator at 37°C for 2 days prior to the experiment. Further, PC3 cells were washed with 1X PBS then fixed in 2% formaldehyde in PBS for 5 minutes at RT. Cells were then rinsed twice with 1X PBS followed by blocking with 5%BSA for 1 hour at RT.

[650] After 1hour incubated with diluted test antibody samples i.e., novel and unique anti-CLEC2D Antibody (at 2µg) and commercial antibody as reference control, for 1hr at RT followed by washing for at least three times in PBS and then incubated with the Alexa Fluor 488 goat anti−human IgG and anti-mouse Alexa 488 (Thermo Fisher Scientific), respectively as applicable, secondary antibody, (at 2 µg) for 1 hour at RT. Cell nuclei were stained using DAPI (1:1000 for 5 min at RT). Cells were then rinsed thrice in 1X PBS and remained submerged in PBS until imaging. Immunofluorescence microscopy was performed on Olympus FV3000- 4 laser scanning confocal microscope with a 60 X magnification with 1.35-NA objective. Cells were imaged at 16 hrs after treatment by using appropriate wavelengths (For DAPI, λex 405 nm and λem 430-470 nm; for Alexa 488, λex 488 nm and λem 510-530 nm. Images were analyzed with Fiji ImageJ software. Variation on CLEC2D antigen binding of mAbs tested and binding data is given as a rating of + (low binding) to +++ (high binding) (Table 19, and FIG. 9C). A variation on surface binding was observed and binding data is given as a rating of + (low binding) to +++ (high binding) on Table 22 As exemplified, surface binding was not detected

with mAbC4252, whereas with antibodyC0610, low binding was observed thereby rated as (+) while other clones have showed differential yet significant surface binding.

Table 22

Sl. No.	Codes	Titer data	Cell surface binding (Flow cytometry)	Imaging
1	C0294	More than 100 µg	5.23	+++
2	C5397	More than 100 µg	4.88	+++
3	C5852	More than 100 µg	5.79	+++
4	C3566	More than 100 µg	10.21	+++
5	C7229	More than 100 µg	4.84	+
6	C2901	More than 100 µg	5.1	+++
7	C4252	More than 100 µg	5.91	Not detected
8	C4577	More than 100 µg	6.73	+++
9	C2685	More than 100 µg	9.78	+++
10	C5355	More than 100 µg	9.9	++
11	C0610	More than 100 µg	8.62	+
12	C8372	More than 100 µg	6.53	+
13	C0694	More than 100 µg	8.43	+++
14	C6525	More than 100 µg	3.27	+
15	C2771	More than 100 µg	7.94	++
16	C0672	More than 100 µg	6.74	+
17	C1063	More than 100 µg	1.96	Not done
18	C4899	More than 100 µg	1.46	Not done
19	C2302	More than 100 µg	7.72	+
20	C3651	10 µg-100 µg	4.73	Not done
21	C6803	More than 100 µg	6.17	Not done
22	C7997	More than 100 µg	4.62	+
23	C2060	More than 100 µg	3.91	+++
24	C0997	More than 100 µg	6.45	+++
25	C2119	More than 100 µg	2.64	++
26	C3482	More than 100 µg	4.17	Not done
27	C9652	More than 100 µg	2.17	Not done
28	C4148	More than 100 µg	6.34	+++
29	C0800	More than 100 µg	7.28	+++
30	C0225	More than 100 µg	5.14	+++
31	C9767	More than 100 µg	4.24	+

32	C9795	More than 100 µg	4.69	+++
33	C5870	More than 100 µg	2.6	+++
34	C7009	More than 100 µg	2.18	+++
35	C8637	10 µg-100 µg	Not done	Not done
36	C5749	10 µg-100 µg	Not done	Not done
37	C3558	10 µg-100 µg	Not done	Not done
38	C5327	10 µg-100 µg	Not done	Not done
39	C4137	10 µg-100 µg	Not done	++
40	C6616	10 µg-100 µg	Not done	+++

[651] Based on all of above mentioned criteria and respective observed results covering biophysical and functional properties of isolated anti CLEC2D antibodies, 9 unique anti-CLEC2D antibody sequences, C5397, C5852, C3566, C2901, C4577, C2685, C0694, C0997, C0800, not limited to, and were selected for stable cell line development.

[652] Generation of stable cell lines

[653] Clinical effectiveness has driven the commercial success of monoclonal antibody (mAb) products. As known to others, mammalian cells are currently the preferred system for large-scale production as the mAbs produced are biochemically similar to human forms. The stable cell line generation process is tedious and time-consuming as clones with high productivity, stable long-term expression and good product quality are rare occurrences. mAb production in mammalian cells can be performed either in transient or stable transfections. As seen in previous section, transient transfections allow relatively fast generation of small amounts of product for use during early stages of drug discovery. However, stably transfected cell lines are more widely used in large scale industrial production. More importantly, stable cell lines used for manufacturing are from a single cell clone in order to obtain high amounts of consistent product.

[654] Antibiotic Selection:

Antibiotic selection was initiated after transfection at 90% cell viability. Cell suspension was centrifuged at 1400 RPM for 4 mins. Pellet was re-suspended in complete Power CHO2 growth

media and concentration of Puromycin Dihydrochloride was adjusted to 2µg /1X10^6 cells. Antibiotic selection was carried out on every 2nd or 3rd day. Refer table 5 for cell count and viability data.

Table 23

Experiment	Viability (%)	Total cells /ml ($x10^6$)	Viable cells /ml ($x10^6$)	Passage No
Transfection R1	95.8	5.42	5.19	35
Antibiotic selection 1 (AB 1)	90.4	3.73	3.37	36
Antibiotic selection 2 (AB 2)	78.7	4.3	3.4	37
Antibiotic selection 3 (AB 3)	82.3	4.4	3.6	38
Antibiotic selection 4 (AB 4)	80.9	4.8	3.9	39
Antibiotic selection 5 (AB 5)	81.8	4.0	3.2	40
Antibiotic selection 6 (AB 6)	77.5	3.9	3.1	41
Antibiotic selection 7 (AB 7)	76.9	4.2	3.2	42
Antibiotic selection 8 (AB 8)	84.5	2.0	1.7	43

[655] Repeat transfection of stable pool

[656] Cell count was taken using Vi-cell XR (Refer Table 10). Cells were subcultured before the transfection. Two more sequential transfections were performed as mentioned previously. On completion of three rounds of transfection the pool was designated as R3 stable pool. See Table 24.

Table 24

Parameters	**Transfection 1**	**Transfection 2**	**Transfection 3**
Total volume of transfection	50 ml	21 ml	21 ml
Cell density	1.25X10^6 cells/ml	1X10^6 cells/ml	1X10^6 cells/ml
OPTIMEM I	12.5ml	1 ml	1ml
Total DNA	25 µg	5 µg	5 µg
HC:LC	1:3	1:3	1:3
Amount of DNA: Lipofectamine	1:3	1:3	1:3
Amount of DNA: Plus reagent	1:1	1:1	1:1

[657] Minipool plating

[658] Minipools were generated by serial dilution method. Continuously growing culture of cell line was subcultured at 0.5 million cells/ml in 30ml complete PowerCHO 2 growth media with 2mM glutamax, 2 days before plating. Cell count and viability data was collected using Vi-cell XR (refer Table 25).

Table 25

Experiment	Viability (%)	Total cells /ml ($x10^6$)	Viable cells /ml ($x10^6$)	Passage No
Minipool plating	97.1	2.5	2.4	50

[659] Serial dilution of the cell suspension was carried out in complete Power CHO2 growth media at 1:10 ratio (refer Table 26). 0.52 ml cell suspension was taken from dilution D and added to 25 ml of cloning media. Cells were seeded at a density of 10 cells/well in a 96 well plate in 200 µl volume per well. These mini-pools were maintained at 37°C temperature in a humidified 5% CO2 incubator.

Table 26

Dilution series	Cell count (cells/ml)	Cell count (cells/ml)
Culture flask	2400000	1370000
Dilution A	240000	137000
Dilution B	24000	13700
Dilution C	2400	1370
Dilution D	240	137

[660] Screening of mini-pools and amplification:

[661] Total 117 mini-pools were screened by flow cytometry and binding to CHO cell surface expressed antigen was estimated. Minipools were ranked based on cell surface binding wherein the method of sample preparation for flow cytometry was as described above while ~200 µl of cell culture supernatant expressing anti CLEC2D antibody proteins and reference positive control, respectively, was used to estimate the membrane bound CLEC2D binding on untransfected CHO cells and C4548 cells (FIG. 10A). Minipools identified from flow cytometry screening, as selected through extend of binding as derived from observed fold change in median fluorescence intensity, were amplified from 96 well plate to 24 well plate and maintained at 37

^{o}C, humidified condition in a 5% CO_2 incubator. These were further amplified from 24 well plate to one well of 6 well plate. After cell were confluent mini-pools were amplified from one well of 6 well plate to a bioreactor tube with 25 ml growth media and maintained at 37 ^{o}C, humidified condition in a 5% CO_2 incubator, 200 rpm.

[662] Single cell cloning

[663] Single cells were generated by serial dilution method. Continuously growing culture of mini-pool was subcultured at 1 million cells/ml in 30ml complete Power CHO 2 growth media with 2 mM glutamax, 1 day before cloning. Cell count and viability data was collected using Vi-cell XR. Serial dilution of the cell suspension was carried out in complete power CHO2 growth media at 1:10 ratio (refer Table 26). Cells were seeded at a density of 0.5 cells/well in a 96 well plate and maintained at 37°C temperature in a humidified 5% CO2 static incubator. Cells were aspirated from dilution D and seeded at density of 0.5 cells/200µl cloning media per well in 96 well plates. The plates were incubated at 37˚C, in a 5% CO2 incubator with 75% relative humidity. Plates were scanned by using CloneSelect Imager (Molecular Devices) for monoclonality report generation from day zero to day ten. The individual well images were collected on day 0, day 1, day 2, day 3, day 6, day 8 and day 10. The clonal population was confirmed from the day zero image of entire well and the monoclonality report generated by CloneSelect Imager. Passage number was P(x+0).The Single cell clones were amplified to 24 well plates after cells were confluent. Passage number was P(x+1).

[664] Screening of single cell clones and clone amplification:

[665] Cell surface binding assay was performed to estimate antibody in cell culture supernatant and to rank the clones. Single cell clones showing higher binding on CHO cell surface expressed antigen were amplified from 24 to 6 well after 2 days. Passage number was (x+2). This was followed by amplification in 3 wells of 6 well plate. Passage number was (x+3). The clones were further amplified to tube bioreactors in 20ml volume, passage number was (x+4). Following amplification RCB vials were prepared for the clones at passage number (x+5).

[666] Stable cell culture supernatant was estimated for binding with CLEC2D surface protein on C4548 cells through flow cytometry, wherein the method of sample preparation and experimentation for flow cytometry was as described above while ~200 µL of cell culture supernatant expressing anti CLEC2D antibody proteins and reference positive control,

respectively, was used to estimate the membrane bound CLEC2D binding on untransfected CHO cells and C4548 cells (FIG. 10B).

Table 27

Experiment	Viability (%)	Total cells /ml (x10^6)	Viable cells /ml (x10^6)	Passage No
Transfection R1	95.8	5.42	5.19	35
Antibiotic selection 1 (AB 1)	90.4	3.73	3.37	36
Antibiotic selection 2 (AB 2)	78.7	4.3	3.4	37
Antibiotic selection 3 (AB 3)	82.3	4.4	3.6	38
Antibiotic selection 4 (AB 4)	80.9	4.8	3.9	39
Antibiotic selection 5 (AB 5)	81.8	4.0	3.2	40
Antibiotic selection 6 (AB 6)	77.5	3.9	3.1	41
Antibiotic selection 7 (AB 7)	76.9	4.2	3.2	42
Antibiotic selection 8 (AB 8)	84.5	2.0	1.7	43
R1 Stable pool Subculture	96.7	2.6	2.5	44
R1 Stable pool Subculture	98.3	3.5	3.4	45
R1 Stable pool Subculture	98.3	3.5	3.4	46
Transfection R2	98.2	0.79	0.78	47
Transfection R3	93.0	1.3	1.2	48
Subculture	93.8	2.3	2.1	49
Minipool plating	97.1	2.5	2.4	50
Minipool screening and amplification	NA	NA	NA	51-53
Mini-pool subculture and RCB	NA	NA	NA	54 to 59
Single cell cloning of Mini-pool	97.50%	1.41	1.37	60

[667] Selection of monoclonal antibody clones expressed and purified from stable cell lines

[668] Culture harvest for protein purification:

[669] Cells were seeded at a density of approximately $0.3X10^6$ cells/ml in 30ml Complete power CHO2 growth media and cultured for 6 days in 37^0C, humidified condition in a 5% CO2 incubator with 120 RPM rotation. 20 ml media top-up was given with complete power CHO2 growth media on 4th day. Cells were harvested by centrifuging the entire cell suspension at 2000

RPM for 10 mins. The supernatant was collected and stored in -20°C for further purification. Here onwards, all respective stable cell clones containing novel, unique anti CLEC2D antibody genes will be referred as Cxxxx, wherein xxxx represents four digit numbers (Table 19). Each code represents a specific stable cell line containing specific antibody gene, otherwise mentioned elsewhere.

[670] Subsequently, culture supernatants of ~221 unique and confirmed stable cell clones were subjected to purification through Protein A followed through rational judgement on parameters as exemplified by yet not limited to, purity, titre. In addition, thermal stability estimation via thermal shift assay (TSA) was incorporated as an additional parameter towards selection/screening.

[671] Higher melting temperature was considered as a characteristic of more stable protein while proteins with melting temperature less than 65°C were decided to be not included for further development. TSA experimentation starts with appropriate dilution of protein sample to 0.5mg/ml concentration in 1x PBS wherein SYPRO-ORANGE fluorescent dye (5000X) was added to the target protein to a final concentration of 5X. Further mixture was centrifuged at 500 RPM for 2 minutes and analyzed by CFX96 Real Time System. Thermal denaturation was carried out by increasing the temperature from 25 °C to 95 °C at a rate of 0.5 °C per minute. Fluorescence intensity was collected at 0.5 °C intervals and analyzed with CFX Maestro software and Tm value was calculated from melt curve.

[672] Flow and /imaging:

[673] In addition, respective purified anti-CLEC2D proteins were also evaluated for Cell surface binding assay by flow-cytometry and confocal microscopy. The rationale behind inclusion of flow cytometry and confocal microscopy studies was to obtain comprehensive list of anti CLEC2D clones through a combination ranking matrix.

[674] The experimentation including the method of sample preparation for flow cytometry was as described above while ~ 1-5 µg of purified anti-CLEC2D antibody proteins and reference positive control, respectively, was used to estimate binding of membrane expressed CLEC2D on untransfected CHO cells and C4548 cells (FIG. 10C).

[675] The experimentation including the method of sample preparation for imaging acquisition through confocal microscopy was as described above while ~2 µg of purified anti CLEC2D antibody proteins, such as, C5848, C8408, C7832, C8800, C5595, C0694, not limited to, and

reference positive control, respectively, was used to monitor the membrane bound CLEC2D antigen binding on PC3 cells. As observed through imaging studies for Anti-CLEC2D purified from stable cell clones, not limited to, C5848, C8408, C8800, C5595, C7832, , exhibits uniform yet differential CLEC2D antigen binding on the surface of PC3 cells (FIG. 10D).

[676] In order to assess/understand the stability of anti CLEC2D antibody genes in stable cell clones, quantitative measurements through RT PCR was adopted wherein amplification of stably integrated anti CLEC2D antibody genes into CHO cell genome would be monitored and estimated. CHO cell pellets were obtained from every passage as part of a continuous subculture of respective clones for 60 generations corresponding to P01 as first passage while P18 represents final 60th generation. Herein, genomic DNA (gDNA) were isolated from cell pellets using the DNeasy® Blood & Tissue kit (QIAGEN GmbH, Hilden, Germany) according to the manufacturer's protocol (protocol for cultured cells with proteinase K treatment). Concentration and purity of gDNA preparations were analyzed spectrophotometrically using Eppendorf BioPhotometer® D30 (Eppendorf AG, Germany). The isolated gDNA were diluted to a concentration of 100 ng/ µL and passed through BD Ultra-Fine™ Needle Insulin Syringes (Becton, Dickinson and Company, NJ, USA) for qPCR. To quantify the Ct values qPCR was performed on a CFX96™Real-Time system with 96-well, thin wall Hard-Shell PCR plates and Microseal® 'B' seal film sealer (all from Bio-Rad, Hercules, CA, USA) using the designed primers. Each qPCR run was performed with each sample in triplicates. GAPDH used as relative control and no template controls (NTC) were included in each qPCR run. Each reaction mix contained 12.5 µL of SYBR™ Green PCR Master Mix (appliedbiosystems by Thermo Fisher Scientific, Life technologies, Woolston Warrington, UK), 10 pmol of each primer (synthesised at Eurofins, Bangalore, India) and 100 ng lysed gDNA adjusted with Water, HPLC (HiMedia Laboratories, Mumbai, India) to a final volume of 25 µL. The qPCR run was performed as a 2-step protocol with an initial denaturation step at 95°C for 10 min followed by 40 cycles of denaturation at 95°C for 15 sec and annealing at 60°C for 60 sec. Raw data were processed by the Bio-Rad CFX Manager™ software application version 3.1.1517.0823 (BioRad) using the settings baseline subtraction, to obtain the Cq (Cycle Quantification) values.

[677] The described quantitative approach was employed for all clones, as exemplified by, for C5511, C4608. The data obtained from the study has been depicted in FIG. 10E. indicating non significant variation of <5% in Ct values for respective antibody chains across all passage

numbers confirming the stable integration of anti CLEC2D antibody genes into CHO cell genome and sustained for at least 60 generations.

[678] Considering the combinatorial matrix, the number of stable cell line was selected to 11 clones, as exemplified by, C4608, C7720, C5093, C3452, C9136, C3641, C5372, C6481, C5511, C6726, C5392. Here onwards, understanding towards large scale production aspect and functionality feature, such as, anti-CLEC2D antibody driven cytotoxicity, was incorporated towards selection of final clones for further development.

[679] For the process of clone selection, it was essential to have a method which is robust, repeatable and produces protein of consistent quality. Therefore, before clone screening was initiated, a platform process was developed to ensure efficient clone screening. A fed batch process was developed using ActiPro as basal media and cell boost 7a and cell boost 7b as the feeding. The interval and quantity of feeding was experimentally optimized and the optimized process was repeated to establish robustness. The fed process was further extended to clone screening to isolate the top performing clones. After the top performing clones were isolated, the clones were verified by culturing cells in a 10L bioreactor using the optimized fed batch process. This step was carried out to ensure manufacturability of clones selected when transferred to a larger scale.

[680] ActiPro media was chosen as the basal media for development of platform process, on the basis of historical data of comparison with different basal media. ActiPro was supplemented with 4mM glutamine to ensure metabolic requirements of cell are met.

[681] Multiple monoclonal cell lines were evaluated in order to understand, rank and select the better performers. Based on the results obtained on Viable Cell Density, Viability, Titer, C5511, C4608, C3452, C5392, C6481 were assessed to be best performers in terms of all the performance parameters.

[682] Surface antigen expression on various prostate cancer cell lines :PC3

[683] Tumor cells expressing CLEC2D antigen were harvested by trypsinization. Cell count was taken by Vi-cell XR automated cell counter. Cells were centrifuged at 1400-1500 rpm for 4-5 minutes. The pellet was re-suspended in 1ml DPBS. 50,000 cells were aliquoted in each well of a 96 well plate.1µg of test samples, as exemplified by C5511, control were added to each well and incubated for 30-60 minutes at room temperature (25ºC). The plate was centrifuged at 1400-1500 rpm for 4-5 minutes, the supernatant was aspirated and cells were washed with 0.1%BSA

in DPBS. 2.5 ml of 2% BSA was diluted to 50ml with DPBS. Goat anti human IgG FITC conjugate was used as secondary antibody. 1:100 dilution of secondary antibody was prepared in DPBS and 100µl was added to each well. Goat anti human IgG FITC conjugate was used as control at dilution of 1:100. The plate was incubated for 30 minutes at room temperature (25^{0}C) in dark. The cells were washed with 0.1% BSA and re-suspended in 100µl of 1% BSA. Samples were analyzed by flow-cytometry.

[684] Binding of test samples were estimated and used for calculation of specific binding on tumor cell surface using following formula:

$$\text{Fold change in MFI} = \frac{\text{Median FITC-A of test sample}}{\text{Median FITC-A of control}}$$

[685] Fold change in MFI of PC3 surface binding, as observed from flow cytometry experiments, as exemplified while not limited to, C5511, C4608, C6481, C2438, C3452, C0949antibody, was found to be increased by more than2 folds when compared against control (FIG. 11A).

[686] Further, surface binding was with various unique anti CLEC2D antibody stable clones on the surface of PC3 through binding of antibody on the surface of PC3 cells through confocal microscopy, as described in Example 4, Section: Cell surface binding assay: through Flow Cytometry and Confocal Microscopy. As depicted in FIG. 11A, the binding of purified novel anti CLEC2D on the surface of PC3 was observed with uniform distribution of CLEC2D antigen through novel antibody on PC3 cells.

[687] Cytotoxicity assay: Through flow cytometry and Imaging methods (Live + end point+) To assess the functional activity of anti-CLEC2D, cytotoxicity assay was performed employing both flow cytometry and confocal microscopy methods, with isolated PBMCs and incubated with target cell and anti-CLEC2D. Prior to this, optimization on mAb concentration and ideal T:E ratio was carried out.

[688] Effector cells, PBMCs from healthy donors were isolated as per previous protocol (Jewett A, J Immunol 1996). Briefly, peripheral blood lymphocytes were obtained after Histopaque-1077 (Sigma) centrifugation. 1:2 diluted blood was layered on 15mL Histopaque. All the reagents were maintained in room temperature. Tube containing histopaque and blood was centrifuged at

400g for 30 minutes at room temperature with zero acceleration and brake. After centrifugation, upper layer was carefully aspirated to within 0.5 cm of the opaque interface containing mononuclear cells and the upper layer was discarded. Opaque interface was carefully transferred into a centrifuge tube. Cells were washed twice by adding 10-15mL of 1XPBS at 250g for 10 minutes. Pellet was resuspended in 2 mL of PBS and PBMCs count was done. Total 10 million PBMC was obtained from 10mL of blood. Quality check of PBMC was done based on flow cytometry with CD45+ population 99%. NK cells were isolated via negative selection using NK isolation kit (Stem cells technologies, Vancouver, BC, Canada). The purity of NK cells was found to be >90% based on flow cytometry CD56+ population.

[689] Target prostate cancer cell line, PC3 cells were labelled with Efluor as per the manufacturer's protocol and were seeded at a density of $0.04x10^6$ in 20% DMEM in 24 well plates. After 24 hours, freshly isolated PBMCs were added in T: E of 1:5. Novel monoclonal anti-CLEC2D antibodies C5511, C6481, C5392, C3452 and C4608, not limited to, were added at ~200 µg/ml in the assay reaction of 0.5ml and incubated for 14 hours. Supernatant was collected from 24 well plate and adherent cells were trypsinized and collected in 1.5ml tubes. Reaction mixture was incubated with sytox green (15nM) for 20min and fluorescence was detected in flow cytometer. Percent specific cell death was determined by subtracting the percent cell death of control from the test samples.

[690] Cytotoxicity was analysed by dual target cell staining by flow cytometry. FIG. 11B shows cytotoxicity of the 3 novel anti CLEC2D monoclonal antibodies, C5511(~41%), C4608(~32%) and C6481(~37%) was observed compared with the control wherein percent cell death was measured from PBMC, isolated from donor 1, and target cell, incubated together at 1:5 ration without treatment. Following similar conditions, C5392 and C3452 clones were tested on donor 2 wherein cytotoxicity was found to be be ~14% and ~28%, respectively (FIG. 11B). More than 80% cytotoxicity of target cells was observed when anti-CLEC2D concentration was increased from 50 µg/ml to 200 µg/ml (FIG 11C) and significant increase in tumour cell killing was also monitored when T:E ratio was increased from 1:5 to 1:10 (FIG. 11D).

[691] For confocal microscopy experiments, PC3 cells were grown on 8-well slides (eppendorf) in complete media (20%FBS +DMEM-F12+ 1x Pen/Strep + 1mM sodium Pyruvate) to 70–80% of confluence. Freshly isolated PBMC cells were left overnight in culture media (RPMI1640 with 10% FBS) prior to be used in cytotoxicity as resting PBMC cells. PC3 cells were stained

with cell tracker dye (100 nM) and PBMC cells were stained with cell proliferation dye EF670 (10 μM) separately. Different concentrations of novel antibodys along with stained PC3 and PBMC cells incubated for 6-7 hrs then images were acquired using Olympus FV3000- 4 laser scanning confocal microscope with a 60 X magnification, 1.35-NA objective. Laser light used for death dye sytox blue (at 5 μM), λex 405 nm and λem 450-500 nm; for cell tracker green, λex 488 nm and λem 510-530 nm; for cell proliferation dye EF670 λex 640 nm and λem 650-750 nm. Images were analyzed with Fiji ImageJ software.

[692] In order to identify the optimal concentration of novel mAb for the cytotoxicity assay, target to effector cells ratio (1:5) and 3 different concentrations (i.e., 10 μg/ml, 20 μg /ml and 50 μg /ml) of novel anti-CLEC2D antibody (C6726) was used and incubated for 6-7 hrs in complete media . Cell death was monitored by disappearance of green fluorescence and appearance of violet fluorescence on PC3 cells. Maximum cytotoxicity observed at 50 μg /ml (FIG. 11E). Further end point cell death assay was continued using a concentration of 50 μg /ml for the same incubation timing for other antibody clones, not limited to, C6726, C4608, C5848, C5511, C6481, clones tested (FIG. 11F) indicating that the target cell death is observed in the presence of novel antibodies while no cell death was monitored when targets cells were not treated with novel antibodies.

[693] Based on available data as described above, C4608, C5511, C6481, C5392 and C3452 clones were selected for final *in vivo* mouse efficacy experimentation.

[694] During the development of therapeutic monoclonal antibodies (mAbs), a strategy for early identification of candidate antibodies with the greatest likelihood of success in the clinic is needed to avoid costly late-stage failures related to inadequate exposure, toxicity or lack of efficacy. Early screening and optimization of mAbs focus on characteristics such as affinity, potency and stability for selection of lead constructs, while confirmation on in vivo efficacy are typically required, although, characterized later in development and on a small number of lead mAb constructs. Herein, confirmed anti CLEC2D clones, C4608, C5511, C6481, C5392 and C3452 were subjected to evaluate for *in vivo* efficacy against prostate cancer xenograft.

[695] Example 6: Deciphering the mechanism of action of novel Anti-CLEC2D antibody molecule

[696] Immune checkpoints consist of inhibitory and stimulatory pathways that maintain self-tolerance and assist with immune response. In cancer, immune checkpoint pathways are often

activated to inhibit the nascent anti-tumor immune response. Immune checkpoint therapies act by blocking or stimulating these pathways and enhance the body's immunological activity against tumors. Under normal circumstances, immune checkpoints allow the immune system to respond against infection and malignancy while protecting tissues from any harm that may derive from this action. However, the expression of some of these immune-checkpoint proteins by malignant cells dysregulates the antitumor immunity and favours the growth and expansion of cancer cells. Understanding the mechanism of action for immunotherapy, especially though monoclonal antibody based therapies, though multiple approaches would further reinvigorates on specific ways whether alone or in combination, that works in favour of tumour cell killing.

[697] In present disclosure, mechanism of anti CLEC2D antibody, as can be understood from in vitro experimentation, usually consists of events occurred at molecular interaction level, such as CLEC2D target dependence, interaction between CLEC2D/CD161, at cellular network level such as involvement of various effector cells, eg., natural killer (NK) cell, T cells on killing of tumour cells in presence or absence of anti CLEC2D antibody, or specific mechanism that are driven by isotype of anti-CLEC2D antibody such as ADCC, CDC, ADCP and/or in combination, tumour cell death induced by elevation of cytokine/chemokine levels or various activating/inhibitory receptor's expression or in combination, and from in vivo experimentation, wherein, tumour regression occurred through lymphocyte infiltration.

[698] Moreover, as the functions and target molecules of antibodies are more diverse, it becomes increasingly necessary to understand how the target molecule functions biologically and what will be the biological response to the modified functions induced by the antibody. Having mentioned this, understanding on mechanism of action will have immense emphasis on prostate cancer treatment, specifically on castration resistant prostate cancer, and will pave avenues for whole spectrum of multiple disease indications with novel immunotherapy strategies. Having mentioned this, a thorough employment of rational approach/stratification will ensure consistent incorporation of better-understood immunology in to cancer therapy and will dramatically impact on the development of overall therapeutic landscape.

[699] The specific cell type involved in cytotoxicity was investigated through flow cytometry and confocal microscopy, wherein, in microscopy based approaches having both end point assay and live cell imaging methods.

[700] NK cell mediated cytotoxicity

PC3 cells were labelled with Efluor as per the manufacturer's protocol and were seeded at a density of $0.04x10^6$ in 20% DMEM in 24 well plates. After 24 hours, freshly isolated NK cell was added in T: E of 1:1. Novel monoclonal anti-CLEC2D antibody C5511 and C6481 were added at 100μg/ml in the assay reaction of 0.5ml and incubated for 14 hours. Supernatant was collected from 24 well plate and adherent cells were trypsinized and collected in 1.5 ml tubes. Reaction mixture was incubated with Sytox green (15nM) for 20min and fluorescence was detected in flow cytometer. Percent specific cell death was determined by subtracting the percent cell death of control from the test samples. NK cell-mediated cytotoxicity (NKCC) was determined by using freshly isolated NK cells co-incubated with prelabelled target tumor cell line and anti-CLEC2D for 14 hours. Assay samples were incubated with dead cell dye sytox green and fluorescence was measured by flow cytometry. As estimated, Anti-CLEC2D antibody exhibited more than 80% cell death in the cytotoxicity assay (FIG. 12A).

[701] Confocal microscopy based approach was employed further to understand the impact of NK cell mediated cytotoxicity through both fixed cell imaging and live cell imaging.

[702] PC3 cells were grown on 8-well slides (eppendorf) in complete media (20%FBS +DMEM-F12+ 1x Pen/Strep + 1mM sodium Pyruvate) to 70–80% confluence. NK cells were isolated as described above. Freshly isolated NK cells were left overnight in in 10%RPMI media overnight prior to be used in cytotoxicity as resting NK cells. PC3 cells were stained with cell tracker dye and NK cells were stained with cell proliferation dye EF670 separately. Different ratio of NK: target cells (1:0.5, 1:5, 1:10) were used along with 50 μg/ml of novel antibodies, not limited to, C5511, C4608, C6481, and were incubated for 6-7 hrs before image acquisition using Olympus FV3000- 4 laser scanning confocal microscope with a 60X magnification, 1.35-NA objective. Laser light used for death dye sytox blue, λex 405 nm and λem 450-500 nm; for cell tracker green, λex 488 nm and λem 510-530 nm; for cell proliferation dye EF670 λex 640 nm and λem 650-750 nm. Images were analyzed with Fiji ImageJ software.

[703] To explore the role of NK cells on cytotoxicity, we have incubated PC3 with different ratio of NK cells along with the fixed concentration of novel antibodies for 6 to 7hrs. We have observed an increase in cell death with increasing in ratio of E:T for all antibodies tested (C5511, C4608, C6481) wherein T:E ratio of 1:10 exhibited highest cell death as indicated in FIGS. 12B, 12C, and 12D).

[704] T cell mediated cytotoxicity

[705] PC3 cells were labelled with Efluor as per the manufacturer's protocol and were seeded at a density of $0.04x10^6$ in 20% DMEM in 24 well plates. Freshly isolated T cell was used in the cytotoxicity assay at T:E of 1:3 and antibody concentration of 100ug/ml. Novel monoclonal anti-CLEC2D antibody C5511 and C6481 were added at 100ug/ml in the assay reaction of 0.5ml and incubated for 14hours. Supernatant was collected from 24 well plate and adherent cells were trypsinized and collected in 1.5ml tubes. Reaction mixture was incubated with sytox green (15nM) for 20min and fluorescence was detected in flow cytometer. Percent specific cell death was determined by subtracting the percent cell death of control from the test samples.

[706] FIG. 13 depicts T cell mediated killing as observed against PC3 cells wherein clone C5511 & C6481was incubated at a concentration of 100 µg/ml eliciting tumor cells cytotoxicity when compared with control having basal level of 6% dead cell. In experimental condition where T:E of 1:3 was used, upto 55% T cell mediated cytotoxicity was observed (FIG. 13)..

[707] To further define the process of cytotoxicity live-cell microscopy experiments were performed to track the target cell killing through effector cells for both PBMC and NK cells. For live cell imaging experimentation, PC3 cells were grown on 8-well slides (eppendorf) in complete media ((20%FBS +DMEM-F12+ 1x Pen/Strep + 1mM sodium Pyruvate)) to 70–80% confluence. PC3 cells were stained with cell tracker dye and PBMC/NK cells were stained with cell proliferation dye EF670 separately. 200 µg/ml of novel antibodies along with stained PC3 and PBMC/NK cells. Target to effector ratio for both PBMC and NK cells were, 1:5 and 1:1, respectively. Cells were kept in a humidifier maintained at 37°C and 5% CO2 during imaging. Live cell imaging was performed on the Zeiss LSM800 confocal microscope with a 63 X magnification, 1.4-NA objective and images were captured at 8 min intervals for up to 20 hrs by using appropriate wavelengths (For sytox blue, λex 405 nm and λem 450-500 nm; for cell tracker green, λex 488 nm and λem 510-530 nm; for cell proliferation dye EF670 λex 630 nm and λem 650-750 nm. Images were analyzed with Zen lite Imaging software.

[708] To further define the process of cytotoxicity, live-cell microscopy was performed to track the target cell killing through effector cells either PBMC or NK cells.

[709] The purpose of live cell imaging was to understand and follow the anti CLEC2D mediated tumour cell killing process in the presence of effector cells, such as PBMC or NK cell, in time dependent manner, under controlled experimental condition. Results obtained from live cell imaging prompted the fact that in the presence of isotype control, PBMC or NK cell made

less direct contact with the PC3 target cells resulting in minor percentage of target cell death. On the contrary, addition of anti-CLEC2D (C5511) antibodies, on PBMC or NK cells and target cells causing an increase in extend of direct contacts between both PBMC or NK cells and PC3 target cells, resulting in significant target cell death. Interestingly, PC3 target cell killing mediated by anti-CLEC2D (C5511) antibody in presence of NK cells elicited more efficient clearance of tumor cells wherein most of the tumor cells lysis occurred within 10 hrs of incubation, while observed tumor cell death in presence of PBMC was found to be significantly lower within the said time point. This indicates that effective elimination of PC3 tumor cells via anti-CLEC2D antibody is predominantly NK cell mediated.

[710] Molecular interaction between Anti-CLEC2D antibody and CLEC2D antigen: through epitope mapping

[711] *In silico* studies

[712] The following protocol was developed to identify the binding site formed by the CLEC2D-Antibody complexes. Briefly the method involves using protein structures of both the antibody and CLEC2D in shape-complementarity based docking to generate CLEC2D-antibody conformations, followed by analysis of the conformation to shortlist mutations to verify the binding sites. (Germain et al, 2011, Rozbesky et al, 2015).

[713] One of the central assumptions of this protocol is that the potential binding site should be more accommodating of a binding partner, i.e., a groove or channel - where an appropriate binding partner may be able to settle, somewhat illustrated by the lock-and-key model of enzymes and substrates, a specific lock (or binding site) would be receptive to a specific key (or binding partner) based on their structural compatibility. This concept was expanded upon to identify the binding site, as following shape-based docking, the largest concentrations of generated conformations were considered to be the possible binding sites.

[714] The conformations were then clustered together on the basis of interacting pairs of residues, conformations that could not be incorporated into clusters were discarded after which the remaining conformations were energy minimized and screened for viability. For conformations found to be viable their interacting residue pairs were more closely scrutinized and mutations were suggested to test the association.

[715] Killer cell lectin-like receptor subfamily B member 1 (NKR-P1) is an inhibitory receptor the regulates NK cell-mediated cytotoxicity. C-type lectin domain family 2 member D

(CLEC2D) is a ligand of NKR-P1, the CLEC2D/CD161 interaction inhibits NK cell-mediated cytotoxicity, blocking the CLEC2D-NKR-P1 complex can enhance primary NK cell activity.

[716] All unique anti CLEC2D antibodies derived from novel library was found to prevent the CLEC2D-NKR-P1 association by binding with CLEC2D, however the exact location and nature of this inhibition was unknown. The following protocol was conceived to identify the likelihood of binding site through the use of modelling, docking and site-directed mutagenesis.

[717] The procedure starts with identifying key interaction residues on CLEC2D wherein, the CLEC2D -antibody complex interactions can be understood by taking a closer look at the CLEC2D -NKR-P1(CD161) complex and was done by studying the crystal structure of the complex, deposited in the PDB as 5MGT (FIG. 15A).

[718] The 5MGT crystal structure describes the association between the CLEC2D and NKR-P1 complex. The residues involved in the association are of interest. If the inhibition mode of the antibody- CLEC2D complex is of a steric variety, the residues involved in both interactions, and their immediate neighbors, would likely overlap. Residues involved from the CLEC2D chains, henceforth called antigen interacting residues were identified by examining the 5MGT structure in Chimera (FIG. 15B) (Pettersen et al, 2004). Essentially all residues within contact distance (up to 6Å) between the chains of CLEC2D and NKR-P1(CD161) were identified (See Table 28).

Table. 28

A list of the residues in CLEC2D Chains within contact distances of NKR-P1(CD161).							
Res No. & Type	6 Å	5 Å	4 Å	Res No. & Type	6 Å	5 Å	4 Å
91 ASP	✓	✓	✗	161 GLY	✓	✓	✗
92 ASP	✓	✗	✗	162 GLU	✓	✓	✓
93 THR	✓	✓	✗				
95 ASN	✓	✗	✗	165 TYR	✓	✓	✓
				167 ASN	✓	✓	✓
124 ARG	✓	✗	✗	168 ASP	✓	✓	✗
126 LYS	✓	✓	✗	169 LYS	✓	✓	✓

127 GLY	✓	✓	✕				
128 PRO	✓	✓	✓	172 SER	✓	✓	✕
129 SER	✓	✓	✓	173 SER	✓	✓	✓
130 ASP	✓	✓	✓	174 ALA	✓	✓	✓
131 HIS	✓	✕	✕	175 ARG	✓	✓	✓
				177 TYR	✓	✓	✓
139 GLN	✓	✓	✓	178 THR	✓	✓	✓
				179 GLU	✓	✓	✓
158 LEU	✓	✓	✕	180 ARG	✓	✓	✓
159 GLY	✓	✓	✕	181 LYS	✓	✓	✓
160 ALA	✓	✓	✓				

[719] These antigen-interacting residues were known to play crucial roles in the NKR-P1(CD161)- CLEC2D complex and would therefore be considered as 'significant' residues in the following conformation analysis.

[720] Building Antibody Structures

[721] Models of the fourteen antibodies were generated through the use of homology modelling program MODELLER. The models generated were limited to the variable regions of the antibody, as that is the main area of interest. The PDB was parsed for structures of complete variable regions of antibodies. Each of the unique antibody variable region sequences were aligned against the available structures' sequences and the best match for each antibody sequence, was used as the template from which the antibody model was built. Multiple models were generated for each sequence and the most energy efficient structure was selected as the main model for the antibody (FIG. 15C).

[722] Antibodies are very well conserved outside their hypervariable Complementarity Determining Regions (CDR) loops, and of the six CDR on the two chains of the antibody, three on each of the heavy and light chains, the CDR3 loop on the heavy chain is known to be the

largest and most influential in the establishment of interactions, and this region along with the light chain CDR3, were run through several rounds of MODELLER's Loop Refinement to generate the most energy efficient structures, with respect to the CDR loops. Once again multiple variants of the main model were generated and the most energy efficient one was taken forward as the refined antibody model.

[723] Docking the antibody on the CLEC2D

[724] The CLEC2D model was acquired from the PDB, deposited as 4QKI a dimer of CLEC2D chains. As the precise location of the interaction is not known, Molecular Docking was used to generate structures of the complex to explore the possible interaction modes. The program used was PatchDock, a shape complementarity docking program which permutes all possible interaction modes based on structural feasibility. (Schneidman-Duhovny et al, 2005)

[725] Docking was carried out between the refined Antibody Variable region structures and the antigen CLEC2D (PDB: 4QKI), using PatchDock's High Accuracy Mode at a cluster distance of 4 Å (preventing conformations within 4 Å of existing conformations from being generated). Constraints were only provided for the antigen structure, wherein both CDR3 loops from the light and heavy chains were specified.

[726] PatchDock generated several docking conformations against each of the provided antibodies. (See Table 29).

Table 29

The number of output structures for each Docking of the unique anti CLEC2D antibody refined structures against CLEC2D.			
Refined Structure	**Conformations Generated**	**Refined Structure**	**Conformations Generated**
1	6424	**8**	5750
2	17370	**9**	18198
3	7338	**10**	7604
4	9245	**11**	10267
5	17976	**12**	12699
6	17170	**13**	15655
7	20617	**14**	6219

[727] Analysing conformations

[728] Following the generation of the docked conformations, their interacting residues were analysed.

[729] In house scripts were used to query the complex structure and identify all residue pairs involving participants from different chains, at a maximum distance of 4Å from one another. These residue pairs were compiled into lists, Table 30 and 31 show such a few lines from such a list, which were then used to cluster the conformations.

92:ASP:B 94:TRP:C	101:ARG:B 211:MET:D
92:ASP:B 95:PRO:C	182:TRP:B 93:THR:C
92:ASP:B 94:TRP:C	106:GLN:B 28:SER:C
94:LYS:B 95:PRO:C	78:SER:B 27:GLN:C
105:SER:B 214:PRO:D	102:PHE:B 28:SER:C
101:ARG:B 214:PRO:D	102:PHE:B 93:THR:C
105:SER:B 32:SER:C	106:GLN:B 32:SER:C
77:GLU:B 25:ALA:C	105:SER:B 30:GLY:C
77:GLU:B 26:SER:C	77:GLU:B 69:THR:C
106:GLN:B 29:VAL:C	79:TRP:B 28:SER:C
94:LYS:B 94:TRP:C	88:TYR:B 27:GLN:C
98:SER:B 93:THR:C	107:ASP:B 31:ASN:C
106:GLN:B 30:GLY:C	77:GLU:B 27:GLN:C
88:TYR:B 94:TRP:C	105:SER:B 29:VAL:C
94:LYS:B 93:THR:C	105:SER:B 31:ASN:C

Table 30: A selection of residue pairs from the contact list generated for C4608 complex 11712. Pairs Highlighted in single underlined, Orange double underlined and Blue dashed underlined denote pairs across the antigen-antibody chains. The single underlined pairs are those between the antibody-antigen chains that involve any of the previously identified "significant" residues" and CDR3 residues from either the antigen or the antibody. The double underlined Pairs involve significant residues on the antigen and non-CDR3 residues on the antibody and dashed underlined pairs involve significant from the antigen as well as CDR3 residues on the antibody.

128:PRO:B 219:LEU:D	165:TYR:B 223:TRP:D
128:PRO:B 220:PHE:D	167:ASN:B 110:GLU:D
129:SER:B 219:LEU:D	168:ASP:B 110:GLU:D
129:SER:B 220:PHE:D	169:LYS:B 110:GLU:D
130:ASP:B 220:PHE:D	175:ARG:B 225:GLN:D
127:GLY:B 219:LEU:D	179:GLU:B 42:GLN:C
130:ASP:B 223:TRP:D	179:GLU:B 40:PRO:C
165:TYR:B 112:GLN:D	180:ARG:B 223:TRP:D

Table 31 : A selection of residue pairs from the contact list generated for C5511 complex 14228. Pairs Highlighted in single underlined, double underlined and dashed underlined denote pairs across the antigen-antibody chains. The Grey pairs are those between the antibody-antigen chains that involve any of the previously identified "significant" residues" and CDR3 residues from either the antigen or the antibody. The Orange Pairs involve significant residues on the antigen and non-CDR3 residues on the antibody and Blue pairs involve significant from the antigen as well as CDR3 residues on the antibody.

[730] Clustering Conformations and Assessing Viability

[731] Conformations were clustered on the basis of overlapping contacts, conformations were clustered together if at least 75% of the residue pairs were in common. Conformations that were not incorporated into a cluster were discarded.

[732] Of the remaining structures, energy minimization was carried out on all the complexes before the next filtration step where the Protein Interaction Z Score Assessment (PIZSA) tool was used to filter out non-binder conformations. PIZSA took in the protein complexes and identified all the likely residue interactions on the basis of a distance threshold applied to the residues' atoms. Following identification it evaluated every contact pair and scored the constituent associations, building up a cumulative score which was ultimately used to determine if the associations it has identified would lead to stable association, if the complex is viable, or not. (Roy et al, 2019) (This viability is based on the composition and combinations of the identified contact pairs.) Conformations identified as viable were the only ones retained. (See Table 32).

Table 32

The Total numbers and membership data of clusters identified when clustering was carried out for 75% identify of interactions. The final column lists the number of conformations that are recognised as PIZSA as being viable.			
Antibody	**Total Clusters**	**Total Conformations**	**Viable Conformations**
C2901	13	100	69
C4608	19	138	117
C3452	6	30	9
C5511	7	44	39
C0694	4	29	9
C0997	6	44	37
C5397	3	21	21
C5392	7	47	36
C0949	6	43	42

[733] These reduced clusters were composed of several tightly grouped structures, all of which formed overlapping associations with the CLEC2D chain.

[734] These cluster formations were taken as likely binding site positions and the validation of each site needed to be carried out (FIGS. 15D, 15E, 15F, and 15G).

[735] Mutation Analysis

[736] Following the short-listing of a smaller number of viable structures to explore, mutation analysis was carried out. PIZSA also had a feature whereby it takes identified contact pair and substitutes each participant residue with the other 19 natural amino acids and determined the impact on the overall score of the structure for that substitution. The impact value would be indicative of the loss of stability the complex would experience if a specific residue was swapped out for another. Residues that were important for the complex, which form strong associations would have high impact values, as mutating those positions could weaken or destabilise the

complex. This information was used to identify which residue pairs mutations would be the most destabilizing to the overall complex. As the conformations were already clustered, an entire cluster could be evaluated by around identifying three to four high impact residue-pairs that were prevalent in all members of the clusters, for mutation. Herein significant considerations were made based on following parameters, such as, Same Cluster Count indicating the total number of times a specific residue was observed in an interaction within same cluster on the same antibody; Same_Cluster_Proportionate indicating proportionate number of times a specific residue was observed in an interaction within same cluster on the same antibody; Same antibody in Other Cluster ccurence count meaning the total number of times a specific residue was observed in an interaction among all clusters on the same antibody that can be seen multiple times in the same cluster; Same antibody Other Cluster count describes the total number of structures in which a specific residue was observed in an interaction among all clusters on the same antibody capturing multiple instances in the same cluster however only counted once; Other antibody Other Cluster occuraece count describes as the total number of times a specific residue was observed in an interaction among all clusters on the other antibodies; Other antibody other Cluster count indicating the total number of structures in which a specific residue was observed in an interaction among all clusters on other antibodies (multiple instances in the same cluster only counted once). Taking together, this approach in turn provided the epitope patch on CLEC2D antigen against respective anti CLEC2D antibody. The similar method was justifyably adopted for all anti CLEC2D antibodies as well.

Table 33. summarizes on significant residues on CLEC2D antigen contacting C4608 anti CLEC2D antibody

Clone No.	Cluster No.	Residue	Position	Same Cluster Count	Same Cluster Propor-tionate	Same Ab Other Cluster occurrence count	Same Ab Other Cluster count	Other Ab Other Cluster occurrence count	Other Ab Other Cluster count	CD161 overlap
C4608	G00001	ARG	101	10	100	26	4	100	22	No
	G00001	SER	105	6	100	15	4	36	11	No
	G00004	ASP	104	8	100	7	3	26	8	No
	G00007	PHE	102	3	100	13	4	27	12	No
	G00007	SER	98	1	100	10	5	37	19	No

	G00007	SER	105	6	100	15	4	36	11	No
	G00008	TYR	177	7	100	10	1	145	25	Yes
	G00008	GLU	179	5	100	14	3	129	20	Yes
	G00009	GLU	138	5	100	7	4	66	20	No
	G00009	GLN	141	10	100	21	5	82	17	No
	G00010	PHE	102	7	100	0	0	14	8	No
	G00010	ARG	101	13	100	2	2	82	17	No
	G00011	THR	152	3	100	10	2	67	21	No
	G00011	ARG	153	12	100	12	2	159	25	No
	G00011	GLN	154	5	100	9	2	72	16	No
	G00011	PRO	156	3	100	1	1	53	16	No
	G00011	GLN	117	4	100	4	2	44	13	No
	G00012	THR	152	5	100	8	2	67	21	No
	G00012	GLU	150	7	100	8	2	96	21	No
	G00014	THR	152	5	100	8	2	67	21	No
	G00014	GLU	150	3	100	12	2	96	21	No
	G00014	ARG	153	4	100	20	2	159	25	No
	G00015	PHE	102	3	100	13	4	27	12	No
	G00016	TRP	151	1	100	4	3	18	10	No
	G00016	GLU	150	6	100	24	5	59	13	No
	G00016	THR	149	3	100	12	3	38	10	No
	G00016	ARG	153	5	100	28	5	60	11	No
	G00016	GLY	140	2	100	19	6	62	19	No
	G00016	GLN	141	5	100	26	5	82	17	No
	G00017	GLN	141	4	100	27	5	82	17	No
	G00017	PRO	142	2	100	16	5	32	14	No
	G00017	ARG	153	5	100	28	5	60	11	No
	G00017	GLU	150	4	100	26	5	59	13	No
	G00017	THR	152	4	100	16	4	34	10	No

	G00018	PRO	156	4	100	2	1	14	6	No
	G00018	LEU	158	3	100	0	0	14	8	No
	G00018	ARG	153	7	100	26	5	60	11	No
	G00018	PHE	155	2	100	3	2	11	5	No
	G00018	LYS	169	4	100	4	1	6	5	Yes
	G00020	ARG	137	1	100	6	5	26	16	No
	G00020	TYR	177	6	100	27	4	158	24	Yes
	G00020	GLU	162	3	100	6	2	49	18	Yes
	G00020	ALA	160	2	100	10	4	44	19	Yes
	G00020	ARG	175	4	100	18	3	90	21	Yes
	G00020	GLN	139	5	100	15	7	77	21	Yes
	G00020	TRP	96	1	100	1	1	9	8	No
	G00020	GLU	138	4	100	8	4	66	20	No
	G00020	ARG	101	1	100	14	2	82	17	No
	G00020	SER	136	2	100	2	1	7	7	No
	G00020	GLY	140	2	100	19	6	62	19	No
	G00021	GLU	150	9	100	21	5	59	13	No
	G00021	THR	149	4	100	11	3	38	10	No
	G00022	THR	93	5	100	9	3	64	20	No
	G00022	TYR	177	10	100	7	1	145	25	Yes
	G00022	GLU	179	10	100	9	3	129	20	Yes
	G00026	TRP	151	1	100	4	3	18	10	No
	G00026	GLU	150	5	100	25	5	59	13	No
	G00026	ARG	153	8	100	25	5	60	11	No
	G00026	GLN	154	3	100	13	4	25	5	No
	G00026	THR	152	6	100	14	4	34	10	No
	G00031	THR	178	4	100	7	1	55	20	Yes
	G00031	GLU	179	3	100	19	3	92	19	Yes
	G00031	TYR	177	8	100	25	4	158	24	Yes

	G00031	ARG	175	5	100	17	3	90	21	Yes

[737] In order to identify which of the clusters describe the true binding sites, a series of mutations would be suggested to key residues. Due to the high number of clusters it was advantageous to identify mutations which were capable of testing multiple clusters concurrently. All the residues identified for all the clusters of a single antibody were analysed to achieve this. The idea was that multiple clusters would be put into combinations and residues that play a major role in all of their potential binding modes be suggested as mutantations to concurrently test many conformations. These combinations were identified by inspecting the overlapping significantly involved residues (those occurring in the top 3 proportions of each cluster.) If clusters shared multiple significantly involved residues they were taken as possible combinations. As exemplified herein, mutations were suggested for C4608 and C5511. These antibodies had 21 and 7 clusters respectively, in order to cluster these, the represented residues from all these clusters were analysed. An inspection of the representative overlaps of significantly occurring residues suggested possible combinations of G00001-G00004-G00007-G00010-G00015, G00012-G00014-G00016-G00017-G00018-G00021-G00026, G00005-G00008-G00020-G00022-G00031 and G00011-G00012-G00014-G00018 for C4608 and possible combinations of G00001-G00005-G00011-G00019-G00020 with G00015 and G00017 by themselves for C5511. Strategy described above was adapted for all anti CLEC2D antibodies.

[738] To identify which residues played a role in combinations of clusters every possible combination of lengths varying from 2 to 13 cluster (depending on the total number of initial clusters available) were generated. For every combination, all the involved residues along with their impact values were identified. Residues that were involved in all or a majority (at most missing in two members) of the members of the combination were retained while the residues that only played a role in some of the clusters in the combination were removed from consideration, leaving only a list of highly occurring residues.

[739] Once a preferable combination was identified based on the overlap of residues the residues that were highly occurring for that combination were scrutinized and residues that were observed to have a high impact value were put forward as mutation options (FIGS. 16E and 16G).

[740] The picks made after all those considerations would possess all the following properties, (a) Be charged or polar residues (although if no such residues were observed other were selected

based on their impact on the interaction.), (b) Be present in all or most of the clusters of a combination, (c) Have a significant on the potential binding mode, and (d) involve the antigen-interacting residues

[741] As exemplified by C4608, wherein the above described strategy was adopted and following combinations of residues are believed to be involved in interaction with CLEC2D antigen. The similar method was justifyably adopted for all anti CLEC2D antibodies as well.

Table 34. The final set of selections of the combinations identified for Antibody clone C4608

Clone Number	Clusters	Remaining Clusters	Residue position	Average Impact	Impact	Present on all Clusters	Unique to clusters
C4608	G00001	G00005	101:ARG:A	-1092.6	yes	yes	no
	G00004	G00008					
	G00007	G00011					
	G00010	G00012					
	G00015	G00014					
		G00016					
		G00017					
		G00018					
		G00020					
		G00021					
		G00022					
		G00026					
		G00031					
	G00012	G00005	150:GLU:A	-382.44	no	yes	no
	G00014	G00008	154:GLN:A	-379.74	no	yes	no
	G00016	G00011					
	G00017	G00020					
	G00018	G00022					
	G00021	G00031					
	G00026						
	G00005	G00011	175:ARG:A	-710.34	yes	yes	no
	G00008		177:TYR:A	-1056.29	yes	yes	no
	G00020		179:GLU:A	-612.15	yes	yes	no
	G00011	-	150:GLU:A	-544.91	yes	yes	no
	G00012		152:THR:A	-577.26	yes	yes	no
	G00014		153:ARG:A	-649.57	yes	yes	no
	G00018		154:GLN:A	-568.9	yes	yes	no

[742] Construct generation as soluble CLEC2D variants

[743] Once the amino acids, which are in combination or independently, are either overlapping or non-overlapping with CD161 interaction points, were generated as CLEC2D antigen variants to map the epitope for novel anti CLEC2D antibody clones. The constructs were generated either by site directed mutagenesis or by gene synthesis. All constructs were having C-term histidine tag, similar to soluble CLEC2D antigen used for screening, to facilitate the further purification. All possible positions were changed into amino acid alanine, as the observed in silico mutation impact was seen to be maximum for the said amino acid. Table 35 describes positions in CLEC2D soluble antigen wherein the mutations were introduced.

Table 35

Positions for mutation
P128A
S129A
D130A
Q139A
E162A
Y165A
K169A
S173A
R175A
Y177A
T178A
E179A
R180A
K181A
K169A & S172A
Y165A & N167A
R101A
Q141A
R153A
S187A
H190A

R175A, Y177A, E179A
R084A, H190A
E150A, T152A, R153A, Q154A
R101A, S105A,
D107A, H190A
Q141A, R153A
D092A, T093A, K094A
Q141A, K144A
E138A, C176A
E138A, Q139A, Q141A, R175A
D092A, Y177A, K181A
F116A, R153A,
T093A, N095A
T093A, Y177A, E179A
K094A, R101A, E179A
R175A, Y177A, R180A

[744] As exemplified herein, site directed mutagenesis was performed using QuikChange Lightning Site-Directed Mutagenesis Kit from Agilent by PCR using synthesizing two complimentary oligonucleotides containing the desired mutation, flanked by unmodified nucleotide sequence, which were synthesized at Eurofins. PCR was performed on an Eppendorf™ Mastercycler™ pro PCR System in 25-µL volumes consisting of 0.2 µM of each primer (Eurofins, India), 1.5 µL of Quick solution, 1 µL Quickchange XL dNTP mix , 10X quick change lightening buffer 2.5 µL. Also included were template DNA 15 ng. Following an initial denaturation at 95°C for 2 min, 18 cycles of 20 seconds denaturation at 95 °C, and 60 seconds annealing at 60 °C, 3 minutes primer extension at 68 °C, 5 minutes final extension at 68 °C were performed. After PCR 2 µL of Dpn I endonuclease was added which is specific for methylated and hemimethylated DNA and is used to digest the parental DNA template and to select for mutation-containing synthesized DNA (DNA isolated from almost all E. coli strains is dam methylated and therefore susceptible to Dpn I digestion.) The nicked vector DNA containing the

desired mutations was then transformed into XL10-Gold ultracompetent cells and plated onto ampicillin -containing LB agar plates. Plasmid DNA from transformed colonies was purified by QIAprep Spin Miniprep kit (Qiagen) and sequenced at Eurofins.

[745] Vector and the SDM construct having specific mutation were restriction endonuclease activity with HindIII and XhoI enzymes and product was extracted using QIAquick Gel Extraction kit, ligated using T4 DNA ligase (NEB) and 50% of mixture were transformed into NEB5α competent cells E.coli. Subsequently clone screening was carried out through restriction digestion and finally through sequencing reaction. Sequencing process confirmed the clones to contain desired mutation.

[746] Anti CLEC2D antibody mediated blocking of CLEC2D and CD161 interaction.Further probing into observations made from epitope mapping studies prompted to the fact that anti CLEC2D antibody binding sites on CLEC2D antigen comprises of contact points having both unique/exclusive contact points established on CLEC2D antigen and binding sites overlapping with contact points established between CLEC2D-CD161 complex. As exemplified herein, epitope patches on CLEC2D antigen for C4608 (FIG. 16A and FIG. 16B) and C5511 (FIG. 16C and FIG. 16D), not limited to, has been represented wherein binding sites for both C4608 and C5511 anti-CLEC2D antibodies interacting with CLEC2D antigen overlaps significantly with contact points between CLEC2D antigen and CD161. Present disclosure explores the impact of identified anti-CLEC2D antibody on the interaction between CLEC2D and CD161 proteins. As tumour cell evades immune system through the said interaction between CLEC2D and CD161, therefore, experimental validation of CLEC2D binder i.e., anti CLEC2D antibody disrupting the interaction has been further proved below. Experimental details starts with confirmation of CLEC2D and CD161 interaction followed by abrogating the same by the use of anti CLEC2D antibody.

[747] As exemplified herein, CLEC2D antigen was conjugated on magnetic beads wherein, 1 ml of 0.1 M phosphate buffer saline was added in to 0.5 mg Dynabeads and vortexed for 30 seconds followed by incubation at rotation, at RT for 10 minutes. After incubation, beads were washed twice with 1 ml of 0.1 M phosphate buffer saline with the help of Dynamag 2, then washed beads were resuspended in to 100 µl of 0.1 M PBS. To conjugate antigen on magnetic beads, 100 µl of washed beads and 100 µl PBS containing 1 µg of CLEC2D antigen were mixed thoroughly in the presence of 100 µl of 3 M ammonium sulphate then incubated at 37°C for

overnight. Overnight incubated mix was washed twice with PBS and blocked with 100 µl PBS containing 0.5% BSA for 2hrs followed by separation of magnetic beads with Dynamag 2.

[748] Finally conjugated antigen beads were resuspended in to 100 µl PBS. To check the identity of antigen, 1µl of above conjugated antigen bead was resuspended in to 99 µl of 1X PBS and washed once with 0.1 M PBS and again resuspended in to 100 µl of 1X PBS. 0.5 µg of anti-CLEC2D monoclonal antibody, commercially available from Novus Biologicals was added in to 100 µl washed conjugated antigen beads then incubated on ice for 2 hrs with constant tapping. After incubation, conjugated antigen beads were washed twice with 100 µl of 1X PBS containing 0.25% BSA then 100 µl of 5 µg/ml Alexa Fluor 488 goat anti−mouse IgG (H+L) was added in to conjugated antigen beads and further incubated for 30 min on ice. After incubation, conjugated antigen beads were washed twice with 100 µl of 1X PBS containing 0.25% BSA and resuspended in to 200 µl of 1X PBS. Fluorescence of all samples including controls were read through CytoFLEX. Bead conjugation efficiency was found to be >95% as judged by flow cytometry analysis as depicted in (FIG. 16E).

[749] To check the binding of CD161-Fc with CLEC2D antigen, 2 µl of above conjugated CLEC2D antigen beads was taken and different concentrations of CD161-FC (purchased from Biolegend) was added and incubated on ice for 2 hrs with constant tapping to avoid settling of beads. After incubation, the beads was washed twice with 100 µl of PBS with 1% BSA. 100 µl of 5 µg/ml of alexa fluor goat anti human IgG, was added and incubated on ice for 20 min on rotation. The beads was washed once with 100 µl of PBS with 1% BSA and resuspended with 100 µl of 1X PBS. Fluorescence of all samples including controls was read through CytoFLEX. As can be seen from FIG. 16F, CLEC2D antigen conjugated on magnetic beads interacts in a dose dependent manner to CD161 protein.

[750] 0.5 µg biotinylayted CD161-FC was added in to 2µl of CLEC2D conjugated beads and incubated on ice for 2 hrs. After incubation the beads were washed twice with 100 µl of PBS containing 1% BSA and 200 ng of Streptavidin, Alexa Fluor™ 633 conjugate was added and further incubated on ice for 20 min. After incubation the beads were washed twice with 100 µl PBS containing 1% BSA and 2 µg of C5511 antibody was added for 2 hrs on ice. After 2 hrs incubation, 5 µg/ml of alexa fluor goat anti human IgG was added and further kept for 20 min on ice with rotation. Finally fluorescence of all samples including controls were read through CytoFLEX. Loss of signal CLEC2D-CD161 interaction at optimal concentration of anti

CLEC2D antibody as seen in FIG. 16G, indicates that anti CLEC2D antibody can compete with CLEC2D-CD61 contact sites and disrupt the interaction.

[751] Immune cell activation: Due to binding of anti-CLEC2D antibody

[752] The prevailing view of NK cell activation is their ability to distinguish healthy cells from sensitive target cells through a balance between signals from activating and inhibitory receptors. The net output of major positive and negative signalling events is viewed to determine the capacity of NK cells to kill target cells. However, the precise molecular check-points where inhibitory signals abrogate activating pathways are not well defined.

[753] However, attempts towards delineating the contribution of individual receptors to NK cell activation, CD 69 surface receptor was considered as an early activation immune cells marker which gets rapidly induced in NK cells shortly after activation. CD69 promoter contains binding site for NF-κB, erythroblast transformation-specific related gene-1 (ERG-1) and AP-1. Its expression is upregulated upon activation in most leukocytes and use as a marker of activated lymphocytes and NK cells. In addition CD69 is also an important regulator of immune responses. CD69 is involved in NK-cells activation via Syk-Src-dependent manner. Whereas in T-cells CD69 is induced after TCR/CD3 engagement where it negatively regulates TH1/TH17 response and control inflammation in vivo also through TGF-B signaling. However in NK cells CD69 cross linking has been shown to induce cytotoxic activity and cytokines production of activated NK cells. Thereby, CD69 can be represented as a putative receptor for target cells in activated NK cells. Effector cells used in this study, PBMC and NK cells, as applicable, were isolated using protocol as described above.

[754] In order to understand the impact of Anti CLEC2D antibody on NK cell status, level of CD69 marker expression on NK cells were monitored in the presence and absence of Anti CLEC2D antibody. For each reaction $0.1X10^6$ of isolated NK cells were taken. IL-2 was used as positive control. 200U of IL-2 (Acro biosystems) and anti-CLEC2D 100 µg/mL and 200 µg /mL was added to each well and incubated overnight. In order to understand the change in CD69 expression through PC3 priming, PC3 cells were added at 1:1 (T:E) ratio to NK cells with or without anti-CLEC2D antibody C5511. NK cells without any treatment or targets were kept as control. Post 12-16hrs of incubation, CD markers not limited to, anti human CD3-FITC and anti human CD69-APC750 (Biolegend) staining was done 0.5 uL of respective antibodies were used against $0.1X10^6$ cells. Cells were washed once with 1XPBS 0.2%BSA and reading was taken

using CytoFLEX (Beckman Coulter). Data was acquired using default gain settings and 5000-10000 events were recorded per sample.

[755] The results showed 40-50% upregulation of CD69 expression as observed in NK cells in presence of C5511 antibody (100 µg /mL and/or 200 µg /mL) when compared to NK control without treatment wherein the baseline expression was recorded to be 1-2% (FIG. 17A). IL-2 was used as positive control and showed 30-40% upregulation (FIG. 17A). In case of tumor (PC3) primed NK cells showed high expression close to 70-75% expression of CD69 while CD69 expression was upregulated to ~85% in presence of both PC3 cell and antibody 100 µg/mL, (FIG. 17B).

[756] Secretion/intra-cellular expression of cytokine/chemokines

[757] NK cells recognition of tumor cells/infected cells induces cytotoxicity and cytokines secretion. Signaling pathways which regulates the cytokines production and the contribution of NK cell activation receptor upon target cell recognition for the process is not well understood. In addition the condition/requirement of cytokines secretion on engagement of specific ligand in target cells is not known. Thereby, to understand the primary initiation of immune response upon target cell recognition by NK cells profile/ screening of cytokines and chemokines are important. Here, the study was designed to detect cytokine secretion in presence of novel antibody C5511. IFN-γ and TNF-α are the two of the most prominent cytokines produced by NK cells and has been implicated in both cytotoxicity and proliferation of various immune cells. Thereby in this study experiments were conducted to detect IFN-γ secretion in PBMCs or isolated NK-cells by a well-established intracellular IFN-γ staining technique on flow based assay.

[758] Cells stimulation and IFN-γ staining protocol:

[759] After overnight rest of PBMCs and NK cells at 37°C, the activation reagents and secretion inhibitor (Brefeldin A (10 µg/mL)/ Monensin (6 µg/mL)) was added to the well. PBMCs and NK cells were left untreated or treated with novel antibody C5511 at 100µg /mL. Cells were stimulated with anti human OKT-3 (1-2 µg /mL) as a positive control, as it is known to induce IFN-γ secretion. Target cells, at an effector to target ratio of 10:1 was used whenever required. Medium alone served as the negative control. Cells were incubated for 4 hours at 37°C, in CO2 incubator.

[760] After incubation EDTA to a final concentration of 2 mM was added and incubated for 15 min at room temperature. Wash the cells with PBS at 1600 rpm, 8 min at room temperature. PBS

wash was repeated at 1600 rpm, 8 min, room temperature and resuspend in 500 µl PBS. Anti-CD3 (Biolegend) cocktail for each sample (20 µl in final) was added. Compensation was done for appropriate amount of single antibodies for compensation controls. Cells were incubated for 30 min at room temperature in the dark. 2ml of FACS buffer was added to each well tube. Cells were washed twice with FACS buffer at 1600 rpm, 8 min, room temperature. Cells are then re-suspended in 100µl of flow buffer (0.1%BSA in DPBS) with or 250µl/tube of BD cytofix/cytoperm, was incubated for 15min at RT. Cells were then centrifuged at 2000 rpm for 8 min at 4°C and supernatant was discarded.

[761] Cells were washed twice in wash buffer. Supernatant was discarded and IFN-γ PE (Invitrogen) intracellular staining was done as per manufacturer's protocol. Cells were incubated for 30 min – 60 min, on ice, in the dark. After the incubation cells were washed twice with 1ml of FACS buffer. Supernatant was discarded and resuspend in a final volume of 150 µl FACS buffer for Flow.

[762] As can be seen from FIG. 18A, release of IFN-γ in PBMCs when induced with C5511, anti CLEC2D antibody, at a concentration of 100 µg/mL was found to be ~2.97% as compared to uninduced control. Anti OKT-3 antibody, an anti CD3 antibody conjugated with FITC, was used as a positive control, showed 3-6 % IFN-γ release when compared with uninduced PBMC (FIG. 18A). Subsequently PBMC cells were gated based on CD3 +ive and -ive populations wherein CD3+ cells from total PBMC showed non-significant increase of IFN-γ release when treated with Anti CLEC2D antibody, either alone or with target cells (at T:E ratio 1:10) (FIG. 18B). On the contrary, CD3-ive population exhibited significant increase of IFN-γ release upon treatment with Anti CLEC2D antibody (FIG. 18C). It should be noted here that there was no or low increase in IFN-γ production in PC3 primed effector cells, either with whole PBMC or CD3+ cells or CD3- cells. Extending the observation to isolated NK cells, IFN-γ release experiments were performed wherein 1-2 % of IFN-γ release, to an approximate, was monitored in the presence of Anti CLEC2D antibody (FIG. 18D). Taken together, release of cytokine, such as IFN-γ, was elevated upon treatment of anti CLEC2D antibody, as described in present disclosure. The said observation mediated through anti CLEC2D antibody is subject to binding to CLEC2D antigen, expressed on effector cells, not limited to CD3-/NK cells, suggesting an independent pathway towards activation of other immune cells and essentially effective clearance of target cells.

[763] Cytotoxicity mechanism:

[764] To understand the functional role of Anti-CLEC2D antibody in the cytotoxicity mechanism, anti-CLEC2D isotype variants were constructed and assessed in cytotoxicity assay.

[765] Generation relevant isotype constructs

[766] As exemplified, mammalian expression vector pZB013 (accession # MTCC 25364) with IgG1, N-> A mutation and pZB014 (accession # MTCC 25365) with IgG4 were generated, wherein selected anti CLEC2D variable heavy chain region could be cloned. Subsequently said constructs with variable heavy chain and pZB008 (accession # MTCC 25359) with variable light chains, will be transfected, expressed and purified for subsequent experimentation. Both the mammalian constructs pZB013 with IgG1, N-> A mutation and pZB014 with IgG4 were custom designed and synthesized (FIGS. 19A and 19B). The plasmid which carries a kanamycinR /puromycinR cassette driven by strong promoter and high-copy-number ColE1/pMB1/pBR322/pUC origin of replication for propagation. The variable heavy chain can be replaced using restriction enzyme *AscI* and *XbaI*. The variable light chain can be replaced by restriction enzyme *EcoRI* and *AscI*.

[767] As exemplified herein, PCR was performed using sequence specific primers which were synthesized at Eurofins, and pZB014 and pZB008 vectors were restriction endonuclease activity with respective enzymes and the PCR amplified product was extracted using QIAquick Gel Extraction kit, infusion cloning was done using Infusion HD Cloning Plus CE from and 50% of mixture were transformed into Stellar competent cells *E.coli* and plated onto Kanamycin - containing LB agar plates. Plasmid DNA from transformed colonies was purified by QIAprep Spin Miniprep kit (Qiagen) and sequenced at Eurofins and large scale plasmid was isolated and used for transfection. Herein, Transformation of plasmid DNA into bacterial cell by heat shock method and Plasmid DNA Isolation from bacterial cells using QIAGEN kit and clone screening was similar to as described in section above. All clones were subsequently sequence verified and found to be error free. Respective anti CLEC2D clones in both IgG4 and/or IgG1 mutant formats, were isolated in large scale for transfection into mammalian expression system, CHO cells.

[768] CHO cell transfection to express novel anti-CLEC2D monoclonal antibody IgG4 variants:

As exemplified, for transfection, cell count and viability data was collected using Vi-cell XR automated cell counter, Beckman coulter. Transfection was carried out as per manufacturer's protocol Lipofectamine® LTX Reagent with PLUS Reagent. Required volume of cell suspension was centrifuged at 1400-1500 RPM for 4-5 mins and re-suspended in specified volume of OPTIMEM I as per Table 36 in 125ml shake flask. Transfection mix was prepared as per Table 3. Refer Table A for DNA details. 2-3 days post transfection 10ml Power CHO2 CD growth media was added and Glutamax was added from 200mM stock to achieve final concentration of 2mM. Day 6 post transfection, cell culture supernatant was harvested by centrifugation at 1400-2000 rpm for 10-15 minutes. IgG4 antibody variants were purified from cell culture supernatant by Protein A affinity chromatography.

Table 36. Example of transfection with IgG4 constructs

Parameters	**Details**
Total volume of transfection	50 ml
Cell density	1.25X10^6 cells/ml
OPTIMEM I	12.5ml
Total DNA	25 µg
HC:LC	1:3
Amount of DNA: Lipofectamine	1:3
Amount of DNA: Plus reagent	1:1

[769] As exemplified by, C4701, C3276, C3256 clones, not limited to, were transfected for further purification and evaluation in cytotoxicity assay.

Table 37. Anti-CLEC2D IgG1 antibody heavy chain and kappa light chain amino acid sequence

SEQ ID	VH+CH AA_IgG1	SEQ ID	VK+CK AA
SEQ ID 1481	EVQLVQSGAEVKKPGASVKV SCKASGYTFTSYAMHWVRQA PGQRLEWMGWINAGNGNTK YSQKFQGRVTITRDTSASTAY MELSSLRSEDTAVYYCARGSL SRSGWYAGLFDYWGQGTLVT VSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYR VVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSP GK	SEQ ID 1589	ETTLTQSPATLSVSLGERATLSC RASQSIGSNLVWYQLKPGQGPR LVIYSATSRATGIPARFSGSGSGT EFILSISNLQSEDLAVYYCQQYGS SPPTTFGQGTRLEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTK SFNRGEC
SEQ ID 1482	QITLKESGGGVVQPGRSLRLS CAASGFTFSSYSMNWVRQAP GKGLQWVAIISDDGSKSYYAD SVQGRFTISRDNSRNTVFLQM NSLRAEDTAMYYCARDRGTK WNQLNDVFDMWGQGTMVTV SSASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1590	EIVMTQSPATLSLSPGERATLSC RASQSVSSSYLAWYQQKPGRAP RLLIYGASNRATGIPDRFSGSGS GTDFTLIISRLEPEDFALYYCQQY GSSPGTFGQGTKVDIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVT KSFNRGEC
SEQ ID 1483	EVQLVQSGAEVKKPGASVKV SCKASGYTFTSYYMHWVRQA PGQGLEWMGIINPSGGSTSY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARGR GYSSSRLYYFDYWGQGTLVT VSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTV	SEQ ID 1591	DVVMTQSPATLSLSPGERATLSC RASQSVSSYLAWYQQKPGQAPR LLIYDASNRATGIPARFSGSGSGT DFTLTISSLEPEDFAVYYCQQRS NWPRTFGQGTKLEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKA

	SWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYR VVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSP GK		DYEKHKVYACEVTHQGLSSPVTK SFNRGEC
SEQ ID 1484	QVTLKESGGGLVRPGGSLRL SCEASGFTFSDPYMDWVRQA PGKGLEWVGRITNKRTGYATT YAASVKDRFTISRDDSRKSVY LQMNSLKTEDTAVYYCATDVS GSFAAYGGQGTLVTVSSAST KGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKT HTCPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK	SEQ ID 1592	EIVLTQSPDSLAVSLGERATITCK SSRNILYSGNNKNFLAWYQHKP GQPPKLLIYWASTRESGVPDRFS GSGSGTDFTLTINSLEAEDAATY YCHQSSSLPHTFGPGTKVDIKRT VAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQ GLSSPVTKSFNRGEC
SEQ ID 1485	EVQLVQSGGGVVQPGRSLRL SCAASGFTFSSYAMHWVRQA PGQRLEWMGWINAGNGNTK YSQKFQGRVTITRDTSASTAY MELSSLRSEDTAVYYCAGEG GAVAGTVYWGQGTLVTVSSA STKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVV SVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQ	SEQ ID 1593	ETTLTQSPGTLSLSPGQRATLSC RASESVSKSYLLWYQQKPGQAP RLLIYGASTRASGIPNRFSGSGS GTDFTLTISRLEPEDSAVYYCQH YGSSRTFGQGTRLEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVT KSFNRGEC

	PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK		
SEQ ID 1486	QVQLVQSGGGLVKPGGSLRL SCAASGFTFSNAWMSWVRQ APGKGLEWVGRIKSKTDGGT TDYAAPVKGRFTISRDDSKNT LYLQMNSLKTEDTAVYYCTTD EYFYWGQGTLVTVSSASTKG PSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCDKTHTCP PCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLP PSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALH NHYTQKSLSLSPGK	SEQ ID 1594	ETTLTQSPGTLSLSPGERATLSC RASQSISSTYLAWYQQKPGQAP RLLIYGASTRATGIPDRFSGSGS GTDFTLSISRLEPEDFAVYYCQQ YGNSPPGATFGQGTRLEIKRTVA APSVFIFPPSDEQLKSGTASVVCL LNNFYPREAKVQWKVDNALQSG NSQESVTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC
SEQ ID 1487	QVQLQQWGAGLLKPSETLSL TCAVYGGSFSGYYWSWIRQP PGKGLEWIGEINHSGSTNYNP SLKSRVTISVDTSKNQFSLKLS SVTAADTAVYYCARVNPGSYT REVSNFDYWGQGTLVTVSSA STKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVV SVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1595	DIQLTQSPSSLSASVGERVTITCR SSQALRNVVGLGDDLAWYQHTP GSAPKILIYSTSTLQSGVSSRFSG GKSGRDFTLTIDRLQPGDSATYY CLQHHDFPFTFGPGTKVEIKRTV AAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWKVDNALQ SGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGEC

SEQ ID 1488	QVQLQQSGPELVKPSQTLTLT CGISGDSVSSNSVTWNWVRQ SPSRGLEWLGRTYYRSQWYY NYAVSVKSRITISPDTSKNQFS LQLNSVTPEDTAVYYCATRGH NYGVDYWGPGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKT HTCPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK	SEQ ID 1596	DVVMTQSPLSLPVTPGEPASISC RSSQSLLNSNGYNYLEWYLQKP GQSPQLLIYLGSNRASGVPDRFS GSGSGTDFTLKISRVEADDAGVY YCMQSLQTPLTFGGGTKLEIKRT VAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQ GLSSPVTKSFNRGEC
SEQ ID 1489	QVQLVQSGGGLVKPGGSLRL SCAASGFTFSNAWMSWVRQ APGKGLEWVCRIKSKTDGETT DYAAPVKGRFTISRDDSKNTL YLQMNSLKTEDTAVYHCTTGV GWSPFQYWGQGTLVTVSSAS TKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDK THTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK	SEQ ID 1597	ETTLTQSPGTLSLSPGERATLSC RASQSVSSSYLAWYQQKPGQAP RLLIYGASSRATGIPDRFSGSGS GTDFTLTISRLEPEDFAVYYCQQ YGSSPRITFGQGTRLEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLS KADYEKHKVYACEVTHQGLSSP VTKSFNRGEC
SEQ ID 1490	EVQLVQSGGGLVQPGRSLRL SCTASGFTFGDYAMSWFRQA PGKGLEWVGFIRSKAYGGTT EYAASVKGRFTISRDDSKSIAY LQMNSLKTEDTAVYYCTRDD KIAAAGFTYWYFDLWGRGTLV TVSSASTKGPSVFPLAPSSKS TSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSSLGTQ TYICNVNHKPSNTKVDKKVEP KSCDKTHTCPPCPAPELLGGP	SEQ ID 1598	DVVMTQSPATLSVSPGERATLSC RASQSVSSNLAWYQQKPGQAPR LLIYGASTRATGIPARFSGSGSGT EFTLTISSLQSEDFAVYYCQQYN NWPPMYTFGQGTKLEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLS KADYEKHKVYACEVTHQGLSSP VTKSFNRGEC

	SVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTY RVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLS PGK		
SEQ ID 1491	QVQLVQSGAEVKKPGASVKV SCKASGYTFAAYYLHWVRQA PGQGLEWMGRISPGNGVTSY AQKFQGRVTMTGDTSINTVY MQLNNLISGDTAVYYCAREAA DDPFDHWGQGALVTVSSAST KGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKT HTCPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK	SEQ ID 1599	DVVMTQSPATLSVSPGERVTLSC RASQSVRDNVGWYKQKPGQPP RLVIYGASTRATGIPARISGSGSG TEFTLTISSLQSEDFAVYYCQQFN NWPYTFGQGTKLEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTK SFNRGEC
SEQ ID 1492	EVQLVQSGGGVVQPGRSLTL SCAASGFTFSSHLMHWVRQA PGKGLEWVAVISYDGTSKYY GDSVKGRFTISRDNSKNTLYL QMNSLRAEDTAIYYCAKADYK YDWGQGTLVTVSSASTKGPS VFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPP CPAPELLGGPSVFLFPPKPKD TLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	SEQ ID 1600	DIQMTQSPSSLSASVGDRVTITC RASQSISSYLNWYQQKPGKAPN LLIYAASSLHTGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSY SIPRTFGQGTKVEIKRTVAAPSVF IFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLTLSKAD YEKHKVYACEVTHQGLSSPVTKS FNRGEC

SEQ ID 1493	EVQLVQSGGGLVKPGGSLRL SCTASGFTFGDYAMSWVRQA PGKGLEWVGFIRSKAYGGTT EYAASVKGRFTISRDDSKSIAY LQMNSLKTEDTAVYYCTTHRR PIYDILTGFDYWGQGTLVTVS SASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1601	DVVMTQSPATLSVTPGERATLSC RASQSVNSNVAWYQQKPGQAP RLLIYDVSTRATDIPARFSGSGSG TDFTLTISRLDPEDFAVYYCQQC ASSPPVTFGGGTKLEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLS KADYEKHKVYACEVTHQGLSSP VTKSFNRGEC
SEQ ID 1494	QLQLQESGGGLVQPGRSLRL SCTASGFTFGDYAMSWVRQA PGKGLEWVGFIRSKAYGGTT EYAASVKGRFTISRDDSKSIAY LQMNSLKTEDTAVYYCTREDT MVRGVIPWGQGTLVTVSSAS TKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDK THTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK	SEQ ID 1602	EIVMTQSPATLSLSPGERATLSC GASQSVSSSYLAWYQQKPGLAP RLLIYDASSRATGIPDRFSGSGS GTDFTLTISRLEPEDFAVYYCQQ YGSSPRVTFGGGTKVDIKRTVAA PSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSTYSLSSTLTL SKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC
SEQ ID 1495	QLQLQESGSGLVKPSQTLSLT CAVSGGSISSGGYSWSWIRQ PPGKGLEWIGYIYHSGSTYYN PSLKSRVTISVDRSKNQFSLKL SSVTAADTAVYYCARDRRYY DSSGYYPAYYFDYWGQGTLV TVSSASTKGPSVFPLAPSSKS TSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSSLGTQ TYICNVNHKPSNTKVDKKVEP KSCDKTHTCPPCPAPELLGGP	SEQ ID 1603	DVVMTQSPGTLSLSPGERATLSC RASQSVSSSALAWFQQKPGQAP RLLIYDSSSRATGIPDSFSGSGSG TEFTLTISSLQPEDFATYYCQQFN TYPNTFGQGTKLEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTK SFNRGEC

	SVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTY RVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLS PGK		
SEQ ID 1496	EVQLVQSGGGLVKPGGSLRL SCAASGFTFSSYSMNWVRQA PGKGLEWVSYISSSGSYTNYA DSVKGRFTISRDNAKNSLYLQI NSLRAEDTAIYYCARDGGYDS SGFHFDYWGQGTLVTVSSAS TKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDK THTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK	SEQ ID 1604	DIQMTQSPLSLPVTPGEPASISCR SSQSLLHSNGYNYLDWFLQKPG QSPRLLIYMGSSRASGVPERFSG SGSGTDFTLKISRVEAEDVGVYY CMQTLHTVTFGGGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCL LNNFYPREAKVQWKVDNALQSG NSQESVTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC
SEQ ID 1497	QVQLQQSGPGLVKPSQTLSL TCAISGDSVSNNRAAWNWIR QSPSRGLEWLGRTYYRSKWY NEYAVSVKSRITINPDTSKNQF SLQLNSMTPEDSAVYYCAILP SSGYLQDHHYYGMDVWGQG TTVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQY NSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQK SLSLSPGK	SEQ ID 1605	ETTLTQSPGTLSLSPGERATLSC RASQSVSSSYLAWYQQKPGQAP RLLIYGASSRATGIPDRFSGSGS GTDFTLTISRLEPEDFAVYYCQQ YGSSLLFGQGTRLEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVT KSFNRGEC

SEQ ID 1498	EVQLVQSGAEVKKPGASVKV SCKASGYTFTSYGISWVRQAP GQGLEWMGWISAYNGNTNY AQKLQGRVTMTTDTSTSTAY MELSSLRSEDTAVYYCARAAV GDGYSYGRLDWGQGTLVTVS SASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1606	DIQLTQSPSFLSASVGDRVTITCR ASQGISSSLAWYQQKPGKAPKLL IYAASTLQSGVPSRFSGSGSGTD FTFTISSLQPEDIATYYCQQYDNL PPLTFGGGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLTLSKAD YEKHKVYACEVTHQGLSSPVTKS FNRGEC
SEQ ID 1499	EVQLVQSGAEVKKPGESLKIS CKGSGYSFTSYWIGWVRQMP GKGLEWMGIIYPGDSDTRYSP SFQGQVTISADKSISTAYLQW SSLKASDTAMYYCARLPSYYY DSSGYFTWYFDLWGRGTLVT VSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYR VVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSP GK	SEQ ID 1607	DVVMTQSPLSLPVTPGEPASISC RSSQSLLHSNGYNYLDWYLQKP GQSPQLLIYLGSNRASGVPDRFS GSGSGTDFTVKISRVEAEDVGVY YCMQALQTPYTFGQGTKLEIKRT VAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQ GLSSPVTKSFNRGEC
SEQ ID 1500	EVQLVQSGAEVKKPGASVKV SCKASGYTFTSYGISWVRQAP GQGLEWMGWIIPIFGIANYAQ KFQGRVTITADKSTSTAYMEL SSLRSEDTAVYYCARELYNYG SKDYFDYWGQGTLVTVSSAS TKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDK	SEQ ID 1608	EIVLTQSPLSLPVTLGQPASISCR SCQSLVYSDGNTYLNCFQQRPG QSPRRLIYKVSNRDSGVPDRFSG SGSGTDFTLEISRVEAEDVGIYFC MQGLQTPFTFGPGTKVDIKRTVA APSVFIFPPSDEQLKSGTASVVCL LNNFYPREAKVQWKVDNALQSG NSQESVTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC

	THTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK		
SEQ ID 1501	EVQLVQSGAEVKKPGESLKIS CKGSGYSFTSYWIGWVRQMP GKGLEWMGIIYPGDSDTRYSP SFQGQVTISADKSISTAYLQW SSLKASDTAMYYCARGGTWD TAMVTGFDYWGQGTLVTVSS ASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVV SVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1609	DVVMTQSPGTLSLSPGERATLSC RASQSVSSSYLAWYQQKPGQAP RLLIYGASSRATGIPDRFSGSGS GTDFTLTISRLEPEDFAVYYCQQ YGSSPALTFGGGTKLEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSTYSLSSTLTL SKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC
SEQ ID 1502	EVQLVQSGAEVKKPGESLKIS CKGSGYSFTSYWIAWVRQMP GKGLEWMGVIYPGDSDTRYS PSFQGQVTISADKSINTAYLQ WSSLKASDTAMYYCARPHYDI LTGSRAPFDYWGQGTLVTVS SASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1610	EIVMTQSPLSLPVTPGEPASISCR SSQSLLHSNGYNYLDWYLQKPG QSPQLLIYLGSTRASGVPDRFSG SGSGTDFTLKISRAEAEDVGVYY CMQALHTPWTFGLGTKVDIKRTV AAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWKVDNALQ SGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGEC

SEQ ID 1503	QVQLQQWGAGLLKPSETLSL TCAVYGGSFSGYYWSWIRQP PGKGLEWIGEINHSGSTNYNP SLKSRVTISVDTSKNQFSLKLS SVTAADTAVYYCARARVESKD GYFDYWGQGTLVTVSSASTK GPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYT LPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK	SEQ ID 1611	DIQMTQSPATLSVSPGERATLFC RASEGLTTNLAWYQHKPGQAPR LLIYAASTRATGVPARFSGSGSG TDFTLTISSLQSEDSAVYYCQQY NHWPLYTFGQGTKVEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLS KADYEKHKVYACEVTHQGLSSP VTKSFNRGEC
SEQ ID 1504	EVQLVESGGGVVQPGRSLRL SCAASGFTFTDAWMNWVRQ APGKGLEWIGRVKNKADGET TDYAAPVKGRITISRDDAKNTL YVQMNSLKTEDTAVYYCTADL RLSTWDAYDFWGQGTMVTV SSASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1612	DIQLTQSPSTLSLSPGERATLSCR ASQSVSSYLAWYQQKSGQAPRL LIYDASNRATGIPARFSGSGSGT DFTLTISSLEPEDFAVYYCQQGS NWPLTFGGGTKVEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTK SFNRGEC
SEQ ID 1505	QITLKESGGGLVQPGGSLRLS CTVSGFTFSNNWMTWVRQTP GKGLEWVANIKQDGTEKHYV DSVKGRFTISRDNAENSLYLQ MNSLRGEDTAVYYCARNSQR SFDYWGQGTLVTVSSASTKG PSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCDKTHTCP PCPAPELLGGPSVFLFPPKPK	SEQ ID 1613	DIVMTHTPLSSPVTLGQPASISCR SSQSLEHTDGNTYLSWLHQRPG QPPRLLIYKVSTRFSGVPDRFSG SGAGTDFTLKISRVEAEDVGVYY CVQATHYPRTFGHGTKVEIKRTV AAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWKVDNALQ SGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGEC

	DTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLP PSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALH NHYTQKSLSLSPGK		
SEQ ID 1506	QVTLKESGGGVVQPGRSLRL SCAASGFTFSSYGMHWVRQA PGKGLEWVAVISYDGSNKYY ADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCAKDLG DPRGGILNYWGQGTLVTVSS ASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVV SVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1614	EIVLTQSPGTLSLSPGERATLSCR ASQSISGSYLAWYQQKRGQAPR LLIYDASSRAEGIPDRFIGSGSGT DFTLTISRLEPEDFAMYYCQQYG SSPIFTFGPGTKVDIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTK SFNRGEC
SEQ ID 1507	EVQLVESGGGVVQPGRSLRL SCAASGFTFSSYAMHWVRQA PGKGLEWVAVISYDGSNKYY ADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARSSP WGELSLYQGAFDIWGQGTMV TVSSASTKGPSVFPLAPSSKS TSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSSLGTQ TYICNVNHKPSNTKVDKKVEP KSCDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTY RVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLS PGK	SEQ ID 1615	EIVLTQSPDSLPVTPGEPASISCR SSQSLLHSNGNNYLDWYLQKPG QSPQLLIYLGSNRASGVPDRFSG SGSGTDFTLKLSRVEAEDVGVYY CMQGLQIPITFGPGTKVDIKRTVA APSVFIFPPSDEQLKSGTASVVCL LNNFYPREAKVQWKVDNALQSG NSQESVTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC

SEQ ID 1508	QITLKESGGGLVQPGRSLRLS CAASGFTFDDYAMHWVRQAP GKGLEWVSAISGSGGSTYYA DSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCAKDNDF WSGKVFDYWGQGTLVTVSSA STKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVV SVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1616	DIQMTQSPSSVSASVGDRVTITC RASQNIRHWLVWYQQKLGQAPK LLIYAASNLQSGVPSRFSGSGSG TEFTLTINSLQAEDFATYYCLQHN SYPWTFGQGTKVEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTK SFNRGEC
SEQ ID 1509	EVQLVQSGGGLVQPGGSLRL SCAASGFTFSSYSMNWVRQA PGKGLEWVSYISSTSSTIYYA DSVKGRFTISRDNSKNMLFLQ MNSLRAEDTAVYYCAKEGGS GWRHYFDYWGQGTLVTVSS ASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVV SVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1617	EIVLTQSPDFQSVTPKQKVTITCR ASQSIGGSLHWYQQKPGQSPKLI IKYASQSFSGVPSRFSGSGSGTD FTLTIDSLEAEDAATYYCHQSISL PLTFGGGTKVDIKRTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESV TEQDSKDSTYSLSSTLTLSKADY EKHKVYACEVTHQGLSSPVTKSF NRGEC
SEQ ID 1510	QVTLKESGGGVVQPGRSLRL SCAASGFTFSSYAMHWVRQA PGKGLEWVAVISYDGSNKYY ADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARDYC SSTSCQNWFDPWGQGTLVTV SSASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSV	SEQ ID 1618	ETTLTQSPGTLSLSPGEGATLSC RASQSVTSNYLAWYQQKPGQAP RLLIYGASYRATGIPDRFSGSGS GTDFTLTISRLEPEDFAVYYCQQ YASSVTFGQGTRLEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVT KSFNRGEC

	FLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK		
SEQ ID 1511	QVQLVQSGGGLVQPGGSLRL SCAASGFTFSNYVMSWVRQA PGKGLEWVSAISGIGDTTYYA DSVKGRFTISRDNAKNTLYLQ MNSLRAEDTAVYYCARGRVA GDAFDIWGQGTMVTVSSAST KGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKT HTCPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK	SEQ ID 1619	DVVMTQSPATLSVSPGERATLSC RASQSISSNLAWYQQKPGQAPR LLIYGASTRATGIPARFSGSGSGT EFTLTISSLQSEDFAVYYCQQYN NWPRTFGQGTKLEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTK SFNRGEC
SEQ ID 1512	QLQLQESGGGLVQPGGSLRL SCAASGFTFSSYAMSWVRQA PGKGLEWVSAISGSGGSTYY ADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCAKDQG AAAGTLGYFDYWGQGTLVTV SSASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1620	DIQLTQSPDSLAVSLGERATINCK SSQSVLYSSNNKNYLAWYQQKP GQPPKLLIYWASARESGVPDRFS GSGSGTDFTLTINSLQAEDVAVY YCQQFYSPPRTFGQGTKVEIKRT VAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQ GLSSPVTKSFNRGEC

SEQ ID 1513	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSYDINWVRQAT GQGLEWMGWMNPNSGNTG YAQKFQGRVTMTRNTSISTAY MELSSLRSEDTAVYYCTRGIY DSSGSSNPFDSWGQGTLVTV SSASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1621	EIVLTQSPGTLSLSPGERATLSCR ASQSVSSSYLAWYQQKPGQAPR LLIYGASSRATGIPDRFSGSGSGT DFTLTISRLEPEDFAVYYCQQYG SSPPGTFGGGTKVDIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVT KSFNRGEC
SEQ ID 1514	EVQLVQSGAEVKKPGASVKIS CEASGYTFTDYAIHWVRQAP GQRLEWMGWINAGDGGTKS SREFQGRVTITRDTSATTAYM EVSSLRSEDTAVYYCARGYC SGGSCPGTDFDYWGQGTLVT VSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYR VVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSP GK	SEQ ID 1622	EIVLTQSPGTLSLSPGERATLSCR ASQSLSTNLAWYQQKPGQAPRL LIYGASTRATGIPARFSGSGSGTE FTLTITSLQSEDFAVYYCQQYHN WPPYTFGQGTKVEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTK SFNRGEC
SEQ ID 1515	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSYYMHWVRQA PGQGLEWMGIINPSGGSTSY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARDG VGGRDGYNFDYWGQGTLVT VSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPK	SEQ ID 1623	DIQMTQSPSTLSASVGDRVTITC RASQSISSWLAWYQQKPGKAPK LLIYKASSLESGVPSRFSGSGSG TEFTLTISSLQPDDFATYYCQQY NSYWTFGQGTKVEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTK SFNRGEC

	SCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYR VVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSP GK		
SEQ ID 1516	EVQLVQSGGGLVQPGGSLRL SCAASGFTVSSNYMSWVRQA PGKGLEWVSVIYSGGSTYYA DSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARAPLAA DGYFDYWGQGTLVTVSSAST KGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKT HTCPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK	SEQ ID 1624	ETTLTQSPGTLSLSPGEGATLSC RASHSVGANYIAWYQQKPGQAP RLLIHTASKRATGVPERFSGSGS GTDFTLSISRLEPEDFAVYHCQQ YAAAPITFGQGTRLEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVT KSFNRGEC
SEQ ID 1517	EVQLVQSGAEVKKPGSSVKV SCKASGGTFSSYAISWVRQA PGQGLEWMGGIIPIFGTANYA QKFQGRVTITADESTSTAYME LSSLRSEDTAVYYCARARGLQ YLIWYFDLWGRGTLVTVSSAS TKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDK THTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK	SEQ ID 1625	EIVMTQSPSSLSASVGDRVIITCR ASQGIANYLAWYQQKPGKGPKL LIYASSTLQSGVPSRFSGSGSGT DFTLTISGLQPEDVATYYCQKYN SVPLTFGGGTKVDIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTK SFNRGEC

SEQ ID 1518	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSYYMHWVRQA PGQGLEWMGIINPSGGSTSY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCASPG MVRGVITAPLDYWGQGTLVT VSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYR VVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSP GK	SEQ ID 1626	DVVMTQSPVSLAVSLGERATINC KSSQSVLYRTNNKNYLAWYQQK PGQPPKLLIYWASTRESGVPDRF SGSGSGTDFTLTISSLQPEDVAV YYCQQYYNLPRSFGQGTKLEIKR TVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQ GLSSPVTKSFNRGEC
SEQ ID 1519	EVQLVQSGGGLVKPGGSLRL SCAASGFTFSSYAISWVRQAP GQGLEWMGGIIPMYGTANYA QKFQGRVTITADESTSTAYME LSSLRSEDTALYYCAREAKW GMYYFDYWGQGTLVTVSSAS TKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDK THTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK	SEQ ID 1627	DIVMTHTPDSLAVSLGERATINCK SNRSVLYSPNNQNYLGWYQQKP GQPPKLLIYWASTRDSGAPDRFS GSGSGTDFTLTINSLQAEDVAVY YCQQYASTPYTFGQGTKVEIKRT VAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQ GLSSPVTKSFNRGEC
SEQ ID 1520	EVQLVESGGGVVQPGRSLRL SCAASGFTFSSYAIHWVRQAP GKGLEWVAIISDDGSKSYYAD SVQGRFTISRDNSRNTVYLQM NSLRAEDTAMYYCARDRGTK WNQLNDVFDMWGQGTMVTV SSASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKS	SEQ ID 1628	DVVMTQSPATLSLSPGERATLSC RASESVNSNFLAWYQQKPGQAP RLLIYAASTRATGIPARFSGSGSG TEFTLIITSLQSEDFAVYYCQQYN NWPLTFGGGTKLEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTK SFNRGEC

	CDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK		
SEQ ID 1521	QMQLVQSGAEVKKPGASVKV SCTASGYTFTSSDINWVRQAT GQGLEWMGWMNPNSGNTG YAEKFQGRVTMTSDSSISTAY MELRSLTTEDTAVYYCARGG GASYTDSWGQGTLVTVSSAS TKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDK THTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK	SEQ ID 1629	DVVMTQSPATLSLSPGERATLSC RASQSVSSYLAWYQQKPGQAPR LLIYDASNRATGIPARFSGSGSGT DFTLTISSLEPEDFAVYYCQQRS NWSLTFGGGTKLEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTK SFNRGEC
SEQ ID 1522	QVQLVQSGGGLVQPGRSLRL SCTASGFTFGDYAMSWFRQA PGKGLEWVGFIRSKAYGGTT EYAASVKGRFTISRDDSKSIAY LQMNSLKTEDTAVYYCTAKG GYVGYSYGPFGGYWGQGTL VTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNST YRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDG SFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSL SPGK	SEQ ID 1630	ETTLTQSPGTLSLSPGERATLSC RASQSVSSSYLAWYQQKPGQAP RLLIYGASTRATGIPDRFSGSGS GTDFTLTIGRLEPEDFAVYYCQH YGPSRRITFGQGTRLEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLS KADYEKHKVYACEVTHQGLSSP VTKSFNRGEC

SEQ ID 1523	QVQLVQSGGGLVQPGRSLRL SCTASGFTFGDYAMSWFRQA PGKGLEWVGFIRSKAYGGTT EYAASVKGRFTISRDDSKSIAY LQMNSLKTEDTAVYYCTRGG TMVRGFGFNYWGQGTLVTVS SASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1631	ETTLTQSPDTLSVSPGGRATLSC RASQSIGSNLAWYQQKPGQSPR LLIYDASTRATGIPARFSGSGSGT EFTLTISSLESEDFVLYYCQQHGE WPTFGQGTRLEIKRTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESV TEQDSKDSTYSLSSTLTLSKADY EKHKVYACEVTHQGLSSPVTKSF NRGEC
SEQ ID 1524	QVQLQQWGAGLLKPSETLSL TCAVYGGSFSGYYWSWIRQP PGKGLEWIGEINHSGSTNYNP SLKSRVTISVDTSKNQFSLKLS SVTAADTAVYYCARARRAMIG PLPRLVGYFDLWGRGTLVTVS SASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1632	DVVMTQSPATLSLSPGERATLSC RASQSVGNSLAWYQQKPGQAP RLLIYDASNRATGIPARFSGSGS GTDFTLTITSLEPEDFAIYYCQQR GTWPPLTFGGGTKLEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLS KADYEKHKVYACEVTHQGLSSP VTKSFNRGEC
SEQ ID 1525	QVQLQQWGAGLLKPSETLSL TCAVYGGSFSGYYWSWIRQP PGKGLEWIGEINHSGSTNYNP SLKSRVTISVDTSKNQFSLKLS SVTAADTAVYYCARGRPAPS WVKTRNWFDPWGQGTLVTV SSASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSV	SEQ ID 1633	DVVMTQSPSSLSASVGDTVTITC RASQSITNWLAWYQQKPGKAPK RLIYGASSLQSGVPSRFSGSGSG TEFTLTISSLQPEDFATYYCQQYT NYPRTFGQGTKLEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTK SFNRGEC

	FLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK		
SEQ ID 1526	QVQLQQSGPGLVKPSQTLSL TCAISGDSVSSNSAAWNWIR QSPSRGLEWLGRTYYRSKWY NDYAVSVKSRITINPDTSKNQF SLQLNSVTPEDTAVYYCAREA SSGWNWGQGTLVTVSSASTK GPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYT LPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK	SEQ ID 1634	DIQMTQSPSTLSASVGDRVTITC RARQSISNRLAWYQQKPGRAPN VLIYKASTLANGVPSRFSGSGSG TEFTLTISSLQPDDFATYYCQQY QSYWTFGPGTKVEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTK SFNRGEC
SEQ ID 1527	QVQLQESGPGLVKPSQTLSLT CAISGDSVSSNNAAWNWIRQ SPSRGLEWLGRTFYRSKWYN DYAVSVKSRLTVNPDTSKNQF SLRLNSVSPEDTAVYYCARG GRYTKGGYFDDWGQGTLVTV SSASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1635	DIQLTQSPATLSLSPGERATLSCK ASQSVSSYLAWYQQKLGQAPRL LIYDASNRATGIPARFSASGSGTD FTLTISSLQPEDVATYYCQKYNSP PRTFGQGTKVEIKRTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESV TEQDSKDSTYSLSSTLTLSKADY EKHKVYACEVTHQGLSSPVTKSF NRGEC

SEQ ID 1528	QVTLKESGPTLVKPTQTLTLT CTFSGFSLSTSGVGVGWIRQ PPGKALEWLALIYWDDDKRYS PSLKSRLTITKDTSKNQVVLTM TNMDPVDTATYYCAHRLDSS GRGGYFDYWGQGTLVTVSSA STKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVV SVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1636	ETTLTQSPGTLSLSPGERVSLSC RASQNVYSNFLAWYQQRPGQAP SLLIYGASSRAAGVPDRFSGSGS GTDFALTISRVEPEDFAVYYCQQ YGTSPITFGQGTRLEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVT KSFNRGEC
SEQ ID 1529	EVQLVESGGGVVQPGRSLRL SCTASGFTFSSYGMHWVRQA PGKGLEWVAVISYDGSNKYY ADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCAKELV GTSSPYYYYYYGMDVWGQG TMVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQY NSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQK SLSLSPGK	SEQ ID 1637	EIVLTQSPRSSPVTLGQPASISCR SSQSLEHGDGNTYLSWLQQRPG QPPRLLIYKVSNRLSGVPDRFSG SGAGTDFTLKISRVEAEDVGVYY CMQGIYWPRTFGQGTRLEIKRTV AAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWKVDNALQ SGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGEC
SEQ ID 1530	QLQLQESGGGLVQPGGSLRL SCAASGFTVSSNYMSWVRQA PGKGLEWVSVIYSGGSTYYA DSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARDYYY GSGSSPWGQGTLVTVSSAST KGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKT	SEQ ID 1638	ETTLTQSPVTLSLSPGDRATLSC RASQSVSSTSLAWYQHKPGQAP RLLIYGASRRATGIPDRFSGSGS GTDFTLTINRLEPEDFAVYYCQH YGSSPPITFGQGTRLEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLS KADYEKHKVYACEVTHQGLSSP VTKSFNRGEC

	HTCPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK		
SEQ ID 1531	QVQLQQWGAGLLKPSETLSL TCAVYGGSFSGYYWSWIRQP PGKGLEWIGEINHSGSTNYNP SLKSRVTISVDTSKNQFSLKLS SVTAADTAVYYCARGRPYCS STSCYPEWFDPWGQGTLVTV SSASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1639	ETTLTQSPATLSVSPGERATLSC RASQSVGSKLAWYQQKPGQAP RLLIYGASTRATGVPVRFSGSGS GTEFTLTISSLQSEDFAVYYCQQ YNNWPPITFGQGTRLEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSTYSLSSTLTL SKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC
SEQ ID 1532	QVTLKESGGGVVQPGRSLRL SCAASGFTFSSYGMHWVRQA PGKGLEWVAVISYDGSNKYY ADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCAKLRGI DYYDSSGYQRGFDYWGQGT LVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNST YRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDG SFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSL SPGK	SEQ ID 1640	EIVLTQSPLSLPVTPGEPASISCR SSQSLLHSNGYNYLDWYLQKPG QSPQLLIYLGSNRASGVPDRFSG SGSGTDFTLKISRVEAEDVGVYY CMQTLQTPLTFGGGTKVDIKRTV AAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWKVDNALQ SGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGEC

SEQ ID 1533	QVQLQESGPGLVKPSETLSLT CTVSGGSISSYYWSWIRQPP GKGLEWIGYIYYTGSTNYNPS LKSRVTISVDTSKNQFSLKLSS VTTADTAVYYCARGGRGDGA AFDIWGQGTMVTVSSASTKG PSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCDKTHTCP PCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLP PSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALH NHYTQKSLSLSPGK	SEQ ID 1641	DVVMTQSPDSLAVSLGERATINC KSSQSVLYSSNNKNYLAWYQQK PGQPPKLLIYWASTRESGVPDRF SGSGSGTDFTLTISSLQAEDVAV YYCQQYYSSTPYTFGQGTKLEIK RTVAAPSVFIFPPSDEQLKSGTA SVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSTYS LSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
SEQ ID 1534	QVQLVQSGGGVVQPGRSLRL SCAASGFTFSSSAMHWVRQA PGKGLEWVAMIWHDESKKYY ADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARPPD GGNSGRWYFDLWGRGTLVT VSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYR VVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSP GK	SEQ ID 1642	DIVMTHTPLSLSVTPGQPASISCK SSQSLLGGDGKTYLYWYLQKPG QPPQLLLYEVSNRFSGVPDRFSG SGAATDFTLKISRVEAEDVGVYY CMQSTQFPWTFGQGTKVEIKRT VAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQ GLSSPVTKSFNRGEC
SEQ ID 1535	QMQLVQSGGGLVQPGGSLRL SCAASGFTFSSYAMSWVRQA PGKGLEWVSAISGSGGSTYY ADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCAKDKN VRKHDYGDHPYGGYFDYWG QGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTF PAVLQSSGLYSLSSVVTVPSS SLGTQTYICNVNHKPSNTKVD	SEQ ID 1643	ETTLTQSPGTLSLSAGERATLSC RASQSVSSSYLAWYQQKPGQAP RLLIYAASYRATGIPDRFSGRGS GTEFTLTISSLQSEDFAVYYCQQ YNNWPPITFGQGTRLEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSTYSLSSTLTL SKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC

	KKVEPKSCDKTHTCPPCPAPE LLGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQY NSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQK SLSLSPGK		
SEQ ID 1536	EVQLVQSGAEVKKPGASVKV SCKASGYTFTSYAMHWVRQA PGQRLEWMGWINAGNGNTK YSQKFQGRVTITRDTSASTAY MELSSLRSEDTAVYYCARVA GATSLWYWGQGTLVTVSSAS TKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDK THTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK	SEQ ID 1644	DVVMTQSPATLSVSPGERATLSC RASQSVSSNLAWYQQKPGQAPR LLIYDASTRATGIPARFSGSGSGT EFTLTISSLQSEDFAVYYCQHYN NWPHTFGQGTKLEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTK SFNRGEC
SEQ ID 1537	QVQLQQSGPGLVKPSQSLSL TCAISGDSVSSNSAAWNWIR QSPSRGLEWLGRTYYRSKWY NDYAVSVKSRITIKPDTSKNQF SLQLNSVTPEDTAVYYCTRLA NSDGVDVWGQGTMVTVSSA STKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVV SVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1645	ETTLTQSPGTLSLSPGERATLSC RASQSVSSNSLAWYQQKPGQAP RLLIYGASSRASGIPDRFNGSGS GTDFTLTINRLEPEDFAVYYCQQ YGNSQTFGQGTRLEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVT KSFNRGEC

SEQ ID 1538	QVQLQQSGPGLVKPSQTLSL TCAISGDSVSSDSAVWTWIRQ SPSRGLEWLGRTYYKSKWYN DYAASVKSRITINPDTSKNQFS LHLNSVTPEDTAVYYCARGVT RTFDYWGQGTTVTVSSASTK GPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYT LPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK	SEQ ID 1646	DVVMTQSPATLSVSPGERATLSC RASQSVSSNLAWYQQKPGQAPR LLIYGASTRATGIPARFSGSGSGT EFTLTISSLQSEDFAVYYCQQYN NWPRTFGQGTKLEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTK SFNRGEC
SEQ ID 1539	QLQLQESGPGLVKPSQTLSLT CAISGDSVSSNSAAWNWIRQ SPSRGLEWLGRTYYRSKWYN DYAVSVKSRITINPDTSKNQFS LQLNSVTPEDTAVYYCAEGN GPFDPWGQGTLVTVSSASTK GPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYT LPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK	SEQ ID 1647	DVVMTQSPLSLPVTLGQPASISC RSSQSLVYSDGNTYLNWFQQRP GQSPRRLIYKVSNRDSGVPDRFS GSGSGTDFTLKISRVEAEDVGVY YCMQGTHWPRTFGGGTKLEIKR TVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQ GLSSPVTKSFNRGEC
SEQ ID 1540	QITLKESGGGVVQPGRSLRLS CVASGFTFSTYPMHWVRQAP GKGLEWVAVISYDGRNEYYA DSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCATRDTPL VGVSIYWGQGTLVTVSSASTK GPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLFPPK	SEQ ID 1648	DIQMTQSPSTLSASVGDRVTITC RASQSISRWLAWYQQKPGKAPK LLIYKASTIKSGVPSRFSASGSGT EFTLTISSLQPEDFATYYCQHYKS DSRTFGQGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLTLSKAD YEKHKVYACEVTHQGLSSPVTKS FNRGEC

	PKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYT LPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK		
SEQ ID 1541	QMQLVQSGGGLVKAGGSLRL SCSASGFTFSSYAMHWVRQA PGKGLEYVSAISSNGGSTYYA DSVKGRFTISRDNSKNTLYLQ MSSLRAEDTAVYYCVNRAGY GDYRHFQHWGQGTLVTVSSA STKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVV SVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1649	DVVMTQSPSSLAASVGDRITITC RPSQDIGTYLNWYQQKAGEAPK LLIYAASNLHSGVSSRFRGVGSG TQFTLTISSLQPEDFATYYCHQSY GPRTFGQGTKLEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLTLSKAD YEKHKVYACEVTHQGLSSPVTKS FNRGEC
SEQ ID 1542	EVQLVQSGGGVVQPGGSLRL SCAASGFTFSSYGMHWVRQA PGKGLEWVAFISYDGSNKYYA DSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCATTGDR FQEFDYWGQGTLVTVSSAST KGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKT HTCPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK	SEQ ID 1650	ETTLTQSPATLSVSPGERATLSC RASQSVSSNLAWYQQKPGQAPR LLIYGASTRATGIPARFSGSGSGT EFTLTISSLQSEDFAVYYCQQYN NWPPITFGQGTRLEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVT KSFNRGEC

SEQ ID 1543	QMQLVQSGGVLLQPGRSLRL SCTASGFTFAAYNINWFRQGP GGGLEWVGFIRANADSGTTE YAASVKGRFFISRDDSRSTAY LQMTSLKTEDTAVYYCARDD RGRGDDFDYWGQGTLVTVSS ASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVV SVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1651	DVVMTQSPGTLSLSPGERATLSC RASQSVSSSYLAWYQQKPGQAP RLLIYGASSRATGIPDRFSGSGS GTDFTLTISRLEPEDFAVYYCQQ YGSSGYTFGQGTKLEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLS KADYEKHKVYACEVTHQGLSSP VTKSFNRGEC
SEQ ID 1544	QVQLVQSGGGLVQPGGSLRL SCAASGFTFSSYGMTWVRQA PGKGLEWVSTISGNGVGTYY PDSVKDRFTISRDSSKNTVYL QMNSLRAEDTAVYYCVKHGR AGINWYFDLWGRGTLVTVSS ASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVV SVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1652	ETTLTQSPGTLSLSPGERATLSC RASQSVSSSYLAWYQQKPGQAP RLLIYGASSRATGIPDRFSGSGS GTDFTLTISRLEPEDFAVYYCQQ YGSSFGQGTRLEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLTLSKAD YEKHKVYACEVTHQGLSSPVTKS FNRGEC
SEQ ID 1545	QVQLQQSGPGLVKPSQTLSL TCAISGDSVSSNSAAWNWIR QSPSRGLEWLGRTYYRSKWY NDYAVSVKSRITINPDTSKNQF SLQLNSVTPEDTAVYYCARG GGLWAFDIWGQGTTVTVSSA STKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPELLGGPSVFL	SEQ ID 1653	EIVLTQSPSTLSASVGDRVTITCR ASQSISSCLAWYQQKPGKAPKLL IYAASTLQSGVPSRFSGSGSGTE FTLTISTLQPEDFATYYCQQLNSY PQTFGQGTKVDIKRTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESV TEQDSKDSTYSLSSTLTLSKADY EKHKVYACEVTHQGLSSPVTKSF NRGEC

	FPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVV SVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK		
SEQ ID 1546	EVQLVQSGAEVKKPGASVKV SCKASGYTFTGYYMHWVRQA PGQGLEWMGWINPNSGGTN YAQKFQGRVTMTRDTSISTAY MELSRLRSDDTAVYYCARDKI GSCPYWGQGTLVTVSSASTK GPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYT LPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK	SEQ ID 1654	DIVMTHTPLSLSVTPGQPASISCK SSQSLLHSDGKTYLYWYLQKPG QPPQLLIYEVSNRFSGVPDRFSG SGSGTDFTLKISRVEAEDVGVYY CMQSIQLPLTFGGGTKVEIKRTV AAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWKVDNALQ SGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGEC
SEQ ID 1547	QVTLKESGPTLVKPTQTLTLT CTFSGFSLSTSGVGVGWIRQ PPGKALEWLALIYWDDDKRYS PSLKSRLTITKDTSKNQVVLTM TNMDPVDTATYYCAHRPDSS SQCFDYWGQGTLVTVSSAST KGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKT HTCPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK	SEQ ID 1655	DVVMTQSPGTLSLSPGERATLSC RASQSVSSSYLAWYQQKPGQAP RLLIYGASSRATGIPDRFSGSGS GTDFTLTISRLEPEDFAVYYCQQ YNNWPLTFGGGTKLEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLS KADYEKHKVYACEVTHQGLSSP VTKSFNRGEC

SEQ ID 1548	QVTLKESGGGVVQPGRSLRL SCAASGFTFSSYAMHWVRQA PGKGLEWVAVISYDGSNKYY ADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARSSG WSLPEDYWGQGTLVTVSSAS TKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDK THTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK	SEQ ID 1656	DIQLTQSPDSLAVSLGERATINCT SSQSVLYSSNNKNYIAWYQQKP GQPPKLLIYWASTRESGVPDRFS GSGSGTDFTLTISSLQAEDVAVY YCQQYYYIPRTFGQGTKVEIKRT VAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQ GLSSPVTKSFNRGEC
SEQ ID 1549	QVQLVQSGAEVKKPGASVKV SCKVSGYTLTELSMHWVRQA PGKGLEWMGGFDPEDGETIY AQKFQGRVTMTEDTSTDTAY MELSSLRSEDTAVYYCATDVN PELLGAGFDYWGQGTLVTVS SASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1657	DVVMTQSPLSLPVTPGEPASISC RSSQSLLHSNGYNYLDWYLQKP GQSPQLLIYLGSNRAPGVPDRFS GSGSGTDFTLKISRVEAEDVGVY YCMQALQTRTFGQGTKLEIKRTV AAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWKVDNALQ SGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGEC
SEQ ID 1550	QVTLKESGGGLVQPGGSLRL SCAASGFTFSDQYMDWVRQA PGKGLEWVGRVRNKANSYTT EYAASVKGRFTISRDDSKNSL YLQMNSLNTEDTAMYFCASSL NSGGYRCFHHWGQGTLVTVS SASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSV	SEQ ID 1658	ETTLTQSPGTLSLSPGERATLSC RASQSLTSSYLAWYQQKPGQAP RLLIYRASSRATGIPDRFSGSGS GTDFTLTISRLEPEDFAVYYCQQ YGSSPNTFGQGTRLEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLS KADYEKHKVYACEVTHQGLSSP VTKSFNRGEC

	FLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK		
SEQ ID 1551	QVQLVQSGGGLVQPGGSLRL SCSASGFTFSSYAMHWVRQA PGKGLEYVSAISSNGGSTYYA DSVKGRFTISRDNSKNTLYLQ MSSLRAEDTAVYYCVKAPRG VVPAAMRGGYWGQGTLVTVS SASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1659	EIVLTQSPLSLPVTLGQPASISCR SSQSLVHSNGHTYLSWFQQRPG QSPRRLIYEVSNRDSGVPDRFSG SGSGTDFTLRISRVEAEDVGVYY CLQGTHWPPLTVGGGTKVDIKRT VAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQ GLSSPVTKSFNRGEC
SEQ ID 1552	QVQLQESGGGLVQPGRSLRL SCTASGFTFGDYAMSWFRQA PGKGLEWVGFIRSKAYGGTT EYAASVKGRFTISRDDSKSIAY LQMNSLKTEDTAVYYCTRLVG NSGSYYPFGYWGQGTLVTVS SASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1660	DVVMTQSPATLSLSPGERATLSC RASQSVGSDLAWYQQKPGQAP RLLIYRASTRAAGIPARFSGSGSG TDFTLTISRLEPEDFAVFYCQQY GRSPYTSGQGTKLEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVT KSFNRGEC

SEQ ID 1553	QVQLQQWGAGLLKPSETLSL TCAVYGGSFSGYYWSWIRQP PGKGLEWIGEINHSGSTNYNP SLKSRVTISVDTSKNQFSLKLS SVTAADTAVYYCARGRSLPYR GLAPRSFGGYYFDYWGQGTL VTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNST YRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDG SFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSL SPGK	SEQ ID 1661	DIVMTHTPDSLAVSLGERATINCK SSQSVLYSSNNKNYLAWYQQKP GQPPKLLIYWASTRESGVPDRFS GSGSGTDFTLTISSLQAEDVAVY YCQQYYSTPLTFGGGTKVEIKRT VAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQ GLSSPVTKSFNRGEC
SEQ ID 1554	QVQLQESGGGLVRPGGSLRL SCGDSGFNFSGYEMNWVRQ APGKGLEWVSYVSTSGSTRY YADSVKGRFTISRDNAKNTLY LQMNSLRVEDTAVYYCARGR THWGPQDFDYWGQGTLVTV SSASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1662	EIVMTQSPLSLSVTPGEPASISCR SSQSLLHSSGYNYLDWYLQKPG QSPQLLIYLGSTRASGVPDRFSG SGSGTDFTLKISRVEAEDVGVYY CMQGLQIPLTFGGGTKVDIKRTV AAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWKVDNALQ SGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGEC
SEQ ID 1555	QVQLQESGGGLVQPGGSLRL SCAASGFTFSSYAMSWVRQA PGKGLEWVSAISGSGGSTYY ADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCAKGGM YYYGSGSSYFDYWGQGTLVT VSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPK	SEQ ID 1663	DIVMTHTPLSLSVTPGQPASISCK SSQSLLHSDGKTYLYWYLQKPG QPPQLLIYEVSNRFSGVPDRFSG SGSGTDFTLKISRVEAEDVGVYY CMQSIQLPWTFGQGTKVEIKRTV AAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWKVDNALQ SGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGEC

	SCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYR VVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSP GK		
SEQ ID 1556	QVQLVQSGGGLVQPGGSLRL SCAASGFTFSSYAMSWVRQA PGKGLEWVSGISGSGGSTYY ADSVKGRFTISRDNSKNMLFL QMNSPRAEDTAVYYCAKKIAA AGKQPVDYWGQGTLVTVSSA STKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVV SVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1664	ETTLTQSPATLSVSPGERATLSC RASQSVSSNLAWYQQKPGQAPR LLIYGASTRATGIPARFSGSGSGT EFTLTISSLQSEDFAVYYCQQYN NWPRFGQGTRLEIKRTVAAPSVF IFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLTLSKAD YEKHKVYACEVTHQGLSSPVTKS FNRGEC
SEQ ID 1557	QVQLQQWGAGLLKPSETLSL TCAVYGGSFSGYYWSWIRQP PGKGLEWIGEINHSGSTNYNP SLKSRVTISVDTSKNQFSLKLS SVTAADTAVYYCARRKVYDYV WGSYRLPGSVSYYFDYWGQ GTLVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQY NSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQ	SEQ ID 1665	DVVMTQSPSTLSASVGDRVTITC RASQTINSWLAWYQQKPGKAPK LLISRASRLESGVPSRFSGSASG TEYILTINSLQPDDFAMYFCHQYN SYSPTFGQGTKLEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTK SFNRGEC

	GNVFSCSVMHEALHNHYTQK SLSLSPGK		
SEQ ID 1558	QVQLVQSGAEVKKPGESLKIS CKGSGYSFTSYWIGWVRQMP GKGLEWMGIIYPGDSDTRYSP SFQGQVTISADKSISTAYLQW SSLKASDTAMYYCARLPGRA ARPDYWGQGTLVTVSSASTK GPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYT LPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK	SEQ ID 1666	ETTLTQSPGTLSLSPGERATLSC RASQSVSSSYLAWYQQKPGQAP RLLIYGASSRATGIPARFSGSGS GTDFTLTISSLEPEDFAVYYCQQ RYNWPITFGQGTRLEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLS KADYEKHKVYACEVTHQGLSSP VTKSFNRGEC
SEQ ID 1559	QVTLKESGGGVVQPGRSLRL SCAASGFTFSSYAMHWVRQA PGKGLEWVAVISYDGSNKYY ADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARGPG AVAGTKPKYYFDYWGQGTLV TVSSASTKGPSVFPLAPSSKS TSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSSLGTQ TYICNVNHKPSNTKVDKKVEP KSCDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTY RVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLS PGK	SEQ ID 1667	EIVLTQSPATLSLSPGETATLSCR ASQTIGPKSFGWYQQRPGQAPR LLIYDSNRATGIPARFSGSGSGTD FTLTISSLEPEDFAVYYCQQRSR WPLTFGPGTKVDIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLTLSKAD YEKHKVYACEVTHQGLSSPVTKS FNRGEC

SEQ ID 1560	EVQLVQSGGGVVQPGRSLRL SCAASGFTFSSYAMHWVRQA PGKGLEWVAVISYDGSNKYY ADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARATY YYDSSGYRFDYWGQGTLVTV SSASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1668	DVVMTQSPLSLPVTLGQPASISC RSSQSLVYSDGNTYLYWFQQRA GQSPRRLIYKVSKRDSGVPDRFS GSGSGTDFTLKISRVEAEDVGIYY CVQGRHWPYTLGQGTKLEIKRT VAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQ GLSSPVTKSFNRGEC
SEQ ID 1561	EVQLVQSGGGLVEPGGSLRL SCAASRFTFSDAWMSWVRQ APGKGLEWVGRIKSKISGGTT DYAAPVQGRFTISRDDSKNTL YLQMDSLKTEDTAVYYCANR NLGYWGQGTLVTVSSASTKG PSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCDKTHTCP PCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLP PSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALH NHYTQKSLSLSPGK	SEQ ID 1669	EIVLTQSPGTLSLSPGERATLSCR ASQSVSSSYLAWYQQKPGQAPR LLIYDASNRATGIPARFSGSGSGT EFTLTISSLQPDDFATYYCQQYN SYSRTFGQGTKVDIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTK SFNRGEC
SEQ ID 1562	EVQLVQSGAEVKKPGASVKV SCKASGYTFTSYAMHWVRQA PGQRLEWMGWINAGNGNTK YSQKFQGRVTMTTDTSTSTA YMELRSLRSDDTAVYYCARA RYYDSSGYIAPSGYFDYWGQ GTLVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPEL	SEQ ID 1670	DVVMTQSPSTLSASVGDRVTITC RASQSITTWLAWSQQQPGKAPK LLIYKASSLTSGVPSRFSGSGSG TEFTLTISSLQPDDFASYYCHHYN GASRMFGQGTKLEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTK SFNRGEC

	LGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQY NSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQK SLSLSPGK		
SEQ ID 1563	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSYAMHWVRQA PGQRLEWMGWINAGNGNTK YSQKFQGRVTITRDTSASTAY MELSSLRSEDTAVYYCARDG PAVDGAEYFQHWGQGTLVTV SSASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1671	ETTLTQSPATLSLSPGERATLSC RASQSVSSYLAWYQQKPGQAPR LLIYDASNRATGIPARFSGSGSGT DFTLTISSLEPEDFAVYYCQQRS NWPFFGQGTRLEIKRTVAAPSVF IFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLTLSKAD YEKHKVYACEVTHQGLSSPVTKS FNRGEC
SEQ ID 1564	QLQLQESGPGLVKPSQTLSLT CAISGDSVSSNSAAWNWIRQ SPSRGLEWLGRTYYRSKWYN DYAVSLKSRITINPDTSKNQFS LQLNSVTPEDTAVYYCASLAS GSPPPGDYWGQGTLVTVSSA STKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVV SVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1672	ETTLTQSPATLTLSPGERVTLSC RASQSIGTYVAWYQQKPGQAPR FLIYDSSNRATGIPARFSGSGSGT DFTLTISSLEPEDFAFYYCQQRAE WPLTFGQGTRLEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLTLSKAD YEKHKVYACEVTHQGLSSPVTKS FNRGEC

SEQ ID 1565	QVTLKESGGGVVQPGRSLRL SCAASGFTFSTYGMHWVRQA PGKGLEWVALISYDGSKKYYA NSVKGRFTISRDNSKNTLYLQ MKSLRAEDTAMYYCAKGPIVG ATMDYWGQGALVTVSSASTK GPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYT LPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK	SEQ ID 1673	DVVMTQSPGTLSLSPGERATLSC RASQSVNSGYLAWYQQKPGQP PRLLISGVSTRATGIPDRFSGSGS GTDFTLTISRLEPEDFAVYYCQEY GNSAMYNFGQGTKLEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLS KADYEKHKVYACEVTHQGLSSP VTKSFNRGEC
SEQ ID 1566	EVQLVQSGAEVKKPGSSVKV SCKASGGTFSSYAISWVRQA PGQGLEWMGWISAYNGNTN YAQKLQGRVTMTTDTSTSTAY MELRSLRSDDTAVYYCARWY GDYGLDYWGQGTLVTVSSAS TKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDK THTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK	SEQ ID 1674	ETTLTQSPATLSVSPGERATLSC RASQSVSSNLAWYQQKPGQAPR LLIYGASTRATGIPARFSGSGSGT EFTLTISSLQSEDFAVYYCQQYN NWPPFTFGQGTRLEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVT KSFNRGEC
SEQ ID 1567	EVQLVQSGAEVKKPGASVKV SCKASGYTFTSYAMHWVRQA PGQRLAWMGWINAGNGNTK YSEKFEGRVTITRDTSASTAY MELSSLRSEDTAVYYCARVAK YYYESGGYRASNWFDPWGQ GTLVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPEL	SEQ ID 1675	DVVMTQSPGTLSLSPGERATLSC RASQSVSSSYLGWYQQKSGQAP RLLIYGASSRATDIPDRFSGSGS GTDFTLTISKLEAEDSAVYYCQQ YGISPLAFGQGTKLEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVT KSFNRGEC

	LGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQY NSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQK SLSLSPGK		
SEQ ID 1568	QVQLQESGPGLVKPSQTLSLT CAISGDSVSSNSAAWNWIRQ SPSRGLEWLGRTYYRSKWYN DYAVSVKSRITINPDTSKNQFS LQLNSVTPEDTAVYYCARAPP PTVGWYAPVFDYWGQGTLVT VSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYR VVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSP GK	SEQ ID 1676	ETTLTQSPATLSVSPGERATLSC RASQSISNNLAWYQQKPGQAPR LLIYGTSTRATGIPARFSGSGSGT EFTLTISSLQSEDFAVYYCQQYN FWPSITFGQGTRLEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTK SFNRGEC
SEQ ID 1569	QLQLQESGGGLVQPGGSLRL SCSASGISFRDYWMHWIRQT PGKGLVWVSRINPDGSSTSY ADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCAKVTG RRVGAHDYWGQGTLVTVSSA STKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVV SVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1677	ETTLTQSPGTLSLSPGERATLSC RASQSVSSSSLAWYQQKPGQAP RLLIYGASSRATGIPDRFSGSGS GTDFTLTISRLEPEDFAVYYCQQ YGSSQTFGQGTRLEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVT KSFNRGEC

SEQ ID 1570	QVQLVQSGAEVKKPGASVKV SCKASGYTFTGYYMHWVRQA PGQGLEWMGWINPNSGGTN YAQKFQGRVTMTRDTSISTAY MELSRLRSDDTAVYYCAFAQ PGAETLNFDLWGRGTLVTVS SASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1678	DVVMTQSPLSLPVSLGQPASISC RSNQSLVYSDGGTYLNWFQQRA GQSPRRLVYKVSNRDSGVPDRF SGSGSGTDFTLRISRVEAEDVGV YYCMQGTHWPYTFGQGTKLEIK RTVAAPSVFIFPPSDEQLKSGTA SVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSTYS LSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
SEQ ID 1571	QVQLQQSGPGLVKPSQTLSL TCAISGDSVSSKSAAWNWIRQ SPSRGLEWLGRTYYRSKWNN DYALSVKSRITINPDTSKNQFS LQLKSVTPEDTALYYCVRQVA GGMDVWGQGTTVTVSSASTK GPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYT LPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK	SEQ ID 1679	DIQLTQSPSSLSASVGDRVTVTC RASQSISSYLNWYQQKPGKAPQ LLIYDASNLETGVPSRFSGSGSG TDFTFTISSLQPEDFATYYCQQF DNVPVTFGGGTKVEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVT KSFNRGEC
SEQ ID 1572	QVQLVQSGGGLVQPGRSLRL SCTASGFTFGDYAMSWFRQA PGKGLEWVSAISGSGGSTYY ADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCAKGSV YSGSYYMLIDYWGQGTLVTV SSASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSV	SEQ ID 1680	EIVLTQSPLSLPVTLGQPASISCR SSQSLVYSDGNTYLNWFQQRPG QSPRRLIYKVSNRDSGVPDRFSG SGSGTDFTLKISRVEAEDVGVYY CMQGTHWPRTFGQGTKLEIKRT VAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQ GLSSPVTKSFNRGEC

	FLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK		
SEQ ID 1573	QVQLQQSGPGLVRPSQTLSL TCVISGDSVSSGSAAWNWIR QSPSRGLEWLGRTYYRAKWY NEYAGSVKSRITISPDTSKNQF SLQLNSVTPEDTAVYFCTRQD KDNTRYSGLGVWGQGTTVTV SSASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1681	DVVMTQSPATLSVSPGERATLSC RASQSVSSNLAWYQQKPGQAPR LLIYGASSRATGIPDRFSGSGSGT DFTLTINRLEPEDFAVYYCQQYG SSSMYTFGQGTKLEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVT KSFNRGEC
SEQ ID 1574	EVQLVETGGGLVQPGGSLRL SCAASEFTLRNYGVSWVRQA PGKGLEWVSGMSGSGYSTYY ADSVKGRFTISRDSSKNTLFL QMDSLRAEDTAIYYCARGPR MWSSGIDAFDIWGHGTMVTV SSASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1682	DVVMTQSPSSLSASVGDSVAITC RASQSISNYLNWYQQRPGKAPK LLIFAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYSCQQSY ITPWTFGQGTKLEIKRTVAAPSVF IFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLTLSKAD YEKHKVYACEVTHQGLSSPVTKS FNRGEC

SEQ ID 1575	QVQLQQWGAGLLKPSETLSL TCAVYGGSVSGYYWSWIRQP PGKGLEWMGEIHHSGSTNYN PSLKSRVTISLDTPKNQFSLKL SSVTAADTAVYYCARRDWAG KRVWGQGTLVTVSSASTKGP SVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPP CPAPELLGGPSVFLFPPKPKD TLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	SEQ ID 1683	DVVMTQSPGTLSLSPGERATLSC RASQSVSTLLAWYQQKPGQAPR LLIYDASNRATGIPGRFSASGSGT DFSLTISSLETEDSAVYYCQHRY VWPFTFGGGTKLEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTK SFNRGEC
SEQ ID 1576	QVQLQQSGPGLLKPSQTLSLT CAISGDSVSSNTATWNWIRQS PSRGLEWLGRTYYRSKWYKD NALSVKSRITINPDTSKNQFSL QLNSVTPEDTAVYYCAGGRA GIAAFDIWGQGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKT HTCPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK	SEQ ID 1684	DIQMTQSPSSLSASVGDRVTITC RASQGIRNDLGWYQQKPGKAPK RLIYGASSLQSGVPSRFSGSGSG TEFTLTIRSLQPEDFATYYCLQHN SYPRTFGQGTKVEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTK SFNRGEC
SEQ ID 1577	QVQLVQSGGGLIQPGGSLRL SCAASGFTVSSNYMSWVRQA PGKGLEWVSLIYSDGRTNYAD SVKGRFTISRDNSKNTLYLQM NSLRAEDTAVYYCAKGALQG EWRRFDYWGQGTLVTVSSAS TKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDK THTCPPCPAPELLGGPSVFLF	SEQ ID 1685	DVVMTQSPATLSLSPGERATLSC RASQSVSSYLAWYQQKPGQAPR LLIYDASNRATGIPARFSGSGSGT DFTLTISSLEPEDFAVYYCQQRS NWPWTFGQGTKLEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVT KSFNRGEC

	PPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK		
SEQ ID 1578	QVQLQQSGPGLVKPSQTLSL TCAISGDSVSSNSAAWNWIR QSPSRGLEWLGRTYYRSKWY NDYAVSVKSRITINPDTSKNQF SLQLNSVTPEDTAVYYCTRTN QGYGGNSGVFDYWGQGTLV TVSSASTKGPSVFPLAPSSKS TSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSSLGTQ TYICNVNHKPSNTKVDKKVEP KSCDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTY RVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLS PGK	SEQ ID 1686	DVVMTQSPLSLPVTLGQAASISC RSSHSLTTTDGRTYVAWFQQRP GQSPRRLLYEVSKRDSGAPDRF SGSGSGTDFTLKISRVEADDVGI YHCMQGTHGPHTFGQGTKLEIK RTVAAPSVFIFPPSDEQLKSGTA SVVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSTYS LSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
SEQ ID 1579	QVQLQQSGPGLVKPSQTLSL TCAISGDSVSGNSAAWNWIR QSPSRGLEWLGRTYYRSKWY NDYAVSVKSRITINPDTSKNQF SLQLNSVTPEDTAVYYCARIV GGAVDCWGQGTLVTVSSAST KGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKT HTCPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK	SEQ ID 1687	ETTLTQSPATLSVSPGERATLSC RASQSVTSNLAWYQQKPGQAPR LLIYGASNRATGIPARFSVSGSGT DFTLTISRLEPEDFAVYYCQQYG SPPPTTFGQGTRLEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVT KSFNRGEC

SEQ ID 1580	EVQLVQSGAEVKKPGASVKV SCKASGYTFTSYAMHWVRQA PGQRLEWMGWINAGNGNTK YSQKFQGRVTITRDTSASTAY MELSSLRSEDTAVYYCARVRV GATTVYDSWFDPWGQGTLVT VSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYR VVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSP GK	SEQ ID 1688	DVVMTQSPGTLSLSPGERATLSC RASQSVSSSYLAWYQQKPGQAP RLLIYGASSRATGIPDRFSGSGS GTDFTLTISRLEPEDFAVYYCQQ YGSSRRTFGQGTKLEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLS KADYEKHKVYACEVTHQGLSSP VTKSFNRGEC
SEQ ID 1581	QVQLVQSGGGLVQPGGSLRL SCAASGFTFSSYAMSWVRQA PGKGLEWVSAISGSGGSTYY ADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCAKDGG SSPYYDSSGLLPWYFDLWGR GTLVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQY NSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQK SLSLSPGK	SEQ ID 1689	ETTLTQSPGTLSLSPGERATLSC RASQSVFNNYLAWYQQRPGQAP RLLIYGASSRATGIPDRFSGGGS GTDFTLTISRLEPEDFAVYCCQQ YGSSPITFGQGTRLEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVT KSFNRGEC
SEQ ID 1582	QVQLQESGGGLVQPGGSLRL SCAASGFTFSSYAMHWVRQA PGKGLEYVSAISSNGGSTYYA NSVKGRFTISRDNSKNTLYLQ MGSLRAEDMAVYYCARAKFW TYYFDYWGQGTLVTVSSAST KGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVN	SEQ ID 1690	EIVLTQSPATLSLSPGERATLSCR ASQSVSSYLAWYQQKPGQAPRL LIYDASNRATGIPARFSGSGSGT DFTLTISRLEPEDFAVYYCQQYG SSLRYTFGQGTKLEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVT KSFNRGEC

	HKPSNTKVDKKVEPKSCDKT HTCPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK		
SEQ ID 1583	QVQLQQWGAGLLKPSETLSL TCAVYGGSFSGYYWSWIRQP PGKGLEWIGEINHSGSTNYNP SLKSRVTISVDTSKNQFSLKLS SVTAADTAVYYCARGGGSGS YYKRFFDYWGQGTLVTVSSA STKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVV SVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1691	EIVLTQSPDSLAVSLGERATINCK SSQSVLYDSNSKNYLSWYQQKP GQPPKLLISWASTRGSGVPDRFS GSGSGTDFTLTISSLQAEDVAVY YCQQFYGIPHFGQGTRLEIKRTV AAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWKVDNALQ SGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGEC
SEQ ID 1584	EVQLVQSGAEVRKPGASVKV SCKASGYTFTSYAISWVRQAP GQGLEWMGWISAYDGNTNY AQKLQGRVTMTTDTSTSTAY MEVRSLRSDDTAVYYCARDG TVRRVVGATTPGNFDYRGQG TLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKK VEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQY NSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQ	SEQ ID 1692	DVVMTQSPATLSLSPGERATLSC RASQSVGTNLAWYQQKPGQAP RLLIYDASNRATGIPARFSGSGS GTEFTLTISSLQSEDFAVYYCQQ YNNWPPITFGGGTKLEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSTYSLSSTLTL SKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC

	GNVFSCSVMHEALHNHYTQK SLSLSPGK		
SEQ ID 1585	EVQLVQSGGGVVQPGRSLRL SCAASGFTFSSYGMHWVRQA PGKGLEWVAVIWYDGSNKYY ADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARDLN RGYCSGGSCFGYWGQGTLV TVSSASTKGPSVFPLAPSSKS TSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSSLGTQ TYICNVNHKPSNTKVDKKVEP KSCDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTY RVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLS PGK	SEQ ID 1693	DVVMTQSPLSLPVTLGQPASISC RSSQSLVYSDGNTYLSWLQQRP GQPPRLLIYKISNRFSGVPDRFS GSGAGTDFTLKISRVEAEDVGVY YCMQGTQFPQTFGQGTKLEIKRT VAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQ GLSSPVTKSFNRGEC
SEQ ID 1586	QVQLQESGGGLVQPGGSLRL SCAASGFTFSSYAMSWVRQA PGKGLEWVSYISSSGTTIYYA DSVKGRFTVSRDNAKNSLYL QMNSLRAEDTAVYYCARDYS SSGECFDYWGQGTLVTVSSA STKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVV SVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1694	EIVLTQSPGTLSLSPGERATLSCR ASQSVISRYLAWYQQKPGQAPR LLIHGASTRATGIPDRFSGSGSGT DFTLTISRLEPEDFAVYYCQQYG SSPPYTFGQGTKVEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVT KSFNRGEC

SEQ ID 1587	EVQLVQSGGGVVQPGRSLRL SCAASGFTFSSYGMHWVRQA PGKGLEWVAVIWYDGSNKYY ADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARDQA AMVGYFDYWGQGTLVTVSSA STKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVV SVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1695	DIQLTQSPSTLAASVGDRVTITCR ASQSISSWLAWYQQKPGKAPKV LIYKASSLESGVPSRFSGSGSGT EFTLTISSLQPDDFATYYCQQYN SYSGTFGQGTKVEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTK SFNRGEC
SEQ ID 1588	QVTLKESGGGVVQPGRSLRL SCAASGFIFSNYAIHWVRQAP GKGLEWVAVISYDGSNKYYA DSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARTFAG YSSKLGYFDLWGRGTLVTVS SASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID 1696	DVVMTQSPAILSVSPGERATLSC RASQSVSSSLAWYQQKPGQPPR LLIYGASTRATAIPARFSGSGSGT EFTLTISSLQSEDFAVYYCQRYD NWPPLFGQGTKLEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTK SFNRGEC

Table 38. Anti-CLEC2D IgG1 antibody Heavy and Kappa Light Chain DNA sequence

SEQ ID	VH+CH DNA_IgG1	SEQ ID	VK+CK DNA
SEQ ID 1697	GAAGTGCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTTTCCTGCAAGGCTTCTG GATACACCTTCACTAGCTATGCTATG CATTGGGTGCGCCAGGCCCCCGGAC AAAGGCTTGAGTGGATGGGATGGAT CAACGCTGGCAATGGTAACACAAAA TATTCACAGAAGTTCCAGGGCAGAG TCACCATTACCAGGGACACATCCGCG AGCACAGCCTACATGGAGCTGAGCA GCCTGAGATCTGAAGACACGGCTGT GTATTACTGTGCGAGAGGCTCCTTGT CCCGAAGTGGCTGGTACGCCGGACT CTTTGACTACTGGGGCCAGGGAACCC TGGTCACCGTCTCCTCAGCATCCACC AAGGGGCCTTCCGTGTTCCCCCTGGC CCCTTCATCCAAGTCGACCTCTGGTG GAACCGCCGCACTCGGTTGCCTGGTC AAAGACTACTTCCCCGAGCCCGTGAC TGTCTCGTGGAACTCGGGCGCCCTCA CATCCGGAGTGCATACCTTTCCCGCC GTGTTGCAGTCCAGCGGCCTGTACAG CCTGAGCTCCGTCGTGACAGTGCCGT CCTCCTCCCTTGGAACCCAGACCTAT ATCTGCAACGTCAATCACAAGCCCTC CAACACCAAAGTGGACAAGAAGGTC GAACCCAAGTCCTGCGACAAGACTC ACACCTGTCCGCCTTGTCCAGCCCCT GAGCTGCTGGGTGGTCCGTCCGTGTT CCTCTTCCCGCCCAAGCCGAAGGACA CTCTGATGATTTCACGCACCCCGGAA GTCACTTGCGTGGTCGTGGACGTGTC GCACGAAGATCCCGAAGTGAAATTC AATTGGTACGTGGATGGGGTCGAAG TGCACAACGCCAAGACCAAGCCTAG GGAAGAACAGTACAACTCTACGTAC CGGGTGGTGTCCGTGCTGACCGTGCT GCACCAGGACTGGCTGAACGGAAAG GAGTACAAGTGCAAAGTGTCAAACA AGGCTCTCCCTGCCCCTATCGAAAAG ACCATCAGCAAGGCCAAGGGTCAAC CTAGGGAGCCCCAGGTCTATACTTTG CCGCCTAGCCGGGAAGAAATGACTA AGAACCAAGTGTCCCTGACTTGCCTT GTCAAGGGCTTTTATCCGTCCGACAT CGCCGTGGAGTGGGAGTCCAACGGA CAACCGGAGAACAACTACAAGACCA CCCCACCGGTGCTCGATTCCGATGGC TCCTTCTTCCTGTACTCCAAGCTGAC TGTGGACAAGTCAAGATGGCAGCAG GGAAACGTGTTCTCCTGCTCCGTGAT GCACGAAGCGCTGCACAACCATTAC	SEQ ID 1805	GAAACGACACTCACGCAGTCTCCA GCCACCCTATCTGTGTCTCTAGGAG AAAGAGCCACCCTTTCTTGCAGGG CCAGTCAGAGTATTGGCAGCAACT TAGTCTGGTACCAGCTGAAACCTG GCCAGGGTCCCAGGCTCGTCATAT ATAGTGCAACCTCTAGGGCCACTG GAATCCCAGCCAGGTTCAGCGGCA GTGGGTCTGGGACAGAGTTCATTC TCTCCATCAGCAACCTGCAGTCTGA AGATCTTGCAGTTTATTACTGTCAG CAGTATGGTAGTTCACCTCCGACC ACCTTCGGCCAAGGGACACGACTG GAGATTAAACGTACTGTGGCTGCT CCCTCCGTGTTCATTTTTCCTCCGT CGGACGAACAGCTGAAGTCCGGAA CCGCGTCCGTGGTCTGTCTCCTGAA CAACTTCTATCCGCGCGAGGCGAA AGTGCAGTGGAAGGTCGACAACGC ACTGCAGTCGGGAAACTCCCAGGA ATCGGTGACCGAGCAGGACTCGAA GGACTCAACCTACTCATTGTCCTCC ACCCTCACCCTGAGCAAGGCCGAT TACGAGAAGCATAAGGTCTACGCC TGCGAAGTGACCCACCAGGGCCTG AGCAGCCCAGTGACGAAGTCCTTC AACCGGGGAGAATGC

	ACCCAGAAATCACTGTCACTTTCGCC GGGAAAA		
SEQ ID 1698	CAGATCACCTTGAAGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTCAGTAGTTATAGCATG AACTGGGTCCGCCAGGCTCCAGGCA AGGGGCTGCAGTGGGTGGCAATTAT ATCAGATGATGGAAGTAAGAGTTAC TACGCAGACTCCGTGCAGGGCCGATT CACCATCTCCAGAGACAATTCGAGG AACACAGTATTTCTGCAAATGAACA GCCTGAGAGCTGAGGACACGGCTAT GTATTACTGTGCGAGAGACAGGGGA ACTAAATGGAACCAATTGAATGATG TTTTTGATATGTGGGGCCAAGGGACA ATGGTCACCGTCTCTTCAGCATCCAC CAAGGGGCCTTCCGTGTTCCCCCTGG CCCCTTCATCCAAGTCGACCTCTGGT GGAACCGCCGCACTCGGTTGCCTGGT CAAAGACTACTTCCCCGAGCCCGTGA CTGTCTCGTGGAACTCGGGCGCCCTC ACATCCGGAGTGCATACCTTTCCCGC CGTGTTGCAGTCCAGCGGCCTGTACA GCCTGAGCTCCGTCGTGACAGTGCCG TCCTCCTCCCTTGGAACCCAGACCTA TATCTGCAACGTCAATCACAAGCCCT CCAACACCAAAGTGGACAAGAAGGT CGAACCCAAGTCCTGCGACAAGACT CACACCTGTCCGCCTTGTCCAGCCCC TGAGCTGCTGGGTGGTCCGTCCGTGT	SEQ ID 1806	GAAATTGTGATGACACAGTCTCCA GCCACCCTGTCTTTGTCTCCAGGGG AAAGAGCCACCCTCTCCTGCAGGG CCAGTCAGAGTGTTAGCAGCAGCT ACTTAGCCTGGTACCAGCAAAAAC CTGGCCGGGCTCCCAGGCTCCTCAT CTATGGCGCATCCAACAGGGCCAC AGGCATCCCAGACAGGTTCAGTGG CAGTGGGTCTGGGACAGACTTCAC TCTCATCATCAGCAGACTGGAGCC TGAAGATTTTGCCTTGTATTACTGT CAGCAGTATGGAAGCTCACCGGGA ACGTTCGGCCAAGGGACCAAAGTG GATATCAAACGTACTGTGGCTGCT CCCTCCGTGTTCATTTTTCCTCCGT CGGACGAACAGCTGAAGTCCGGAA CCGCGTCCGTGGTCTGTCTCCTGAA CAACTTCTATCCGCGCGAGGCGAA AGTGCAGTGGAAGGTCGACAACGC ACTGCAGTCGGGAAACTCCCAGGA ATCGGTGACCGAGCAGGACTCGAA GGACTCAACCTACTCATTGTCCTCC ACCCTCACCCTGAGCAAGGCCGAT TACGAGAAGCATAAGGTCTACGCC TGCGAAGTGACCCACCAGGGCCTG AGCAGCCCAGTGACGAAGTCCTTC AACCGGGGAGAATGC

	TCCTCTTCCCGCCCAAGCCGAAGGAC ACTCTGATGATTTCACGCACCCCGGA AGTCACTTGCGTGGTCGTGGACGTGT CGCACGAAGATCCCGAAGTGAAATT CAATTGGTACGTGGATGGGGTCGAA GTGCACAACGCCAAGACCAAGCCTA GGGAAGAACAGTACAACTCTACGTA CCGGGTGGTGTCCGTGCTGACCGTGC TGCACCAGGACTGGCTGAACGGAAA GGAGTACAAGTGCAAAGTGTCAAAC AAGGCTCTCCCTGCCCCTATCGAAAA GACCATCAGCAAGGCCAAGGGTCAA CCTAGGGAGCCCCAGGTCTATACTTT GCCGCCTAGCCGGGAAGAAATGACT AAGAACCAAGTGTCCCTGACTTGCCT TGTCAAGGGCTTTTATCCGTCCGACA TCGCCGTGGAGTGGGAGTCCAACGG ACAACCGGAGAACAACTACAAGACC ACCCCACCGGTGCTCGATTCCGATGG CTCCTTCTTCCTGTACTCCAAGCTGA CTGTGGACAAGTCAAGATGGCAGCA GGGAAACGTGTTCTCCTGCTCCGTGA TGCACGAAGCGCTGCACAACCATTA CACCCAGAAATCACTGTCACTTTCGC CGGGAAAA		
SEQ ID 1699	GAAGTGCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTTTCCTGCAAGGCATCTG GATACACCTTCACCAGCTACTATATG CACTGGGTGCGACAGGCCCCTGGAC AAGGGCTTGAGTGGATGGGAATAAT CAACCCTAGTGGTGGTAGCACAAGC TACGCACAGAAGTTCCAGGGCAGAG TCACCATGACCAGGGACACGTCCAC GAGCACAGTCTACATGGAGCTGAGC AGCCTGAGATCTGAGGACACGGCCG TGTATTACTGTGCGAGAGGCCGAGG GTATAGCAGCAGTCGGCTCTACTACT TTGACTACTGGGGCCAGGGAACCCT GGTCACCGTCTCCTCAGCATCCACCA AGGGGCCTTCCGTGTTCCCCCTGGCC CCTTCATCCAAGTCGACCTCTGGTGG AACCGCCGCACTCGGTTGCCTGGTCA AAGACTACTTCCCCGAGCCCGTGACT GTCTCGTGGAACTCGGGCGCCCTCAC ATCCGGAGTGCATACCTTTCCCGCCG TGTTGCAGTCCAGCGGCCTGTACAGC CTGAGCTCCGTCGTGACAGTGCCGTC CTCCTCCCTTGGAACCCAGACCTATA TCTGCAACGTCAATCACAAGCCCTCC AACACCAAAGTGGACAAGAAGGTCG AACCCAAGTCCTGCGACAAGACTCA CACCTGTCCGCCTTGTCCAGCCCCTG AGCTGCTGGGTGGTCCGTCCGTGTTC	SEQ ID 1807	GATGTTGTGATGACTCAGTCTCCAG CCACCCTGTCTTTGTCTCCAGGGGA AAGAGCCACCCTCTCCTGCAGGGC CAGTCAGAGTGTTAGCAGCTACTT AGCCTGGTACCAACAGAAACCTGG CCAGGCTCCCAGGCTCCTCATCTAT GATGCATCCAACAGGGCCACTGGC ATCCCAGCCAGGTTCAGTGGCAGT GGGTCTGGGACAGACTTCACTCTC ACCATCAGCAGCCTAGAGCCTGAA GATTTTGCAGTTTATTACTGTCAGC AGCGTAGCAACTGGCCTCGGACGT TCGGCCAAGGGACCAAGCTGGAGA TCAAACGTACTGTGGCTGCTCCCTC CGTGTTCATTTTTCCTCCGTCGGAC GAACAGCTGAAGTCCGGAACCGCG TCCGTGGTCTGTCTCCTGAACAACT TCTATCCGCGCGAGGCGAAAGTGC AGTGGAAGGTCGACAACGCACTGC AGTCGGGAAACTCCCAGGAATCGG TGACCGAGCAGGACTCGAAGGACT CAACCTACTCATTGTCCTCCACCCT CACCCTGAGCAAGGCCGATTACGA GAAGCATAAGGTCTACGCCTGCGA AGTGACCCACCAGGGCCTGAGCAG CCCAGTGACGAAGTCCTTCAACCG GGGAGAATGC

	CTCTTCCCGCCCAAGCCGAAGGACAC TCTGATGATTTCACGCACCCCGGAAG TCACTTGCGTGGTCGTGGACGTGTCG CACGAAGATCCCGAAGTGAAATTCA ATTGGTACGTGGATGGGGTCGAAGT GCACAACGCCAAGACCAAGCCTAGG GAAGAACAGTACAACTCTACGTACC GGGTGGTGTCCGTGCTGACCGTGCTG CACCAGGACTGGCTGAACGGAAAGG AGTACAAGTGCAAAGTGTCAAACAA GGCTCTCCCTGCCCCTATCGAAAAGA CCATCAGCAAGGCCAAGGGTCAACC TAGGGAGCCCCAGGTCTATACTTTGC CGCCTAGCCGGGAAGAAATGACTAA GAACCAAGTGTCCCTGACTTGCCTTG TCAAGGGCTTTTATCCGTCCGACATC GCCGTGGAGTGGGAGTCCAACGGAC AACCGGAGAACAACTACAAGACCAC CCCACCGGTGCTCGATTCCGATGGCT CCTTCTTCCTGTACTCCAAGCTGACT GTGGACAAGTCAAGATGGCAGCAGG GAAACGTGTTCTCCTGCTCCGTGATG CACGAAGCGCTGCACAACCATTACA CCCAGAAATCACTGTCACTTTCGCCG GGAAAA		
SEQ ID 1700	CAGGTCACCTTGAAGGAGTCTGGGG GAGGCTTGGTCCGGCCTGGAGGGTC CCTGAGACTCTCCTGTGAAGCCTCTG GATTCACCTTCAGTGACCCCTACATG GACTGGGTCCGCCAGGCTCCAGGCA AGGGGCTGGAGTGGGTTGGCCGAAT TACAAATAAGCGTACCGGTTACGCC ACAACATATGCCGCGTCTGTGAAGG ACAGATTCACCATCTCAAGAGATGAT TCAAGGAAGTCAGTATATCTGCAAAT GAACAGCCTGAAGACCGAGGACACG GCCGTATATTATTGTGCAACAGATGT CAGTGGGTCCTTCGCGGCCTACGGGG GCCAGGGCACCCTGGTCACCGTCTCC TCAGCATCCACCAAGGGGCCTTCCGT GTTCCCCCTGGCCCCTTCATCCAAGT CGACCTCTGGTGGAACCGCCGCACTC GGTTGCCTGGTCAAAGACTACTTCCC CGAGCCCGTGACTGTCTCGTGGAACT CGGGCGCCCTCACATCCGGAGTGCAT ACCTTTCCCGCCGTGTTGCAGTCCAG CGGCCTGTACAGCCTGAGCTCCGTCG TGACAGTGCCGTCCTCCTCCCTTGGA ACCCAGACCTATATCTGCAACGTCAA TCACAAGCCCTCCAACACCAAAGTG GACAAGAAGGTCGAACCCAAGTCCT GCGACAAGACTCACACCTGTCCGCCT TGTCCAGCCCCTGAGCTGCTGGGTGG TCCGTCCGTGTTCCTCTTCCCGCCCA	SEQ ID 1808	GAAATTGTGTTGACGCAGTCTCCA GACTCCCTGGCTGTGTCTCTGGGCG AGAGGGCCACCATCACCTGCAAGT CCAGCCGGAATATTTTATACAGCG GCAACAATAAAAACTTCTTGGCTT GGTATCAGCACAAACCAGGACAGC CTCCTAAGTTGCTCATTTACTGGGC ATCTACCCGGGAATCCGGGGTCCC TGACCGATTTAGTGGCAGCGGGTC TGGGACAGATTTCACCCTCACCATC AATAGCCTGGAAGCTGAAGATGCT GCAACGTATTACTGTCATCAGAGT AGTAGTTTACCTCACACTTTCGGCC CTGGGACCAAAGTGGATATCAAAC GTACTGTGGCTGCTCCCTCCGTGTT CATTTTTCCTCCGTCGGACGAACAG CTGAAGTCCGGAACCGCGTCCGTG GTCTGTCTCCTGAACAACTTCTATC CGCGCGAGGCGAAAGTGCAGTGGA AGGTCGACAACGCACTGCAGTCGG GAAACTCCCAGGAATCGGTGACCG AGCAGGACTCGAAGGACTCAACCT ACTCATTGTCCTCCACCCTCACCCT GAGCAAGGCCGATTACGAGAAGCA TAAGGTCTACGCCTGCGAAGTGAC CCACCAGGGCCTGAGCAGCCCAGT GACGAAGTCCTTCAACCGGGGAGA ATGC

	AGCCGAAGGACACTCTGATGATTTCA CGCACCCCGGAAGTCACTTGCGTGGT CGTGGACGTGTCGCACGAAGATCCC GAAGTGAAATTCAATTGGTACGTGG ATGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTAC AACTCTACGTACCGGGTGGTGTCCGT GCTGACCGTGCTGCACCAGGACTGG CTGAACGGAAAGGAGTACAAGTGCA AAGTGTCAAACAAGGCTCTCCCTGCC CCTATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTATACTTTGCCGCCTAGCCGGG AAGAAATGACTAAGAACCAAGTGTC CCTGACTTGCCTTGTCAAGGGCTTTT ATCCGTCCGACATCGCCGTGGAGTGG GAGTCCAACGGACAACCGGAGAACA ACTACAAGACCACCCCACCGGTGCTC GATTCCGATGGCTCCTTCTTCCTGTA CTCCAAGCTGACTGTGGACAAGTCA AGATGGCAGCAGGGAAACGTGTTCT CCTGCTCCGTGATGCACGAAGCGCTG CACAACCATTACACCCAGAAATCACT GTCACTTTCGCCGGGAAAA		
SEQ ID 1701	GAGGTCCAGCTGGTACAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCGTCTG GATTCACCTTCAGTAGCTATGCTATG CATTGGGTGCGCCAGGCCCCCGGAC AAAGGCTTGAGTGGATGGGATGGAT CAACGCTGGCAATGGTAACACAAAA TATTCACAGAAGTTCCAGGGCAGAG TCACCATTACCAGGGACACATCCGCG AGCACAGCCTACATGGAGCTGAGCA GCCTGAGATCTGAAGACACGGCTGT GTATTACTGTGCGGGAGAGGGCGGA GCAGTGGCTGGTACTGTCTACTGGGG CCAGGGAACCCTGGTCACCGTCTCCT CAGCATCCACCAAGGGGCCTTCCGTG TTCCCCCTGGCCCCTTCATCCAAGTC GACCTCTGGTGGAACCGCCGCACTCG GTTGCCTGGTCAAAGACTACTTCCCC GAGCCCGTGACTGTCTCGTGGAACTC GGGCGCCCTCACATCCGGAGTGCAT ACCTTTCCCGCCGTGTTGCAGTCCAG CGGCCTGTACAGCCTGAGCTCCGTCG TGACAGTGCCGTCCTCCTCCCTTGGA ACCCAGACCTATATCTGCAACGTCAA TCACAAGCCCTCCAACACCAAAGTG GACAAGAAGGTCGAACCCAAGTCCT GCGACAAGACTCACACCTGTCCGCCT TGTCCAGCCCCTGAGCTGCTGGGTGG TCCGTCCGTGTTCCTCTTCCCGCCCA	SEQ ID 1809	GAAACGACACTCACGCAGTCTCCA GGCACCCTGTCTTTGTCTCCAGGGC AAAGAGCCACCCTCTCCTGCAGGG CCAGTGAGAGTGTTAGCAAGAGCT ACTTACTCTGGTACCAGCAGAAAC CTGGCCAGGCTCCCAGACTCCTCAT CTATGGTGCATCCACCAGGGCCAG TGGCATCCCAAACAGGTTCAGTGG CAGTGGGTCTGGGACAGACTTCAC TCTCACCATCAGCAGACTGGAGCC TGAAGATTCTGCAGTGTATTACTGT CAGCACTATGGCAGCTCTCGCACC TTCGGCCAAGGGACACGACTGGAG ATTAAACGTACTGTGGCTGCTCCCT CCGTGTTCATTTTTCCTCCGTCGGA CGAACAGCTGAAGTCCGGAACCGC GTCCGTGGTCTGTCTCCTGAACAAC TTCTATCCGCGCGAGGCGAAAGTG CAGTGGAAGGTCGACAACGCACTG CAGTCGGGAAACTCCCAGGAATCG GTGACCGAGCAGGACTCGAAGGAC TCAACCTACTCATTGTCCTCCACCC TCACCCTGAGCAAGGCCGATTACG AGAAGCATAAGGTCTACGCCTGCG AAGTGACCCACCAGGGCCTGAGCA GCCCAGTGACGAAGTCCTTCAACC GGGGAGAATGC

	AGCCGAAGGACACTCTGATGATTTCA CGCACCCCGGAAGTCACTTGCGTGGT CGTGGACGTGTCGCACGAAGATCCC GAAGTGAAATTCAATTGGTACGTGG ATGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTAC AACTCTACGTACCGGGTGGTGTCCGT GCTGACCGTGCTGCACCAGGACTGG CTGAACGGAAAGGAGTACAAGTGCA AAGTGTCAAACAAGGCTCTCCCTGCC CCTATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTATACTTTGCCGCCTAGCCGGG AAGAAATGACTAAGAACCAAGTGTC CCTGACTTGCCTTGTCAAGGGCTTTT ATCCGTCCGACATCGCCGTGGAGTGG GAGTCCAACGGACAACCGGAGAACA ACTACAAGACCACCCCACCGGTGCTC GATTCCGATGGCTCCTTCTTCCTGTA CTCCAAGCTGACTGTGGACAAGTCA AGATGGCAGCAGGGAAACGTGTTCT CCTGCTCCGTGATGCACGAAGCGCTG CACAACCATTACACCCAGAAATCACT GTCACTTTCGCCGGGAAAA		
SEQ ID 1702	CAGGTCCAGCTGGTGCAGTCTGGGG GAGGCTTGGTAAAGCCTGGGGGGTC CCTTAGACTCTCCTGTGCAGCCTCTG GATTCACTTTCAGTAACGCCTGGATG AGCTGGGTCCGCCAGGCTCCAGGGA AGGGGCTGGAGTGGGTTGGCCGTAT TAAAAGCAAAACTGATGGTGGGACA ACAGACTACGCTGCACCCGTGAAAG GCAGATTCACCATCTCAAGAGATGAT TCAAAAAACACGCTGTATCTGCAAAT GAACAGCCTGAAAACCGAGGACACA GCCGTGTATTACTGTACCACAGACGA GTATTTCTACTGGGGCCAGGGAACCC TGGTCACCGTCTCCTCAGCATCCACC AAGGGGCCTTCCGTGTTCCCCCTGGC CCCTTCATCCAAGTCGACCTCTGGTG GAACCGCCGCACTCGGTTGCCTGGTC AAAGACTACTTCCCCGAGCCCGTGAC TGTCTCGTGGAACTCGGGCGCCCTCA CATCCGGAGTGCATACCTTTCCCGCC GTGTTGCAGTCCAGCGGCCTGTACAG CCTGAGCTCCGTCGTGACAGTGCCGT CCTCCTCCCTTGGAACCCAGACCTAT ATCTGCAACGTCAATCACAAGCCCTC CAACACCAAAGTGGACAAGAAGGTC GAACCCAAGTCCTGCGACAAGACTC ACACCTGTCCGCCTTGTCCAGCCCCT GAGCTGCTGGGTGGTCCGTCCGTGTT CCTCTTCCCGCCCAAGCCGAAGGACA	SEQ ID 1810	GAAACGACACTCACGCAGTCTCCA GGCACCCTGTCTTTGTCTCCAGGGG AAAGAGCCACCCTCTCCTGCAGGG CCAGTCAGAGTATTAGCAGCACCT ACTTAGCCTGGTACCAGCAGAAAC CTGGCCAGGCTCCCAGGCTCCTCAT CTATGGTGCATCCACCAGGGCCAC TGGCATCCCAGACAGGTTCAGTGG CAGTGGGTCTGGGACAGACTTCAC TCTCAGCATCAGCAGACTGGAGCC TGAAGATTTTGCAGTGTATTACTGT CAGCAGTATGGTAACTCACCTCCG GGAGCCACCTTCGGCCAAGGGACA CGACTGGAGATTAAACGTACTGTG GCTGCTCCCTCCGTGTTCATTTTTC CTCCGTCGGACGAACAGCTGAAGT CCGGAACCGCGTCCGTGGTCTGTCT CCTGAACAACTTCTATCCGCGCGA GGCGAAAGTGCAGTGGAAGGTCGA CAACGCACTGCAGTCGGGAAACTC CCAGGAATCGGTGACCGAGCAGGA CTCGAAGGACTCAACCTACTCATT GTCCTCCACCCTCACCCTGAGCAA GGCCGATTACGAGAAGCATAAGGT CTACGCCTGCGAAGTGACCCACCA GGGCCTGAGCAGCCCAGTGACGAA GTCCTTCAACCGGGGAGAATGC

	CTCTGATGATTTCACGCACCCCGGAA GTCACTTGCGTGGTCGTGGACGTGTC GCACGAAGATCCCGAAGTGAAATTC AATTGGTACGTGGATGGGGTCGAAG TGCACAACGCCAAGACCAAGCCTAG GGAAGAACAGTACAACTCTACGTAC CGGGTGGTGTCCGTGCTGACCGTGCT GCACCAGGACTGGCTGAACGGAAAG GAGTACAAGTGCAAAGTGTCAAACA AGGCTCTCCCTGCCCCTATCGAAAAG ACCATCAGCAAGGCCAAGGGTCAAC CTAGGGAGCCCCAGGTCTATACTTTG CCGCCTAGCCGGGAAGAAATGACTA AGAACCAAGTGTCCCTGACTTGCCTT GTCAAGGGCTTTTATCCGTCCGACAT CGCCGTGGAGTGGGAGTCCAACGGA CAACCGGAGAACAACTACAAGACCA CCCCACCGGTGCTCGATTCCGATGGC TCCTTCTTCCTGTACTCCAAGCTGAC TGTGGACAAGTCAAGATGGCAGCAG GGAAACGTGTTCTCCTGCTCCGTGAT GCACGAAGCGCTGCACAACCATTAC ACCCAGAAATCACTGTCACTTTCGCC GGGAAAA		
SEQ ID 1703	CAGGTGCAGCTACAGCAGTGGGGCG CAGGACTGTTGAAGCCTTCGGAGAC CCTGTCCCTCACCTGCGCTGTCTATG GTGGGTCCTTCAGTGGTTACTACTGG AGCTGGATCCGCCAGCCCCCAGGGA AGGGGCTGGAGTGGATTGGGGAAAT CAATCATAGTGGAAGCACCAACTAC AACCCGTCCCTCAAGAGTCGAGTCAC CATATCAGTAGACACGTCCAAGAAC CAGTTCTCCCTGAAGCTGAGCTCTGT GACCGCCGCGGACACGGCTGTGTATT ACTGTGCGAGAGTAAATCCGGGGAG TTATACGAGGGAGGTGAGCAACTTT GACTACTGGGGCCAGGGAACCCTGG TGACCGTCTCCTCAGCATCCACCAAG GGGCCTTCCGTGTTCCCCCTGGCCCC TTCATCCAAGTCGACCTCTGGTGGAA CCGCCGCACTCGGTTGCCTGGTCAAA GACTACTTCCCCGAGCCCGTGACTGT CTCGTGGAACTCGGGCGCCCTCACAT CCGGAGTGCATACCTTTCCCGCCGTG TTGCAGTCCAGCGGCCTGTACAGCCT GAGCTCCGTCGTGACAGTGCCGTCCT CCTCCCTTGGAACCCAGACCTATATC TGCAACGTCAATCACAAGCCCTCCAA CACCAAAGTGGACAAGAAGGTCGAA CCCAAGTCCTGCGACAAGACTCACA CCTGTCCGCCTTGTCCAGCCCCTGAG CTGCTGGGTGGTCCGTCCGTGTTCCT CTTCCCGCCCAAGCCGAAGGACACTC	SEQ ID 1811	GACATCCAGTTGACCCAGTCTCCTT CCTCCCTGTCTGCATCTGTGGGAGA AAGAGTCACCATCACTTGCCGGTC CAGCCAGGCCCTGCGAAATGTTGT CGGCCTTGGCGATGATTTAGCCTG GTATCAACACACGCCAGGCAGCGC CCCCAAGATCCTGATCTACTCTACA TCGACTTTACAAAGTGGAGTCTCAT CAAGATTCAGCGGCGGAAAGTCTG GGAGAGACTTCACTCTCACGATCG ATCGTCTGCAGCCTGGAGATTCTGC AACTTATTACTGTCTCCAGCACCAT GATTTCCCTTTCACTTTCGGCCCTG GGACCAAGGTGGAAATCAAACGTA CTGTGGCTGCTCCCTCCGTGTTCAT TTTTCCTCCGTCGGACGAACAGCTG AAGTCCGGAACCGCGTCCGTGGTC TGTCTCCTGAACAACTTCTATCCGC GCGAGGCGAAAGTGCAGTGGAAG GTCGACAACGCACTGCAGTCGGGA AACTCCCAGGAATCGGTGACCGAG CAGGACTCGAAGGACTCAACCTAC TCATTGTCCTCCACCCTCACCCTGA GCAAGGCCGATTACGAGAAGCATA AGGTCTACGCCTGCGAAGTGACCC ACCAGGGCCTGAGCAGCCCAGTGA CGAAGTCCTTCAACCGGGGAGAAT GC

	TGATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGCA CGAAGATCCCGAAGTGAAATTCAAT TGGTACGTGGATGGGGTCGAAGTGC ACAACGCCAAGACCAAGCCTAGGGA AGAACAGTACAACTCTACGTACCGG GTGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGAG TACAAGTGCAAAGTGTCAAACAAGG CTCTCCCTGCCCCTATCGAAAAGACC ATCAGCAAGGCCAAGGGTCAACCTA GGGAGCCCCAGGTCTATACTTTGCCG CCTAGCCGGGAAGAAATGACTAAGA ACCAAGTGTCCCTGACTTGCCTTGTC AAGGGCTTTTATCCGTCCGACATCGC CGTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTCC TTCTTCCTGTACTCCAAGCTGACTGT GGACAAGTCAAGATGGCAGCAGGGA AACGTGTTCTCCTGCTCCGTGATGCA CGAAGCGCTGCACAACCATTACACC CAGAAATCACTGTCACTTTCGCCGGG AAAA		
SEQ ID 1704	CAGGTACAGCTGCAGCAGTCAGGTC CAGAATTGGTGAAGCCCTCGCAGAC CCTCACACTCACCTGTGGCATCTCCG GGGACAGTGTCTCTAGCAACAGTGTT ACTTGGAACTGGGTCAGGCAGTCCCC ATCGAGAGGCCTTGAGTGGCTGGGA AGGACTTACTACCGGTCCCAGTGGTA TTATAATTATGCGGTGTCTGTGAAAA GTCGAATAACCATCAGCCCAGACAC ATCCAAGAACCAGTTCTCCCTGCAGT TGAATTCTGTGACTCCCGAGGACACG GCTGTCTATTACTGTGCAACCAGGGG ACATAACTACGGTGTAGATTACTGGG GCCCGGGGACCACGGTCACCGTCTCC TCAGCATCCACCAAGGGGCCTTCCGT GTTCCCCCTGGCCCCTTCATCCAAGT CGACCTCTGGTGGAACCGCCGCACTC GGTTGCCTGGTCAAAGACTACTTCCC CGAGCCCGTGACTGTCTCGTGGAACT CGGGCGCCCTCACATCCGGAGTGCAT ACCTTTCCCGCCGTGTTGCAGTCCAG CGGCCTGTACAGCCTGAGCTCCGTCG TGACAGTGCCGTCCTCCTCCCTTGGA ACCCAGACCTATATCTGCAACGTCAA TCACAAGCCCTCCAACACCAAAGTG GACAAGAAGGTCGAACCCAAGTCCT GCGACAAGACTCACACCTGTCCGCCT TGTCCAGCCCCTGAGCTGCTGGGTGG TCCGTCCGTGTTCCTCTTCCCGCCCA	SEQ ID 1812	GATGTTGTGATGACTCAGTCTCCAC TCTCCCTGCCCGTCACCCCTGGAGA GCCGGCCTCCATCTCCTGCAGGTCT AGTCAGAGCCTCCTGAATAGTAAT GGATACAACTATTTGGAGTGGTAC CTGCAGAAGCCGGGGCAGTCTCCA CAGCTCCTGATCTATTTGGGTTCTA ATCGGGCCTCCGGGGTCCCTGACA GGTTCAGTGGCAGTGGATCAGGCA CAGATTTTACACTGAAAATCAGCA GAGTGGAGGCTGACGATGCTGGTG TTTATTACTGCATGCAGTCTCTACA AACTCCTCTCACTTTCGGCGGTGGG ACCAAGCTGGAGATCAAACGTACT GTGGCTGCTCCCTCCGTGTTCATTT TTCCTCCGTCGGACGAACAGCTGA AGTCCGGAACCGCGTCCGTGGTCT GTCTCCTGAACAACTTCTATCCGCG CGAGGCGAAAGTGCAGTGGAAGGT CGACAACGCACTGCAGTCGGGAAA CTCCCAGGAATCGGTGACCGAGCA GGACTCGAAGGACTCAACCTACTC ATTGTCCTCCACCCTCACCCTGAGC AAGGCCGATTACGAGAAGCATAAG GTCTACGCCTGCGAAGTGACCCAC CAGGGCCTGAGCAGCCCAGTGACG AAGTCCTTCAACCGGGGAGAATGC

	AGCCGAAGGACACTCTGATGATTTCA CGCACCCCGGAAGTCACTTGCGTGGT CGTGGACGTGTCGCACGAAGATCCC GAAGTGAAATTCAATTGGTACGTGG ATGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTAC AACTCTACGTACCGGGTGGTGTCCGT GCTGACCGTGCTGCACCAGGACTGG CTGAACGGAAAGGAGTACAAGTGCA AAGTGTCAAACAAGGCTCTCCCTGCC CCTATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTATACTTTGCCGCCTAGCCGGG AAGAAATGACTAAGAACCAAGTGTC CCTGACTTGCCTTGTCAAGGGCTTTT ATCCGTCCGACATCGCCGTGGAGTGG GAGTCCAACGGACAACCGGAGAACA ACTACAAGACCACCCCACCGGTGCTC GATTCCGATGGCTCCTTCTTCCTGTA CTCCAAGCTGACTGTGGACAAGTCA AGATGGCAGCAGGGAAACGTGTTCT CCTGCTCCGTGATGCACGAAGCGCTG CACAACCATTACACCCAGAAATCACT GTCACTTTCGCCGGGAAAA		
SEQ ID 1705	CAGGTGCAGCTGGTGCAGTCTGGGG GAGGCTTGGTAAAGCCTGGGGGGTC CCTTAGACTCTCCTGTGCAGCCTCTG GATTCACTTTCAGTAACGCCTGGATG AGCTGGGTCCGCCAGGCTCCAGGGA AGGGGCTGGAGTGGGTTTGCCGTATT AAAAGCAAAACTGATGGTGAGACAA CAGACTACGCTGCACCCGTGAAAGG CAGATTCACCATCTCAAGAGATGATT CAAAAAACACGCTGTATCTGCAAAT GAACAGCCTGAAAACTGAGGACACA GCCGTGTATCACTGTACCACAGGGGT GGGATGGTCGCCCTTCCAATACTGGG GCCAGGGCACCCTGGTCACCGTCTCC TCAGCATCCACCAAGGGGCCTTCCGT GTTCCCCCTGGCCCCTTCATCCAAGT CGACCTCTGGTGGAACCGCCGCACTC GGTTGCCTGGTCAAAGACTACTTCCC CGAGCCCGTGACTGTCTCGTGGAACT CGGGCGCCCTCACATCCGGAGTGCAT ACCTTTCCCGCCGTGTTGCAGTCCAG CGGCCTGTACAGCCTGAGCTCCGTCG TGACAGTGCCGTCCTCCTCCCTTGGA ACCCAGACCTATATCTGCAACGTCAA TCACAAGCCCTCCAACACCAAAGTG GACAAGAAGGTCGAACCCAAGTCCT GCGACAAGACTCACACCTGTCCGCCT TGTCCAGCCCCTGAGCTGCTGGGTGG TCCGTCCGTGTTCCTCTTCCCGCCCA	SEQ ID 1813	GAAACGACACTCACGCAGTCTCCA GGCACCCTGTCTTTGTCTCCAGGGG AAAGAGCCACCCTCTCCTGCAGGG CCAGTCAGAGTGTTAGCAGCAGCT ACTTAGCCTGGTACCAGCAGAAAC CTGGCCAGGCTCCCAGGCTCCTCAT CTATGGTGCATCCAGCAGGGCCAC TGGCATCCCAGACAGGTTCAGTGG CAGTGGGTCTGGGACAGACTTCAC TCTCACCATCAGCAGACTGGAGCC TGAAGATTTTGCAGTGTATTACTGT CAGCAGTATGGTAGCTCACCCCGG ATCACCTTCGGCCAAGGGACACGA CTGGAGATTAAACGTACTGTGGCT GCTCCCTCCGTGTTCATTTTTCCTC CGTCGGACGAACAGCTGAAGTCCG GAACCGCGTCCGTGGTCTGTCTCCT GAACAACTTCTATCCGCGCGAGGC GAAAGTGCAGTGGAAGGTCGACAA CGCACTGCAGTCGGGAAACTCCCA GGAATCGGTGACCGAGCAGGACTC GAAGGACTCAACCTACTCATTGTC CTCCACCCTCACCCTGAGCAAGGC CGATTACGAGAAGCATAAGGTCTA CGCCTGCGAAGTGACCCACCAGGG CCTGAGCAGCCCAGTGACGAAGTC CTTCAACCGGGGAGAATGC

	AGCCGAAGGACACTCTGATGATTTCA CGCACCCCGGAAGTCACTTGCGTGGT CGTGGACGTGTCGCACGAAGATCCC GAAGTGAAATTCAATTGGTACGTGG ATGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTAC AACTCTACGTACCGGGTGGTGTCCGT GCTGACCGTGCTGCACCAGGACTGG CTGAACGGAAAGGAGTACAAGTGCA AAGTGTCAAACAAGGCTCTCCCTGCC CCTATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTATACTTTGCCGCCTAGCCGGG AAGAAATGACTAAGAACCAAGTGTC CCTGACTTGCCTTGTCAAGGGCTTTT ATCCGTCCGACATCGCCGTGGAGTGG GAGTCCAACGGACAACCGGAGAACA ACTACAAGACCACCCCACCGGTGCTC GATTCCGATGGCTCCTTCTTCCTGTA CTCCAAGCTGACTGTGGACAAGTCA AGATGGCAGCAGGGAAACGTGTTCT CCTGCTCCGTGATGCACGAAGCGCTG CACAACCATTACACCCAGAAATCACT GTCACTTTCGCCGGGAAAA		
SEQ ID 1706	GAGGTCCAGCTGGTACAGTCTGGGG GAGGCTTGGTACAGCCAGGGCGGTC CCTGAGACTCTCCTGTACAGCTTCTG GATTCACCTTTGGTGATTATGCTATG AGCTGGTTCCGCCAGGCTCCAGGGA AGGGGCTGGAGTGGGTAGGTTTCATT AGAAGCAAAGCTTATGGTGGGACAA CAGAATACGCCGCGTCTGTGAAAGG CAGATTCACCATCTCAAGAGATGATT CCAAAAGCATCGCCTATCTGCAAATG AACAGCCTGAAAACCGAGGACACAG CCGTGTATTACTGTACTAGAGACGAC AAAATAGCAGCAGCTGGATTCACAT ACTGGTACTTCGATCTCTGGGGCCGT GGCACCCTGGTCACCGTCTCCTCAGC ATCCACCAAGGGGCCTTCCGTGTTCC CCCTGGCCCCTTCATCCAAGTCGACC TCTGGTGGAACCGCCGCACTCGGTTG CCTGGTCAAAGACTACTTCCCCGAGC CCGTGACTGTCTCGTGGAACTCGGGC GCCCTCACATCCGGAGTGCATACCTT TCCCGCCGTGTTGCAGTCCAGCGGCC TGTACAGCCTGAGCTCCGTCGTGACA GTGCCGTCCTCCTCCCTTGGAACCCA GACCTATATCTGCAACGTCAATCACA AGCCCTCCAACACCAAAGTGGACAA GAAGGTCGAACCCAAGTCCTGCGAC AAGACTCACACCTGTCCGCCTTGTCC AGCCCCTGAGCTGCTGGGTGGTCCGT	SEQ ID 1814	GATGTTGTGATGACTCAGTCTCCAG CCACCCTGTCTGTGTCTCCAGGGGA AAGAGCCACCCTCTCCTGCAGGGC CAGTCAGAGTGTTAGCAGCAACTT AGCCTGGTACCAGCAGAAACCTGG CCAGGCTCCCAGGCTCCTCATCTAT GGTGCATCCACCAGGGCCACTGGT ATCCCAGCCAGGTTCAGTGGCAGT GGGTCTGGGACAGAGTTCACTCTC ACCATCAGCAGCCTGCAGTCTGAA GATTTTGCAGTTTATTACTGTCAGC AGTATAATAACTGGCCTCCTATGTA CACTTTTGGCCAGGGGACCAAGCT GGAGATCAAACGTACTGTGGCTGC TCCCTCCGTGTTCATTTTTCCTCCGT CGGACGAACAGCTGAAGTCCGGAA CCGCGTCCGTGGTCTGTCTCCTGAA CAACTTCTATCCGCGCGAGGCGAA AGTGCAGTGGAAGGTCGACAACGC ACTGCAGTCGGGAAACTCCCAGGA ATCGGTGACCGAGCAGGACTCGAA GGACTCAACCTACTCATTGTCCTCC ACCCTCACCCTGAGCAAGGCCGAT TACGAGAAGCATAAGGTCTACGCC TGCGAAGTGACCCACCAGGGCCTG AGCAGCCCAGTGACGAAGTCCTTC AACCGGGGAGAATGC

	CCGTGTTCCTCTTCCCGCCCAAGCCG AAGGACACTCTGATGATTTCACGCAC CCCGGAAGTCACTTGCGTGGTCGTGG ACGTGTCGCACGAAGATCCCGAAGT GAAATTCAATTGGTACGTGGATGGG GTCGAAGTGCACAACGCCAAGACCA AGCCTAGGGAAGAACAGTACAACTC TACGTACCGGGTGGTGTCCGTGCTGA CCGTGCTGCACCAGGACTGGCTGAA CGGAAAGGAGTACAAGTGCAAAGTG TCAAACAAGGCTCTCCCTGCCCCTAT CGAAAAGACCATCAGCAAGGCCAAG GGTCAACCTAGGGAGCCCCAGGTCT ATACTTTGCCGCCTAGCCGGGAAGA AATGACTAAGAACCAAGTGTCCCTG ACTTGCCTTGTCAAGGGCTTTTATCC GTCCGACATCGCCGTGGAGTGGGAG TCCAACGGACAACCGGAGAACAACT ACAAGACCACCCCACCGGTGCTCGA TTCCGATGGCTCCTTCTTCCTGTACTC CAAGCTGACTGTGGACAAGTCAAGA TGGCAGCAGGGAAACGTGTTCTCCTG CTCCGTGATGCACGAAGCGCTGCAC AACCATTACACCCAGAAATCACTGTC ACTTTCGCCGGGAAAA		
SEQ ID 1707	CAGGTGCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTCTCCTGCAAGGCTTCTG GATACACCTTCGCCGCCTATTATTTA CACTGGGTGCGACAGGCCCCTGGAC AAGGCCTTGAGTGGATGGGGCGGAT CAGCCCTGGTAACGGTGTCACAAGTT ATGCACAGAAATTTCAGGGCAGAGT CACCATGACCGGGGACACGTCCATT AACACAGTCTACATGCAACTGAACA ATTTGATTTCTGGCGACACGGCCGTA TATTACTGTGCGAGAGAGGCTGCCG ACGACCCGTTTGACCATTGGGGCCAG GGAGCCCTGGTCACCGTCTCCTCAGC ATCCACCAAGGGGCCTTCCGTGTTCC CCCTGGCCCCTTCATCCAAGTCGACC TCTGGTGGAACCGCCGCACTCGGTTG CCTGGTCAAAGACTACTTCCCCGAGC CCGTGACTGTCTCGTGGAACTCGGGC GCCCTCACATCCGGAGTGCATACCTT TCCCGCCGTGTTGCAGTCCAGCGGCC TGTACAGCCTGAGCTCCGTCGTGACA GTGCCGTCCTCCTCCCTTGGAACCCA GACCTATATCTGCAACGTCAATCACA AGCCCTCCAACACCAAAGTGGACAA GAAGGTCGAACCCAAGTCCTGCGAC AAGACTCACACCTGTCCGCCTTGTCC AGCCCCTGAGCTGCTGGGTGGTCCGT CCGTGTTCCTCTTCCCGCCCAAGCCG	SEQ ID 1815	GATGTTGTGATGACTCAGTCTCCAG CCACCCTGTCTGTGTCTCCAGGGGA AAGAGTCACACTCTCCTGCAGGGC CAGTCAGAGTGTTAGAGACAACGT AGGTTGGTACAAGCAGAAACCTGG CCAACCTCCCAGGCTCGTCATCTAT GGTGCATCCACCAGGGCCACTGGT ATCCCAGCCAGGATCAGTGGCAGT GGGTCTGGGACAGAGTTCACTCTC ACCATCAGCAGCCTGCAGTCTGAA GATTTTGCAGTTTATTACTGTCAGC AGTTTAATAATTGGCCTTACACTTT TGGCCAGGGGACCAAGCTGGAGAT CAAACGTACTGTGGCTGCTCCCTCC GTGTTCATTTTTCCTCCGTCGGACG AACAGCTGAAGTCCGGAACCGCGT CCGTGGTCTGTCTCCTGAACAACTT CTATCCGCGCGAGGCGAAAGTGCA GTGGAAGGTCGACAACGCACTGCA GTCGGGAAACTCCCAGGAATCGGT GACCGAGCAGGACTCGAAGGACTC AACCTACTCATTGTCCTCCACCCTC ACCCTGAGCAAGGCCGATTACGAG AAGCATAAGGTCTACGCCTGCGAA GTGACCCACCAGGGCCTGAGCAGC CCAGTGACGAAGTCCTTCAACCGG GGAGAATGC

	AAGGACACTCTGATGATTTCACGCAC CCCGGAAGTCACTTGCGTGGTCGTGG ACGTGTCGCACGAAGATCCCGAAGT GAAATTCAATTGGTACGTGGATGGG GTCGAAGTGCACAACGCCAAGACCA AGCCTAGGGAAGAACAGTACAACTC TACGTACCGGGTGGTGTCCGTGCTGA CCGTGCTGCACCAGGACTGGCTGAA CGGAAAGGAGTACAAGTGCAAAGTG TCAAACAAGGCTCTCCCTGCCCCTAT CGAAAAGACCATCAGCAAGGCCAAG GGTCAACCTAGGGAGCCCCAGGTCT ATACTTTGCCGCCTAGCCGGGAAGA AATGACTAAGAACCAAGTGTCCCTG ACTTGCCTTGTCAAGGGCTTTTATCC GTCCGACATCGCCGTGGAGTGGGAG TCCAACGGACAACCGGAGAACAACT ACAAGACCACCCCACCGGTGCTCGA TTCCGATGGCTCCTTCTTCCTGTACTC CAAGCTGACTGTGGACAAGTCAAGA TGGCAGCAGGGAAACGTGTTCTCCTG CTCCGTGATGCACGAAGCGCTGCAC AACCATTACACCCAGAAATCACTGTC ACTTTCGCCGGGAAAA		
SEQ ID 1708	GAAGTGCAGCTGGTGCAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGACACTCTCCTGTGCAGCCTCTG GATTCACCTTCAGTTCCCATCTTATG CACTGGGTCCGCCAGGCTCCAGGCA AGGGGCTGGAGTGGGTGGCAGTTAT ATCATATGATGGAACTAGTAAATATT ACGGAGACTCCGTGAAGGGCCGCTT CACCATCTCCAGAGACAATTCCAAG AACACGTTGTATCTGCAAATGAACA GCCTGCGAGCTGAAGACACGGCTAT ATATTACTGTGCGAAAGCAGATTATA AATATGACTGGGGCCAGGGAACCCT GGTCACCGTCTCCTCAGCATCCACCA AGGGGCCTTCCGTGTTCCCCCTGGCC CCTTCATCCAAGTCGACCTCTGGTGG AACCGCCGCACTCGGTTGCCTGGTCA AAGACTACTTCCCCGAGCCCGTGACT GTCTCGTGGAACTCGGGCGCCCTCAC ATCCGGAGTGCATACCTTTCCCGCCG TGTTGCAGTCCAGCGGCCTGTACAGC CTGAGCTCCGTCGTGACAGTGCCGTC CTCCTCCCTTGGAACCCAGACCTATA TCTGCAACGTCAATCACAAGCCCTCC AACACCAAAGTGGACAAGAAGGTCG AACCCAAGTCCTGCGACAAGACTCA CACCTGTCCGCCTTGTCCAGCCCCTG AGCTGCTGGGTGGTCCGTCCGTGTTC CTCTTCCCGCCCAAGCCGAAGGACAC	SEQ ID 1816	GACATCCAGATGACCCAGTCTCCA TCCTCCCTGTCTGCATCTGTAGGAG ACAGAGTCACCATCACTTGCCGGG CAAGTCAGAGCATTAGCAGCTATT TAAATTGGTATCAGCAGAAACCAG GGAAAGCCCCTAACCTCCTGATCT ATGCTGCATCCAGTTTGCACACTGG GGTCCCATCAAGGTTCAGTGGCAG TGGATCTGGGACAGATTTCACTCTC ACCATCAGCAGTCTGCAACCTGAA GATTTTGCAACTTACTACTGTCAAC AGAGTTACAGTATTCCTCGAACGTT CGGCCAAGGGACCAAGGTGGAAAT CAAACGTACTGTGGCTGCTCCCTCC GTGTTCATTTTTCCTCCGTCGGACG AACAGCTGAAGTCCGGAACCGCGT CCGTGGTCTGTCTCCTGAACAACTT CTATCCGCGCGAGGCGAAAGTGCA GTGGAAGGTCGACAACGCACTGCA GTCGGGAAACTCCCAGGAATCGGT GACCGAGCAGGACTCGAAGGACTC AACCTACTCATTGTCCTCCACCCTC ACCCTGAGCAAGGCCGATTACGAG AAGCATAAGGTCTACGCCTGCGAA GTGACCCACCAGGGCCTGAGCAGC CCAGTGACGAAGTCCTTCAACCGG GGAGAATGC

	TCTGATGATTTCACGCACCCCGGAAG TCACTTGCGTGGTCGTGGACGTGTCG CACGAAGATCCCGAAGTGAAATTCA ATTGGTACGTGGATGGGGTCGAAGT GCACAACGCCAAGACCAAGCCTAGG GAAGAACAGTACAACTCTACGTACC GGGTGGTGTCCGTGCTGACCGTGCTG CACCAGGACTGGCTGAACGGAAAGG AGTACAAGTGCAAAGTGTCAAACAA GGCTCTCCCTGCCCCTATCGAAAAGA CCATCAGCAAGGCCAAGGGTCAACC TAGGGAGCCCCAGGTCTATACTTTGC CGCCTAGCCGGGAAGAAATGACTAA GAACCAAGTGTCCCTGACTTGCCTTG TCAAGGGCTTTTATCCGTCCGACATC GCCGTGGAGTGGGAGTCCAACGGAC AACCGGAGAACAACTACAAGACCAC CCCACCGGTGCTCGATTCCGATGGCT CCTTCTTCCTGTACTCCAAGCTGACT GTGGACAAGTCAAGATGGCAGCAGG GAAACGTGTTCTCCTGCTCCGTGATG CACGAAGCGCTGCACAACCATTACA CCCAGAAATCACTGTCACTTTCGCCG GGAAAA		
SEQ ID 1709	GAGGTGCAGCTGGTGCAGTCTGGGG GAGGCTTGGTCAAGCCTGGAGGGTC CCTGAGACTCTCCTGTACAGCTTCTG GATTCACCTTTGGTGATTATGCTATG AGCTGGGTCCGCCAGGCTCCAGGGA AGGGGCTGGAGTGGGTAGGTTTCATT AGAAGCAAAGCTTATGGTGGGACAA CAGAATACGCCGCGTCTGTGAAAGG CAGATTCACCATCTCAAGAGATGATT CCAAAAGCATCGCCTATCTGCAAATG AACAGCCTGAAAACCGAGGACACAG CCGTGTATTACTGTACTACTCATAGA CGCCCAATTTACGATATTTTGACTGG TTTTGACTACTGGGGCCAGGGAACCC TGGTCACCGTCTCCTCAGCATCCACC AAGGGGCCTTCCGTGTTCCCCCTGGC CCCTTCATCCAAGTCGACCTCTGGTG GAACCGCCGCACTCGGTTGCCTGGTC AAAGACTACTTCCCCGAGCCCGTGAC TGTCTCGTGGAACTCGGGCGCCCTCA CATCCGGAGTGCATACCTTTCCCGCC GTGTTGCAGTCCAGCGGCCTGTACAG CCTGAGCTCCGTCGTGACAGTGCCGT CCTCCTCCCTTGGAACCCAGACCTAT ATCTGCAACGTCAATCACAAGCCCTC CAACACCAAAGTGGACAAGAAGGTC GAACCCAAGTCCTGCGACAAGACTC ACACCTGTCCGCCTTGTCCAGCCCCT GAGCTGCTGGGTGGTCCGTCCGTGTT CCTCTTCCCGCCCAAGCCGAAGGACA	SEQ ID 1817	GATGTTGTGATGACTCAGTCTCCAG CCACCCTGTCTGTGACTCCAGGGG AAAGGGCCACCCTCTCCTGCAGGG CCAGTCAAAGTGTTAACAGCAACG TAGCCTGGTACCAGCAGAAACCTG GCCAGGCTCCCAGGCTCCTCATCTA TGATGTATCCACCAGGGCCACTGA TATCCCAGCCAGGTTCAGTGGCAG TGGGTCTGGGACAGACTTCACTCTC ACCATCAGCAGACTTGACCCTGAA GATTTTGCAGTGTATTACTGTCAGC AGTGTGCTAGCTCACCTCCTGTCAC TTTCGGCGGAGGGACCAAGCTGGA GATCAAACGTACTGTGGCTGCTCC CTCCGTGTTCATTTTTCCTCCGTCG GACGAACAGCTGAAGTCCGGAACC GCGTCCGTGGTCTGTCTCCTGAACA ACTTCTATCCGCGCGAGGCGAAAG TGCAGTGGAAGGTCGACAACGCAC TGCAGTCGGGAAACTCCCAGGAAT CGGTGACCGAGCAGGACTCGAAGG ACTCAACCTACTCATTGTCCTCCAC CCTCACCCTGAGCAAGGCCGATTA CGAGAAGCATAAGGTCTACGCCTG CGAAGTGACCCACCAGGGCCTGAG CAGCCCAGTGACGAAGTCCTTCAA CCGGGGAGAATGC

	CTCTGATGATTTCACGCACCCCGGAA GTCACTTGCGTGGTCGTGGACGTGTC GCACGAAGATCCCGAAGTGAAATTC AATTGGTACGTGGATGGGGTCGAAG TGCACAACGCCAAGACCAAGCCTAG GGAAGAACAGTACAACTCTACGTAC CGGGTGGTGTCCGTGCTGACCGTGCT GCACCAGGACTGGCTGAACGGAAAG GAGTACAAGTGCAAAGTGTCAAACA AGGCTCTCCCTGCCCCTATCGAAAAG ACCATCAGCAAGGCCAAGGGTCAAC CTAGGGAGCCCCAGGTCTATACTTTG CCGCCTAGCCGGGAAGAAATGACTA AGAACCAAGTGTCCCTGACTTGCCTT GTCAAGGGCTTTTATCCGTCCGACAT CGCCGTGGAGTGGGAGTCCAACGGA CAACCGGAGAACAACTACAAGACCA CCCCACCGGTGCTCGATTCCGATGGC TCCTTCTTCCTGTACTCCAAGCTGAC TGTGGACAAGTCAAGATGGCAGCAG GGAAACGTGTTCTCCTGCTCCGTGAT GCACGAAGCGCTGCACAACCATTAC ACCCAGAAATCACTGTCACTTTCGCC GGGAAAA		
SEQ ID 1710	CAGCTGCAGCTGCAGGAGTCCGGGG GAGGCTTGGTACAGCCAGGGCGGTC CCTGAGACTCTCCTGTACAGCTTCTG GATTCACCTTTGGTGATTATGCTATG AGCTGGGTCCGCCAGGCTCCAGGGA AGGGGCTGGAGTGGGTAGGTTTCATT AGAAGCAAAGCTTATGGTGGGACAA CAGAATACGCCGCGTCTGTGAAAGG CAGATTCACCATCTCAAGAGATGATT CCAAAAGCATCGCCTATCTGCAAATG AACAGCCTGAAAACCGAGGACACAG CCGTGTATTACTGTACTAGAGAGGAT ACTATGGTTCGGGGAGTTATTCCCTG GGGCCAGGGAACCCTGGTCACCGTC TCCTCAGCATCCACCAAGGGGCCTTC CGTGTTCCCCCTGGCCCCTTCATCCA AGTCGACCTCTGGTGGAACCGCCGC ACTCGGTTGCCTGGTCAAAGACTACT TCCCCGAGCCCGTGACTGTCTCGTGG AACTCGGGCGCCCTCACATCCGGAGT GCATACCTTTCCCGCCGTGTTGCAGT CCAGCGGCCTGTACAGCCTGAGCTCC GTCGTGACAGTGCCGTCCTCCTCCCT TGGAACCCAGACCTATATCTGCAACG TCAATCACAAGCCCTCCAACACCAA AGTGGACAAGAAGGTCGAACCCAAG TCCTGCGACAAGACTCACACCTGTCC GCCTTGTCCAGCCCCTGAGCTGCTGG GTGGTCCGTCCGTGTTCCTCTTCCCG	SEQ ID 1818	GAAATTGTGATGACGCAGTCTCCA GCCACCCTGTCTTTGTCTCCAGGGG AAAGAGCCACCCTCTCCTGCGGGG CCAGTCAGAGTGTTAGCAGCAGCT ACTTAGCCTGGTACCAGCAGAAAC CTGGCCTGGCGCCCAGGCTCCTCAT CTATGATGCATCCAGCAGGGCCAC TGGCATCCCAGACAGGTTCAGTGG CAGTGGGTCTGGGACAGACTTCAC TCTCACCATCAGCAGACTGGAGCC TGAAGATTTTGCAGTGTATTACTGT CAGCAGTATGGTAGCTCACCTCGG GTCACTTTCGGCGGAGGGACCAAA GTGGATATCAAACGTACTGTGGCT GCTCCCTCCGTGTTCATTTTTCCTC CGTCGGACGAACAGCTGAAGTCCG GAACCGCGTCCGTGGTCTGTCTCCT GAACAACTTCTATCCGCGCGAGGC GAAAGTGCAGTGGAAGGTCGACAA CGCACTGCAGTCGGGAAACTCCCA GGAATCGGTGACCGAGCAGGACTC GAAGGACTCAACCTACTCATTGTC CTCCACCCTCACCCTGAGCAAGGC CGATTACGAGAAGCATAAGGTCTA CGCCTGCGAAGTGACCCACCAGGG CCTGAGCAGCCCAGTGACGAAGTC CTTCAACCGGGGAGAATGC

	CCCAAGCCGAAGGACACTCTGATGA TTTCACGCACCCCGGAAGTCACTTGC GTGGTCGTGGACGTGTCGCACGAAG ATCCCGAAGTGAAATTCAATTGGTAC GTGGATGGGGTCGAAGTGCACAACG CCAAGACCAAGCCTAGGGAAGAACA GTACAACTCTACGTACCGGGTGGTGT CCGTGCTGACCGTGCTGCACCAGGAC TGGCTGAACGGAAAGGAGTACAAGT GCAAAGTGTCAAACAAGGCTCTCCCT GCCCCTATCGAAAAGACCATCAGCA AGGCCAAGGGTCAACCTAGGGAGCC CCAGGTCTATACTTTGCCGCCTAGCC GGGAAGAAATGACTAAGAACCAAGT GTCCCTGACTTGCCTTGTCAAGGGCT TTTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAGA ACAACTACAAGACCACCCCACCGGT GCTCGATTCCGATGGCTCCTTCTTCC TGTACTCCAAGCTGACTGTGGACAAG TCAAGATGGCAGCAGGGAAACGTGT TCTCCTGCTCCGTGATGCACGAAGCG CTGCACAACCATTACACCCAGAAATC ACTGTCACTTTCGCCGGGAAAA		
SEQ ID 1711	CAGCTGCAGCTGCAGGAGTCCGGCT CAGGACTGGTGAAGCCTTCACAGAC CCTGTCCCTCACCTGCGCTGTCTCTG GTGGCTCCATCAGCAGTGGTGGTTAC TCCTGGAGCTGGATCCGGCAGCCACC AGGGAAGGGCCTGGAGTGGATTGGG TACATCTATCATAGTGGGAGCACCTA CTACAACCCGTCCCTCAAGAGTCGAG TCACCATATCAGTAGACAGGTCCAA GAACCAGTTCTCCCTGAAGCTGAGCT CTGTGACCGCCGCGGACACGGCTGT GTATTACTGTGCGAGAGATCGGCGTT ACTATGATAGTAGTGGTTATTATCCC GCCTACTACTTTGACTACTGGGGCCA GGGAACCCTGGTCACCGTCTCCTCAG CATCCACCAAGGGGCCTTCCGTGTTC CCCCTGGCCCCTTCATCCAAGTCGAC CTCTGGTGGAACCGCCGCACTCGGTT GCCTGGTCAAAGACTACTTCCCCGAG CCCGTGACTGTCTCGTGGAACTCGGG CGCCCTCACATCCGGAGTGCATACCT TTCCCGCCGTGTTGCAGTCCAGCGGC CTGTACAGCCTGAGCTCCGTCGTGAC AGTGCCGTCCTCCTCCCTTGGAACCC AGACCTATATCTGCAACGTCAATCAC AAGCCCTCCAACACCAAAGTGGACA AGAAGGTCGAACCCAAGTCCTGCGA CAAGACTCACACCTGTCCGCCTTGTC CAGCCCCTGAGCTGCTGGGTGGTCCG	SEQ ID 1819	GATGTTGTGATGACTCAGTCTCCAG GCACCCTGTCTTTGTCTCCAGGGGA AAGAGCCACCCTCTCCTGCAGGGC CAGTCAGAGTGTTAGCAGCAGCGC CTTAGCCTGGTTCCAGCAGAAACC TGGCCAGGCTCCCAGGCTCCTCATC TATGATTCATCCAGCAGGGCCACT GGCATCCCAGACAGCTTCAGCGGC AGTGGATCTGGGACAGAATTCACA CTCACAATCAGTAGCCTGCAGCCT GAAGATTTTGCAACTTATTACTGTC AACAGTTTAATACCTACCCCAACA CTTTTGGCCAGGGGACCAAGCTGG AGATCAAACGTACTGTGGCTGCTC CCTCCGTGTTCATTTTTCCTCCGTC GGACGAACAGCTGAAGTCCGGAAC CGCGTCCGTGGTCTGTCTCCTGAAC AACTTCTATCCGCGCGAGGCGAAA GTGCAGTGGAAGGTCGACAACGCA CTGCAGTCGGGAAACTCCCAGGAA TCGGTGACCGAGCAGGACTCGAAG GACTCAACCTACTCATTGTCCTCCA CCCTCACCCTGAGCAAGGCCGATT ACGAGAAGCATAAGGTCTACGCCT GCGAAGTGACCCACCAGGGCCTGA GCAGCCCAGTGACGAAGTCCTTCA ACCGGGGAGAATGC

	TCCGTGTTCCTCTTCCCGCCCAAGCC GAAGGACACTCTGATGATTTCACGCA CCCCGGAAGTCACTTGCGTGGTCGTG GACGTGTCGCACGAAGATCCCGAAG TGAAATTCAATTGGTACGTGGATGGG GTCGAAGTGCACAACGCCAAGACCA AGCCTAGGGAAGAACAGTACAACTC TACGTACCGGGTGGTGTCCGTGCTGA CCGTGCTGCACCAGGACTGGCTGAA CGGAAAGGAGTACAAGTGCAAAGTG TCAAACAAGGCTCTCCCTGCCCCTAT CGAAAAGACCATCAGCAAGGCCAAG GGTCAACCTAGGGAGCCCCAGGTCT ATACTTTGCCGCCTAGCCGGGAAGA AATGACTAAGAACCAAGTGTCCCTG ACTTGCCTTGTCAAGGGCTTTTATCC GTCCGACATCGCCGTGGAGTGGGAG TCCAACGGACAACCGGAGAACAACT ACAAGACCACCCCACCGGTGCTCGA TTCCGATGGCTCCTTCTTCCTGTACTC CAAGCTGACTGTGGACAAGTCAAGA TGGCAGCAGGGAAACGTGTTCTCCTG CTCCGTGATGCACGAAGCGCTGCAC AACCATTACACCCAGAAATCACTGTC ACTTTCGCCGGGAAAA		
SEQ ID 1712	GAAGTGCAGCTGGTGCAGTCTGGGG GAGGCCTGGTCAAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTCAGTAGCTATAGCATG AACTGGGTCCGCCAGGCTCCAGGGA AGGGGCTGGAGTGGGTTTCATACATT AGTAGTAGTGGTAGTTACACAAACT ACGCAGACTCTGTGAAGGGCCGATT CACCATCTCCAGAGACAACGCCAAG AACTCACTGTATCTGCAAATAAACAG CCTGAGAGCCGAGGACACGGCCATT TATTACTGTGCGAGAGACGGGGGCT ATGATAGTAGTGGTTTTCACTTTGAC TACTGGGGCCAGGGAACCCTGGTCA CCGTCTCCTCAGCATCCACCAAGGGG CCTTCCGTGTTCCCCCTGGCCCCTTC ATCCAAGTCGACCTCTGGTGGAACCG CCGCACTCGGTTGCCTGGTCAAAGAC TACTTCCCCGAGCCCGTGACTGTCTC GTGGAACTCGGGCGCCCTCACATCCG GAGTGCATACCTTTCCCGCCGTGTTG CAGTCCAGCGGCCTGTACAGCCTGA GCTCCGTCGTGACAGTGCCGTCCTCC TCCCTTGGAACCCAGACCTATATCTG CAACGTCAATCACAAGCCCTCCAAC ACCAAAGTGGACAAGAAGGTCGAAC CCAAGTCCTGCGACAAGACTCACAC CTGTCCGCCTTGTCCAGCCCCTGAGC TGCTGGGTGGTCCGTCCGTGTTCCTC	SEQ ID 1820	GACATCCAGATGACCCAGTCTCCA CTCTCCCTGCCCGTCACCCCTGGAG AGCCGGCCTCCATCTCCTGCAGGTC TAGTCAGAGCCTCCTGCATAGTAA TGGATACAACTATTTGGATTGGTTC CTGCAGAAGCCAGGGCAGTCTCCA CGGCTCCTGATCTATATGGGTTCTA GTCGGGCCTCCGGGGTCCCTGAGA GGTTCAGTGGCAGTGGATCAGGCA CAGATTTTACACTGAAAATCAGCA GAGTGGAGGCTGAGGATGTTGGGG TCTATTACTGCATGCAAACTTTACA CACTGTCACTTTCGGCGGCGGGAC CAAGGTGGAAATCAAACGTACTGT GGCTGCTCCCTCCGTGTTCATTTTT CCTCCGTCGGACGAACAGCTGAAG TCCGGAACCGCGTCCGTGGTCTGTC TCCTGAACAACTTCTATCCGCGCGA GGCGAAAGTGCAGTGGAAGGTCGA CAACGCACTGCAGTCGGGAAACTC CCAGGAATCGGTGACCGAGCAGGA CTCGAAGGACTCAACCTACTCATT GTCCTCCACCCTCACCCTGAGCAA GGCCGATTACGAGAAGCATAAGGT CTACGCCTGCGAAGTGACCCACCA GGGCCTGAGCAGCCCAGTGACGAA GTCCTTCAACCGGGGAGAATGC

	TTCCCGCCCAAGCCGAAGGACACTCT GATGATTTCACGCACCCCGGAAGTCA CTTGCGTGGTCGTGGACGTGTCGCAC GAAGATCCCGAAGTGAAATTCAATT GGTACGTGGATGGGGTCGAAGTGCA CAACGCCAAGACCAAGCCTAGGGAA GAACAGTACAACTCTACGTACCGGG TGGTGTCCGTGCTGACCGTGCTGCAC CAGGACTGGCTGAACGGAAAGGAGT ACAAGTGCAAAGTGTCAAACAAGGC TCTCCCTGCCCCTATCGAAAAGACCA TCAGCAAGGCCAAGGGTCAACCTAG GGAGCCCCAGGTCTATACTTTGCCGC CTAGCCGGGAAGAAATGACTAAGAA CCAAGTGTCCCTGACTTGCCTTGTCA AGGGCTTTTATCCGTCCGACATCGCC GTGGAGTGGGAGTCCAACGGACAAC CGGAGAACAACTACAAGACCACCCC ACCGGTGCTCGATTCCGATGGCTCCT TCTTCCTGTACTCCAAGCTGACTGTG GACAAGTCAAGATGGCAGCAGGGAA ACGTGTTCTCCTGCTCCGTGATGCAC GAAGCGCTGCACAACCATTACACCC AGAAATCACTGTCACTTTCGCCGGGA AAA		
SEQ ID 1713	CAGGTACAGCTGCAGCAGTCAGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAACAACAGGGC TGCTTGGAACTGGATCAGGCAGTCGC CATCGAGAGGCCTTGAGTGGCTGGG AAGGACATACTACAGGTCCAAGTGG TATAATGAATATGCAGTCTCTGTGAA AAGTCGAATAACCATCAACCCAGAC ACATCCAAGAACCAGTTCTCCCTGCA GCTGAACTCTATGACTCCCGAGGACT CGGCTGTGTATTACTGTGCAATTTTG CCTAGTAGTGGTTATCTACAGGACCA CCACTACTACGGTATGGACGTCTGGG GCCAAGGGACCACGGTCACCGTCTC CTCAGCATCCACCAAGGGGCCTTCCG TGTTCCCCCTGGCCCCTTCATCCAAG TCGACCTCTGGTGGAACCGCCGCACT CGGTTGCCTGGTCAAAGACTACTTCC CCGAGCCCGTGACTGTCTCGTGGAAC TCGGGCGCCCTCACATCCGGAGTGCA TACCTTTCCCGCCGTGTTGCAGTCCA GCGGCCTGTACAGCCTGAGCTCCGTC GTGACAGTGCCGTCCTCCTCCCTTGG AACCCAGACCTATATCTGCAACGTCA ATCACAAGCCCTCCAACACCAAAGT GGACAAGAAGGTCGAACCCAAGTCC TGCGACAAGACTCACACCTGTCCGCC TTGTCCAGCCCCTGAGCTGCTGGGTG	SEQ ID 1821	GAAACGACACTCACGCAGTCTCCA GGCACCCTGTCTTTGTCTCCAGGGG AAAGAGCCACCCTCTCCTGCAGGG CCAGTCAGAGTGTTAGCAGCAGCT ACTTAGCCTGGTACCAGCAGAAAC CTGGCCAGGCTCCCAGGCTCCTCAT CTATGGTGCATCCAGCAGGGCCAC TGGCATCCCAGACAGGTTCAGTGG CAGTGGGTCTGGGACAGACTTCAC TCTCACCATCAGCAGACTGGAGCC TGAAGATTTTGCAGTGTATTACTGT CAGCAGTATGGTAGCTCACTCCTCT TCGGCCAAGGGACACGACTGGAGA TTAAACGTACTGTGGCTGCTCCCTC CGTGTTCATTTTTCCTCCGTCGGAC GAACAGCTGAAGTCCGGAACCGCG TCCGTGGTCTGTCTCCTGAACAACT TCTATCCGCGCGAGGCGAAAGTGC AGTGGAAGGTCGACAACGCACTGC AGTCGGGAAACTCCCAGGAATCGG TGACCGAGCAGGACTCGAAGGACT CAACCTACTCATTGTCCTCCACCCT CACCCTGAGCAAGGCCGATTACGA GAAGCATAAGGTCTACGCCTGCGA AGTGACCCACCAGGGCCTGAGCAG CCCAGTGACGAAGTCCTTCAACCG GGGAGAATGC

	GTCCGTCCGTGTTCCTCTTCCCGCCC AAGCCGAAGGACACTCTGATGATTTC ACGCACCCCGGAAGTCACTTGCGTG GTCGTGGACGTGTCGCACGAAGATC CCGAAGTGAAATTCAATTGGTACGTG GATGGGGTCGAAGTGCACAACGCCA AGACCAAGCCTAGGGAAGAACAGTA CAACTCTACGTACCGGGTGGTGTCCG TGCTGACCGTGCTGCACCAGGACTGG CTGAACGGAAAGGAGTACAAGTGCA AAGTGTCAAACAAGGCTCTCCCTGCC CCTATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTATACTTTGCCGCCTAGCCGGG AAGAAATGACTAAGAACCAAGTGTC CCTGACTTGCCTTGTCAAGGGCTTTT ATCCGTCCGACATCGCCGTGGAGTGG GAGTCCAACGGACAACCGGAGAACA ACTACAAGACCACCCCACCGGTGCTC GATTCCGATGGCTCCTTCTTCCTGTA CTCCAAGCTGACTGTGGACAAGTCA AGATGGCAGCAGGGAAACGTGTTCT CCTGCTCCGTGATGCACGAAGCGCTG CACAACCATTACACCCAGAAATCACT GTCACTTTCGCCGGGAAAA		
SEQ ID 1714	GAGGTGCAGCTGGTGCAGTCTGGAG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTCTCCTGCAAGGCTTCTG GTTACACCTTTACCAGCTACGGTATC AGCTGGGTGCGACAGGCCCCTGGAC AAGGGCTTGAGTGGATGGGATGGAT CAGCGCTTACAATGGTAACACAAAC TATGCACAGAAGCTCCAGGGCAGAG TCACCATGACCACAGACACATCCAC GAGCACAGCCTACATGGAGCTGAGC AGCCTGAGATCTGAGGACACGGCCG TGTATTACTGTGCGAGAGCCGCGGTG GGGGATGGATACAGCTATGGTCGGC TCGATTGGGGCCAGGGAACCCTGGT CACCGTCTCCTCAGCATCCACCAAGG GGCCTTCCGTGTTCCCCCTGGCCCCT TCATCCAAGTCGACCTCTGGTGGAAC CGCCGCACTCGGTTGCCTGGTCAAAG ACTACTTCCCCGAGCCCGTGACTGTC TCGTGGAACTCGGGCGCCCTCACATC CGGAGTGCATACCTTTCCCGCCGTGT TGCAGTCCAGCGGCCTGTACAGCCTG AGCTCCGTCGTGACAGTGCCGTCCTC CTCCCTTGGAACCCAGACCTATATCT GCAACGTCAATCACAAGCCCTCCAA CACCAAAGTGGACAAGAAGGTCGAA CCCAAGTCCTGCGACAAGACTCACA CCTGTCCGCCTTGTCCAGCCCCTGAG CTGCTGGGTGGTCCGTCCGTGTTCCT	SEQ ID 1822	GACATCCAGTTGACCCAGTCTCCAT CCTTCCTGTCTGCATCTGTTGGAGA CAGAGTCACCATCACTTGCCGGGC CAGTCAGGGCATTAGCAGTTCTTTG GCCTGGTATCAGCAAAAGCCAGGG AAAGCCCCTAAGCTCCTGATCTAT GCTGCATCCACTTTGCAAAGTGGG GTCCCATCAAGGTTCAGTGGAAGT GGATCTGGGACAGATTTTACTTTCA CCATCAGCAGCCTGCAGCCTGAAG ATATTGCAACATATTACTGTCAACA GTATGATAATCTCCCTCCTCTCACT TTCGGCGGAGGGACCAAGGTGGAA ATCAAACGTACTGTGGCTGCTCCCT CCGTGTTCATTTTTCCTCCGTCGGA CGAACAGCTGAAGTCCGGAACCGC GTCCGTGGTCTGTCTCCTGAACAAC TTCTATCCGCGCGAGGCGAAAGTG CAGTGGAAGGTCGACAACGCACTG CAGTCGGGAAACTCCCAGGAATCG GTGACCGAGCAGGACTCGAAGGAC TCAACCTACTCATTGTCCTCCACCC TCACCCTGAGCAAGGCCGATTACG AGAAGCATAAGGTCTACGCCTGCG AAGTGACCCACCAGGGCCTGAGCA GCCCAGTGACGAAGTCCTTCAACC GGGGAGAATGC

	CTTCCCGCCCAAGCCGAAGGACACTC TGATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGCA CGAAGATCCCGAAGTGAAATTCAAT TGGTACGTGGATGGGGTCGAAGTGC ACAACGCCAAGACCAAGCCTAGGGA AGAACAGTACAACTCTACGTACCGG GTGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGAG TACAAGTGCAAAGTGTCAAACAAGG CTCTCCCTGCCCCTATCGAAAAGACC ATCAGCAAGGCCAAGGGTCAACCTA GGGAGCCCCAGGTCTATACTTTGCCG CCTAGCCGGGAAGAAATGACTAAGA ACCAAGTGTCCCTGACTTGCCTTGTC AAGGGCTTTTATCCGTCCGACATCGC CGTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTCC TTCTTCCTGTACTCCAAGCTGACTGT GGACAAGTCAAGATGGCAGCAGGGA AACGTGTTCTCCTGCTCCGTGATGCA CGAAGCGCTGCACAACCATTACACC CAGAAATCACTGTCACTTTCGCCGGG AAAA		
SEQ ID 1715	GAGGTCCAGCTGGTACAGTCTGGAG CAGAGGTGAAAAAGCCCGGGGAGTC TCTGAAGATCTCCTGTAAGGGTTCTG GATACAGCTTTACCAGCTACTGGATC GGCTGGGTGCGCCAGATGCCCGGGA AAGGCCTGGAGTGGATGGGGATCAT CTATCCTGGTGACTCTGATACCAGAT ACAGCCCGTCCTTCCAAGGCCAGGTC ACCATCTCAGCCGACAAGTCCATCAG CACCGCCTACCTGCAGTGGAGCAGC CTGAAGGCCTCGGACACCGCCATGT ATTACTGTGCGAGACTCCCCTCGTAT TACTATGATAGTAGTGGTTACTTTAC CTGGTACTTCGATCTCTGGGGCCGTG GCACCCTGGTGACCGTCTCTTCAGCA TCCACCAAGGGGCCTTCCGTGTTCCC CCTGGCCCCTTCATCCAAGTCGACCT CTGGTGGAACCGCCGCACTCGGTTGC CTGGTCAAAGACTACTTCCCCGAGCC CGTGACTGTCTCGTGGAACTCGGGCG CCCTCACATCCGGAGTGCATACCTTT CCCGCCGTGTTGCAGTCCAGCGGCCT GTACAGCCTGAGCTCCGTCGTGACAG TGCCGTCCTCCTCCCTTGGAACCCAG ACCTATATCTGCAACGTCAATCACAA GCCCTCCAACACCAAAGTGGACAAG AAGGTCGAACCCAAGTCCTGCGACA AGACTCACACCTGTCCGCCTTGTCCA GCCCCTGAGCTGCTGGGTGGTCCGTC	SEQ ID 1823	GATGTTGTGATGACTCAGTCTCCAC TCTCCCTGCCCGTCACCCCTGGAGA GCCGGCCTCCATCTCCTGCAGGTCT AGTCAGAGCCTCCTGCATAGTAAT GGATACAACTATTTGGATTGGTAC CTGCAGAAGCCAGGGCAGTCTCCA CAGCTCCTGATCTATTTGGGTTCTA ATCGGGCCTCCGGGGTCCCTGACA GGTTCAGTGGCAGTGGATCAGGCA CAGATTTCACAGTGAAAATCAGCA GAGTGGAGGCTGAGGATGTTGGGG TTTATTACTGCATGCAAGCTCTACA AACTCCGTACACTTTTGGCCAGGG GACCAAGCTGGAGATCAAACGTAC TGTGGCTGCTCCCTCCGTGTTCATT TTTCCTCCGTCGGACGAACAGCTG AAGTCCGGAACCGCGTCCGTGGTC TGTCTCCTGAACAACTTCTATCCGC GCGAGGCGAAAGTGCAGTGGAAG GTCGACAACGCACTGCAGTCGGGA AACTCCCAGGAATCGGTGACCGAG CAGGACTCGAAGGACTCAACCTAC TCATTGTCCTCCACCCTCACCCTGA GCAAGGCCGATTACGAGAAGCATA AGGTCTACGCCTGCGAAGTGACCC ACCAGGGCCTGAGCAGCCCAGTGA CGAAGTCCTTCAACCGGGGAGAAT GC

	CGTGTTCCTCTTCCCGCCCAAGCCGA AGGACACTCTGATGATTTCACGCACC CCGGAAGTCACTTGCGTGGTCGTGGA CGTGTCGCACGAAGATCCCGAAGTG AAATTCAATTGGTACGTGGATGGGGT CGAAGTGCACAACGCCAAGACCAAG CCTAGGGAAGAACAGTACAACTCTA CGTACCGGGTGGTGTCCGTGCTGACC GTGCTGCACCAGGACTGGCTGAACG GAAAGGAGTACAAGTGCAAAGTGTC AAACAAGGCTCTCCCTGCCCCTATCG AAAAGACCATCAGCAAGGCCAAGGG TCAACCTAGGGAGCCCCAGGTCTATA CTTTGCCGCCTAGCCGGGAAGAAAT GACTAAGAACCAAGTGTCCCTGACTT GCCTTGTCAAGGGCTTTTATCCGTCC GACATCGCCGTGGAGTGGGAGTCCA ACGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCCG ATGGCTCCTTCTTCCTGTACTCCAAG CTGACTGTGGACAAGTCAAGATGGC AGCAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACTT TCGCCGGGAAAA		
SEQ ID 1716	GAGGTCCAGCTGGTACAGTCTGGAG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTCTCCTGCAAGGCTTCTG GTTACACCTTTACCAGCTATGGTATC AGCTGGGTGCGACAGGCCCCTGGAC AAGGGCTTGAGTGGATGGGATGGAT CATCCCTATCTTTGGTATAGCAAACT ACGCACAGAAGTTCCAGGGCAGAGT CACGATTACCGCGGACAAATCCACG AGCACAGCCTACATGGAGCTGAGCA GCCTGAGATCTGAGGACACGGCCGT GTATTACTGTGCGAGAGAACTATACA ACTATGGTTCAAAGGACTACTTTGAC TACTGGGGCCAGGGAACCCTGGTCA CCGTCTCCTCAGCATCCACCAAGGGG CCTTCCGTGTTCCCCCTGGCCCCTTC ATCCAAGTCGACCTCTGGTGGAACCG CCGCACTCGGTTGCCTGGTCAAAGAC TACTTCCCCGAGCCCGTGACTGTCTC GTGGAACTCGGGCGCCCTCACATCCG GAGTGCATACCTTTCCCGCCGTGTTG CAGTCCAGCGGCCTGTACAGCCTGA GCTCCGTCGTGACAGTGCCGTCCTCC TCCCTTGGAACCCAGACCTATATCTG CAACGTCAATCACAAGCCCTCCAAC ACCAAAGTGGACAAGAAGGTCGAAC CCAAGTCCTGCGACAAGACTCACAC CTGTCCGCCTTGTCCAGCCCCTGAGC TGCTGGGTGGTCCGTCCGTGTTCCTC	SEQ ID 1824	GAAATTGTGTTGACGCAGTCTCCA CTCTCCCTGCCCGTCACCCTTGGAC AGCCGGCCTCCATCTCCTGCAGGTC TTGTCAAAGCCTCGTATACAGTGAT GGCAACACCTACTTGAATTGCTTTC AGCAGAGGCCAGGCCAATCTCCAA GGCGCCTAATTTATAAGGTTTCTAA CCGGGACTCTGGGGTCCCAGACAG ATTCAGCGGCAGTGGGTCAGGCAC AGATTTTACACTGGAAATCAGCAG AGTGGAGGCTGAGGATGTTGGGAT TTATTTCTGCATGCAAGGTCTACAA ACTCCATTCACTTTCGGCCCTGGGA CCAAAGTGGATATCAAACGTACTG TGGCTGCTCCCTCCGTGTTCATTTT TCCTCCGTCGGACGAACAGCTGAA GTCCGGAACCGCGTCCGTGGTCTG TCTCCTGAACAACTTCTATCCGCGC GAGGCGAAAGTGCAGTGGAAGGTC GACAACGCACTGCAGTCGGGAAAC TCCCAGGAATCGGTGACCGAGCAG GACTCGAAGGACTCAACCTACTCA TTGTCCTCCACCCTCACCCTGAGCA AGGCCGATTACGAGAAGCATAAGG TCTACGCCTGCGAAGTGACCCACC AGGGCCTGAGCAGCCCAGTGACGA AGTCCTTCAACCGGGGAGAATGC

	TTCCCGCCCAAGCCGAAGGACACTCT GATGATTTCACGCACCCCGGAAGTCA CTTGCGTGGTCGTGGACGTGTCGCAC GAAGATCCCGAAGTGAAATTCAATT GGTACGTGGATGGGGTCGAAGTGCA CAACGCCAAGACCAAGCCTAGGGAA GAACAGTACAACTCTACGTACCGGG TGGTGTCCGTGCTGACCGTGCTGCAC CAGGACTGGCTGAACGGAAAGGAGT ACAAGTGCAAAGTGTCAAACAAGGC TCTCCCTGCCCCTATCGAAAAGACCA TCAGCAAGGCCAAGGGTCAACCTAG GGAGCCCCAGGTCTATACTTTGCCGC CTAGCCGGGAAGAAATGACTAAGAA CCAAGTGTCCCTGACTTGCCTTGTCA AGGGCTTTTATCCGTCCGACATCGCC GTGGAGTGGGAGTCCAACGGACAAC CGGAGAACAACTACAAGACCACCCC ACCGGTGCTCGATTCCGATGGCTCCT TCTTCCTGTACTCCAAGCTGACTGTG GACAAGTCAAGATGGCAGCAGGGAA ACGTGTTCTCCTGCTCCGTGATGCAC GAAGCGCTGCACAACCATTACACCC AGAAATCACTGTCACTTTCGCCGGGA AAA		
SEQ ID 1717	GAAGTGCAGCTGGTGCAGTCTGGAG CAGAGGTGAAAAAGCCCGGGGAGTC TCTGAAGATCTCCTGTAAGGGTTCTG GATACAGCTTTACCAGCTACTGGATC GGCTGGGTGCGCCAGATGCCCGGGA AAGGCCTGGAGTGGATGGGGATCAT CTATCCTGGTGACTCTGATACCAGAT ACAGCCCGTCCTTCCAAGGCCAGGTC ACCATCTCAGCCGACAAGTCCATCAG CACCGCCTACCTGCAGTGGAGCAGC CTGAAGGCCTCGGACACCGCCATGT ATTACTGTGCGAGGGGCGGTACTTGG GATACAGCTATGGTTACGGGCTTTGA CTACTGGGGCCAGGGAACCCTGGTC ACCGTCTCCTCAGCATCCACCAAGGG GCCTTCCGTGTTCCCCCTGGCCCCTT CATCCAAGTCGACCTCTGGTGGAACC GCCGCACTCGGTTGCCTGGTCAAAGA CTACTTCCCCGAGCCCGTGACTGTCT CGTGGAACTCGGGCGCCCTCACATCC GGAGTGCATACCTTTCCCGCCGTGTT GCAGTCCAGCGGCCTGTACAGCCTG AGCTCCGTCGTGACAGTGCCGTCCTC CTCCCTTGGAACCCAGACCTATATCT GCAACGTCAATCACAAGCCCTCCAA CACCAAAGTGGACAAGAAGGTCGAA CCCAAGTCCTGCGACAAGACTCACA CCTGTCCGCCTTGTCCAGCCCCTGAG CTGCTGGGTGGTCCGTCCGTGTTCCT	SEQ ID 1825	GATGTTGTGATGACTCAGTCTCCAG GCACCCTGTCTTTGTCTCCAGGGGA AAGAGCCACCCTCTCCTGCAGGGC CAGTCAGAGTGTTAGCAGCAGCTA CTTAGCCTGGTACCAGCAGAAACC TGGCCAGGCTCCCAGGCTCCTCATC TATGGTGCATCCAGCAGGGCCACT GGCATCCCAGACAGGTTCAGTGGC AGTGGGTCTGGGACAGACTTCACT CTCACCATCAGCAGACTGGAGCCT GAAGATTTTGCAGTGTATTACTGTC AGCAGTATGGTAGCTCACCTGCGC TCACTTTCGGCGGAGGGACCAAGC TGGAGATCAAACGTACTGTGGCTG CTCCCTCCGTGTTCATTTTTCCTCC GTCGGACGAACAGCTGAAGTCCGG AACCGCGTCCGTGGTCTGTCTCCTG AACAACTTCTATCCGCGCGAGGCG AAAGTGCAGTGGAAGGTCGACAAC GCACTGCAGTCGGGAAACTCCCAG GAATCGGTGACCGAGCAGGACTCG AAGGACTCAACCTACTCATTGTCCT CCACCCTCACCCTGAGCAAGGCCG ATTACGAGAAGCATAAGGTCTACG CCTGCGAAGTGACCCACCAGGGCC TGAGCAGCCCAGTGACGAAGTCCT TCAACCGGGGAGAATGC

	CTTCCCGCCCAAGCCGAAGGACACTC TGATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGCA CGAAGATCCCGAAGTGAAATTCAAT TGGTACGTGGATGGGGTCGAAGTGC ACAACGCCAAGACCAAGCCTAGGGA AGAACAGTACAACTCTACGTACCGG GTGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGAG TACAAGTGCAAAGTGTCAAACAAGG CTCTCCCTGCCCCTATCGAAAAGACC ATCAGCAAGGCCAAGGGTCAACCTA GGGAGCCCCAGGTCTATACTTTGCCG CCTAGCCGGGAAGAAATGACTAAGA ACCAAGTGTCCCTGACTTGCCTTGTC AAGGGCTTTTATCCGTCCGACATCGC CGTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTCC TTCTTCCTGTACTCCAAGCTGACTGT GGACAAGTCAAGATGGCAGCAGGGA AACGTGTTCTCCTGCTCCGTGATGCA CGAAGCGCTGCACAACCATTACACC CAGAAATCACTGTCACTTTCGCCGGG AAAA		
SEQ ID 1718	GAAGTGCAGCTGGTGCAGTCTGGAG CAGAGGTGAAAAAGCCCGGGGAGTC TCTGAAGATCTCCTGTAAGGGTTCTG GATACAGCTTTACCAGCTACTGGATC GCCTGGGTGCGCCAGATGCCCGGGA AAGGCCTGGAGTGGATGGGGGTCAT CTATCCTGGTGACTCTGATACCAGAT ACAGCCCGTCCTTCCAAGGCCAGGTC ACCATCTCAGCCGACAAGTCCATCAA TACCGCCTACCTGCAGTGGAGCAGCC TGAAGGCCTCGGACACCGCCATGTAT TACTGTGCGAGACCCCATTACGATAT TTTGACTGGTTCCCGGGCGCCCTTTG ACTACTGGGGCCAGGGAACCCTGGT CACCGTCTCCTCAGCATCCACCAAGG GGCCTTCCGTGTTCCCCCTGGCCCCT TCATCCAAGTCGACCTCTGGTGGAAC CGCCGCACTCGGTTGCCTGGTCAAAG ACTACTTCCCCGAGCCCGTGACTGTC TCGTGGAACTCGGGCGCCCTCACATC CGGAGTGCATACCTTTCCCGCCGTGT TGCAGTCCAGCGGCCTGTACAGCCTG AGCTCCGTCGTGACAGTGCCGTCCTC CTCCCTTGGAACCCAGACCTATATCT GCAACGTCAATCACAAGCCCTCCAA CACCAAAGTGGACAAGAAGGTCGAA CCCAAGTCCTGCGACAAGACTCACA CCTGTCCGCCTTGTCCAGCCCCTGAG CTGCTGGGTGGTCCGTCCGTGTTCCT	SEQ ID 1826	GAAATTGTGATGACGCAGTCTCCA CTCTCCCTGCCCGTCACCCCTGGAG AGCCGGCCTCCATCTCCTGCAGGTC TAGTCAGAGCCTCCTGCATAGTAA TGGATACAACTATTTGGATTGGTAC CTGCAGAAGCCAGGGCAGTCTCCA CAGCTCCTGATCTATTTGGGTTCTA CTCGGGCCTCCGGGGTCCCTGACA GGTTCAGTGGCAGTGGATCAGGCA CAGACTTTACACTGAAAATCAGCA GAGCGGAGGCTGAGGATGTTGGGG TTTATTACTGCATGCAAGCTCTACA CACTCCGTGGACGTTCGGCCTAGG GACCAAAGTGGATATCAAACGTAC TGTGGCTGCTCCCTCCGTGTTCATT TTTCCTCCGTCGGACGAACAGCTG AAGTCCGGAACCGCGTCCGTGGTC TGTCTCCTGAACAACTTCTATCCGC GCGAGGCGAAAGTGCAGTGGAAG GTCGACAACGCACTGCAGTCGGGA AACTCCCAGGAATCGGTGACCGAG CAGGACTCGAAGGACTCAACCTAC TCATTGTCCTCCACCCTCACCCTGA GCAAGGCCGATTACGAGAAGCATA AGGTCTACGCCTGCGAAGTGACCC ACCAGGGCCTGAGCAGCCCAGTGA CGAAGTCCTTCAACCGGGGAGAAT GC

	CTTCCCGCCCAAGCCGAAGGACACTC TGATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGCA CGAAGATCCCGAAGTGAAATTCAAT TGGTACGTGGATGGGGTCGAAGTGC ACAACGCCAAGACCAAGCCTAGGGA AGAACAGTACAACTCTACGTACCGG GTGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGAG TACAAGTGCAAAGTGTCAAACAAGG CTCTCCCTGCCCCTATCGAAAAGACC ATCAGCAAGGCCAAGGGTCAACCTA GGGAGCCCCAGGTCTATACTTTGCCG CCTAGCCGGGAAGAAATGACTAAGA ACCAAGTGTCCCTGACTTGCCTTGTC AAGGGCTTTTATCCGTCCGACATCGC CGTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTCC TTCTTCCTGTACTCCAAGCTGACTGT GGACAAGTCAAGATGGCAGCAGGGA AACGTGTTCTCCTGCTCCGTGATGCA CGAAGCGCTGCACAACCATTACACC CAGAAATCACTGTCACTTTCGCCGGG AAAA		
SEQ ID 1719	CAGGTGCAGCTACAGCAGTGGGGCG CAGGACTGTTGAAGCCTTCGGAGAC CCTGTCCCTCACCTGCGCTGTCTATG GTGGGTCCTTCAGTGGTTACTACTGG AGCTGGATCCGCCAGCCCCCAGGGA AGGGGCTGGAGTGGATTGGGGAAAT CAATCATAGTGGAAGCACCAACTAC AACCCGTCCCTCAAGAGTCGAGTCAC CATATCAGTAGACACGTCCAAGAAC CAGTTCTCCCTGAAGCTGAGCTCTGT GACCGCCGCGGACACGGCTGTGTATT ACTGTGCGAGAGCCCGAGTGGAATC CAAGGATGGGTACTTTGACTACTGGG GCCAGGGAACCCTGGTCACCGTCTCC TCAGCATCCACCAAGGGGCCTTCCGT GTTCCCCCTGGCCCCTTCATCCAAGT CGACCTCTGGTGGAACCGCCGCACTC GGTTGCCTGGTCAAAGACTACTTCCC CGAGCCCGTGACTGTCTCGTGGAACT CGGGCGCCCTCACATCCGGAGTGCAT ACCTTTCCCGCCGTGTTGCAGTCCAG CGGCCTGTACAGCCTGAGCTCCGTCG TGACAGTGCCGTCCTCCTCCCTTGGA ACCCAGACCTATATCTGCAACGTCAA TCACAAGCCCTCCAACACCAAAGTG GACAAGAAGGTCGAACCCAAGTCCT GCGACAAGACTCACACCTGTCCGCCT TGTCCAGCCCCTGAGCTGCTGGGTGG TCCGTCCGTGTTCCTCTTCCCGCCCA	SEQ ID 1827	GACATCCAGATGACCCAGTCTCCA GCCACCCTGTCTGTGTCTCCAGGGG AAAGGGCCACCCTCTTTTGCCGGG CCAGTGAAGGTCTTACCACCAACT TAGCCTGGTACCAGCACAAACCTG GCCAGGCTCCCAGGCTCCTCATCTA TGCTGCCTCCACCAGGGCCACTGG TGTCCCAGCCAGGTTCAGTGGCAG TGGGTCTGGGACAGACTTCACTCTC ACCATCAGCAGCCTGCAGTCTGAA GATTCCGCAGTTTATTACTGTCAGC AGTATAATCACTGGCCTCTCTACAC TTTTGGCCAGGGGACCAAGGTGGA AATCAAACGTACTGTGGCTGCTCC CTCCGTGTTCATTTTTCCTCCGTCG GACGAACAGCTGAAGTCCGGAACC GCGTCCGTGGTCTGTCTCCTGAACA ACTTCTATCCGCGCGAGGCGAAAG TGCAGTGGAAGGTCGACAACGCAC TGCAGTCGGGAAACTCCCAGGAAT CGGTGACCGAGCAGGACTCGAAGG ACTCAACCTACTCATTGTCCTCCAC CCTCACCCTGAGCAAGGCCGATTA CGAGAAGCATAAGGTCTACGCCTG CGAAGTGACCCACCAGGGCCTGAG CAGCCCAGTGACGAAGTCCTTCAA CCGGGGAGAATGC

	AGCCGAAGGACACTCTGATGATTTCA CGCACCCCGGAAGTCACTTGCGTGGT CGTGGACGTGTCGCACGAAGATCCC GAAGTGAAATTCAATTGGTACGTGG ATGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTAC AACTCTACGTACCGGGTGGTGTCCGT GCTGACCGTGCTGCACCAGGACTGG CTGAACGGAAAGGAGTACAAGTGCA AAGTGTCAAACAAGGCTCTCCCTGCC CCTATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTATACTTTGCCGCCTAGCCGGG AAGAAATGACTAAGAACCAAGTGTC CCTGACTTGCCTTGTCAAGGGCTTTT ATCCGTCCGACATCGCCGTGGAGTGG GAGTCCAACGGACAACCGGAGAACA ACTACAAGACCACCCCACCGGTGCTC GATTCCGATGGCTCCTTCTTCCTGTA CTCCAAGCTGACTGTGGACAAGTCA AGATGGCAGCAGGGAAACGTGTTCT CCTGCTCCGTGATGCACGAAGCGCTG CACAACCATTACACCCAGAAATCACT GTCACTTTCGCCGGGAAAA		
SEQ ID 1720	GAGGTGCAGCTGGTGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCCTCTG GATTCACTTTCACTGATGCCTGGATG AACTGGGTCCGCCAGGCTCCAGGGA AGGGGCTGGAGTGGATTGGCCGTGT TAAAAACAAAGCTGATGGTGAGACA ACGGACTACGCTGCACCCGTCAAAG GCAGAATCACCATCTCAAGAGATGA TGCAAAGAACACTCTGTATGTGCAA ATGAACAGCCTGAAAACCGAGGACA CAGCCGTGTATTATTGTACCGCTGAC CTGCGACTTTCTACGTGGGATGCTTA TGATTTCTGGGGCCAAGGGACAATG GTCACCGTCTCTTCAGCATCCACCAA GGGGCCTTCCGTGTTCCCCCTGGCCC CTTCATCCAAGTCGACCTCTGGTGGA ACCGCCGCACTCGGTTGCCTGGTCAA AGACTACTTCCCCGAGCCCGTGACTG TCTCGTGGAACTCGGGCGCCCTCACA TCCGGAGTGCATACCTTTCCCGCCGT GTTGCAGTCCAGCGGCCTGTACAGCC TGAGCTCCGTCGTGACAGTGCCGTCC TCCTCCCTTGGAACCCAGACCTATAT CTGCAACGTCAATCACAAGCCCTCCA ACACCAAAGTGGACAAGAAGGTCGA ACCCAAGTCCTGCGACAAGACTCAC ACCTGTCCGCCTTGTCCAGCCCCTGA GCTGCTGGGTGGTCCGTCCGTGTTCC	SEQ ID 1828	GACATCCAGTTGACCCAGTCTCCTT CCACCCTGTCTTTGTCTCCAGGGGA AAGAGCCACCCTCTCCTGCAGGGC CAGTCAGAGTGTTAGCAGCTACTT AGCCTGGTACCAACAGAAATCTGG CCAGGCTCCCAGGCTCCTCATCTAT GATGCATCCAACAGGGCCACTGGC ATCCCAGCCAGGTTCAGTGGCAGT GGGTCTGGGACAGACTTCACTCTC ACCATCAGCAGCCTAGAGCCTGAA GATTTTGCAGTTTATTACTGTCAGC AGGGTAGCAACTGGCCGCTCACTT TCGGCGGAGGGACCAAGGTGGAAA TCAAACGTACTGTGGCTGCTCCCTC CGTGTTCATTTTTCCTCCGTCGGAC GAACAGCTGAAGTCCGGAACCGCG TCCGTGGTCTGTCTCCTGAACAACT TCTATCCGCGCGAGGCGAAAGTGC AGTGGAAGGTCGACAACGCACTGC AGTCGGGAAACTCCCAGGAATCGG TGACCGAGCAGGACTCGAAGGACT CAACCTACTCATTGTCCTCCACCCT CACCCTGAGCAAGGCCGATTACGA GAAGCATAAGGTCTACGCCTGCGA AGTGACCCACCAGGGCCTGAGCAG CCCAGTGACGAAGTCCTTCAACCG GGGAGAATGC

	TCTTCCCGCCCAAGCCGAAGGACACT CTGATGATTTCACGCACCCCGGAAGT CACTTGCGTGGTCGTGGACGTGTCGC ACGAAGATCCCGAAGTGAAATTCAA TTGGTACGTGGATGGGGTCGAAGTG CACAACGCCAAGACCAAGCCTAGGG AAGAACAGTACAACTCTACGTACCG GGTGGTGTCCGTGCTGACCGTGCTGC ACCAGGACTGGCTGAACGGAAAGGA GTACAAGTGCAAAGTGTCAAACAAG GCTCTCCCTGCCCCTATCGAAAAGAC CATCAGCAAGGCCAAGGGTCAACCT AGGGAGCCCCAGGTCTATACTTTGCC GCCTAGCCGGGAAGAAATGACTAAG AACCAAGTGTCCCTGACTTGCCTTGT CAAGGGCTTTTATCCGTCCGACATCG CCGTGGAGTGGGAGTCCAACGGACA ACCGGAGAACAACTACAAGACCACC CCACCGGTGCTCGATTCCGATGGCTC CTTCTTCCTGTACTCCAAGCTGACTG TGGACAAGTCAAGATGGCAGCAGGG AAACGTGTTCTCCTGCTCCGTGATGC ACGAAGCGCTGCACAACCATTACAC CCAGAAATCACTGTCACTTTCGCCGG GAAAA		
SEQ ID 1721	CAGATCACCTTGAAGGAGTCTGGGG GAGGCTTGGTCCAGCCTGGGGGGTC CCTAAGACTCTCTTGTACAGTCTCAG GATTCACCTTTAGTAACAATTGGATG ACCTGGGTCCGCCAGACTCCAGGGA AGGGGCTGGAGTGGGTGGCCAACAT AAAGCAAGATGGAACTGAGAAACAC TATGTGGACTCTGTGAAGGGCCGATT CACCATCTCCAGAGACAACGCCGAG AACTCACTGTATCTGCAGATGAACAG CCTGAGAGGTGAGGACACGGCCGTG TATTATTGTGCGAGAAACAGTCAACG TTCGTTTGACTACTGGGGCCAGGGCA CCCTGGTGACCGTCTCCTCAGCATCC ACCAAGGGGCCTTCCGTGTTCCCCCT GGCCCCTTCATCCAAGTCGACCTCTG GTGGAACCGCCGCACTCGGTTGCCTG GTCAAAGACTACTTCCCCGAGCCCGT GACTGTCTCGTGGAACTCGGGCGCCC TCACATCCGGAGTGCATACCTTTCCC GCCGTGTTGCAGTCCAGCGGCCTGTA CAGCCTGAGCTCCGTCGTGACAGTGC CGTCCTCCTCCCTTGGAACCCAGACC TATATCTGCAACGTCAATCACAAGCC CTCCAACACCAAAGTGGACAAGAAG GTCGAACCCAAGTCCTGCGACAAGA CTCACACCTGTCCGCCTTGTCCAGCC CCTGAGCTGCTGGGTGGTCCGTCCGT GTTCCTCTTCCCGCCCAAGCCGAAGG	SEQ ID 1829	GATATTGTGATGACCCACACTCCA CTCTCCTCACCTGTCACCCTTGGAC AGCCGGCCTCCATCTCCTGCAGGTC TAGTCAAAGCCTCGAACACACTGA TGGAAACACCTACTTAAGTTGGCTT CACCAGAGGCCAGGCCAGCCCCCA AGACTGTTAATTTATAAGGTTTCTA CCCGGTTCTCTGGGGTCCCAGACA GATTCAGTGGCAGTGGGGCAGGGA CAGATTTCACACTGAAAATCAGCA GGGTGGAGGCTGAGGATGTCGGCG TTTATTACTGCGTGCAGGCTACACA CTATCCTCGGACGTTCGGCCATGG GACCAAGGTGGAGATCAAACGTAC TGTGGCTGCTCCCTCCGTGTTCATT TTTCCTCCGTCGGACGAACAGCTG AAGTCCGGAACCGCGTCCGTGGTC TGTCTCCTGAACAACTTCTATCCGC GCGAGGCGAAAGTGCAGTGGAAG GTCGACAACGCACTGCAGTCGGGA AACTCCCAGGAATCGGTGACCGAG CAGGACTCGAAGGACTCAACCTAC TCATTGTCCTCCACCCTCACCCTGA GCAAGGCCGATTACGAGAAGCATA AGGTCTACGCCTGCGAAGTGACCC ACCAGGGCCTGAGCAGCCCAGTGA CGAAGTCCTTCAACCGGGGAGAAT GC

	ACACTCTGATGATTTCACGCACCCCG GAAGTCACTTGCGTGGTCGTGGACGT GTCGCACGAAGATCCCGAAGTGAAA TTCAATTGGTACGTGGATGGGGTCGA AGTGCACAACGCCAAGACCAAGCCT AGGGAAGAACAGTACAACTCTACGT ACCGGGTGGTGTCCGTGCTGACCGTG CTGCACCAGGACTGGCTGAACGGAA AGGAGTACAAGTGCAAAGTGTCAAA CAAGGCTCTCCCTGCCCCTATCGAAA AGACCATCAGCAAGGCCAAGGGTCA ACCTAGGGAGCCCCAGGTCTATACTT TGCCGCCTAGCCGGGAAGAAATGAC TAAGAACCAAGTGTCCCTGACTTGCC TTGTCAAGGGCTTTTATCCGTCCGAC ATCGCCGTGGAGTGGGAGTCCAACG GACAACCGGAGAACAACTACAAGAC CACCCCACCGGTGCTCGATTCCGATG GCTCCTTCTTCCTGTACTCCAAGCTG ACTGTGGACAAGTCAAGATGGCAGC AGGGAAACGTGTTCTCCTGCTCCGTG ATGCACGAAGCGCTGCACAACCATT ACACCCAGAAATCACTGTCACTTTCG CCGGGAAAA		
SEQ ID 1722	CAGGTCACCTTGAAGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTCAGTAGCTATGGCATG CACTGGGTCCGCCAGGCTCCAGGCA AGGGGCTGGAGTGGGTGGCAGTTAT ATCATATGATGGAAGTAATAAATACT ATGCAGACTCCGTGAAGGGCCGATT CACCATCTCCAGAGACAATTCCAAG AACACGCTGTATCTGCAAATGAACA GCCTGAGAGCTGAGGACACGGCTGT GTATTACTGTGCGAAAGATTTAGGGG ATCCCCGGGGTGGTATTTTGAACTAC TGGGGCCAGGGCACCCTGGTCACCG TCTCCTCAGCATCCACCAAGGGGCCT TCCGTGTTCCCCCTGGCCCCTTCATC CAAGTCGACCTCTGGTGGAACCGCC GCACTCGGTTGCCTGGTCAAAGACTA CTTCCCCGAGCCCGTGACTGTCTCGT GGAACTCGGGCGCCCTCACATCCGG AGTGCATACCTTTCCCGCCGTGTTGC AGTCCAGCGGCCTGTACAGCCTGAG CTCCGTCGTGACAGTGCCGTCCTCCT CCCTTGGAACCCAGACCTATATCTGC AACGTCAATCACAAGCCCTCCAACA CCAAAGTGGACAAGAAGGTCGAACC CAAGTCCTGCGACAAGACTCACACCT GTCCGCCTTGTCCAGCCCCTGAGCTG CTGGGTGGTCCGTCCGTGTTCCTCTT	SEQ ID 1830	GAAATTGTGCTGACTCAGTCTCCA GGCACCCTGTCCTTGTCTCCAGGGG AAAGAGCCACCCTCTCCTGCAGGG CCAGTCAGAGTATTAGCGGCAGTT ACTTAGCCTGGTACCAGCAGAAAC GTGGCCAGGCTCCCAGGCTCCTCA TCTATGATGCGTCCAGCAGGGCCG AAGGCATCCCAGACAGGTTCATTG GCAGTGGGTCTGGGACAGACTTCA CTCTCACCATCAGCAGACTGGAGC CTGAAGACTTTGCTATGTATTACTG TCAGCAGTATGGTAGCTCACCAAT ATTCACTTTCGGCCCTGGGACCAA AGTGGATATCAAACGTACTGTGGC TGCTCCCTCCGTGTTCATTTTTCCTC CGTCGGACGAACAGCTGAAGTCCG GAACCGCGTCCGTGGTCTGTCTCCT GAACAACTTCTATCCGCGCGAGGC GAAAGTGCAGTGGAAGGTCGACAA CGCACTGCAGTCGGGAAACTCCCA GGAATCGGTGACCGAGCAGGACTC GAAGGACTCAACCTACTCATTGTC CTCCACCCTCACCCTGAGCAAGGC CGATTACGAGAAGCATAAGGTCTA CGCCTGCGAAGTGACCCACCAGGG CCTGAGCAGCCCAGTGACGAAGTC CTTCAACCGGGGAGAATGC

	CCCGCCCAAGCCGAAGGACACTCTG ATGATTTCACGCACCCCGGAAGTCAC TTGCGTGGTCGTGGACGTGTCGCACG AAGATCCCGAAGTGAAATTCAATTG GTACGTGGATGGGGTCGAAGTGCAC AACGCCAAGACCAAGCCTAGGGAAG AACAGTACAACTCTACGTACCGGGT GGTGTCCGTGCTGACCGTGCTGCACC AGGACTGGCTGAACGGAAAGGAGTA CAAGTGCAAAGTGTCAAACAAGGCT CTCCCTGCCCCTATCGAAAAGACCAT CAGCAAGGCCAAGGGTCAACCTAGG GAGCCCCAGGTCTATACTTTGCCGCC TAGCCGGGAAGAAATGACTAAGAAC CAAGTGTCCCTGACTTGCCTTGTCAA GGGCTTTTATCCGTCCGACATCGCCG TGGAGTGGGAGTCCAACGGACAACC GGAGAACAACTACAAGACCACCCCA CCGGTGCTCGATTCCGATGGCTCCTT CTTCCTGTACTCCAAGCTGACTGTGG ACAAGTCAAGATGGCAGCAGGGAAA CGTGTTCTCCTGCTCCGTGATGCACG AAGCGCTGCACAACCATTACACCCA GAAATCACTGTCACTTTCGCCGGGAA AA		
SEQ ID 1723	GAGGTGCAGCTGGTGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTCAGTAGCTATGCTATG CACTGGGTCCGCCAGGCTCCAGGCA AGGGGCTGGAGTGGGTGGCAGTTAT ATCATATGATGGAAGTAATAAATACT ACGCAGACTCCGTGAAGGGCCGATT CACCATCTCCAGAGACAATTCCAAG AACACGCTGTATCTGCAAATGAACA GCCTGAGAGCTGAGGACACGGCTGT GTATTACTGTGCCCGGTCGAGCCCCT GGGGGGAGTTATCGTTATACCAGGG GGCTTTTGATATCTGGGGCCAAGGGA CAATGGTCACCGTCTCTTCAGCATCC ACCAAGGGGCCTTCCGTGTTCCCCCT GGCCCCTTCATCCAAGTCGACCTCTG GTGGAACCGCCGCACTCGGTTGCCTG GTCAAAGACTACTTCCCCGAGCCCGT GACTGTCTCGTGGAACTCGGGCGCCC TCACATCCGGAGTGCATACCTTTCCC GCCGTGTTGCAGTCCAGCGGCCTGTA CAGCCTGAGCTCCGTCGTGACAGTGC CGTCCTCCTCCCTTGGAACCCAGACC TATATCTGCAACGTCAATCACAAGCC CTCCAACACCAAAGTGGACAAGAAG GTCGAACCCAAGTCCTGCGACAAGA CTCACACCTGTCCGCCTTGTCCAGCC CCTGAGCTGCTGGGTGGTCCGTCCGT	SEQ ID 1831	GAAATTGTGCTGACTCAGTCTCCA GACTCCCTGCCCGTCACCCCTGGA GAGCCGGCCTCCATCTCCTGCAGG TCTAGTCAGAGCCTCCTGCATAGTA ATGGAAACAACTATTTGGATTGGT ACCTGCAGAAGCCAGGGCAGTCTC CACAGCTCCTGATCTATTTGGGTTC TAATCGGGCCTCCGGGGTCCCTGA CAGGTTCAGTGGCAGTGGATCAGG CACAGATTTTACACTGAAACTCAG CAGAGTGGAGGCTGAGGATGTTGG GGTTTATTACTGCATGCAAGGTCTA CAAATCCCTATCACTTTCGGCCCTG GGACCAAAGTGGATATCAAACGTA CTGTGGCTGCTCCCTCCGTGTTCAT TTTTCCTCCGTCGGACGAACAGCTG AAGTCCGGAACCGCGTCCGTGGTC TGTCTCCTGAACAACTTCTATCCGC GCGAGGCGAAAGTGCAGTGGAAG GTCGACAACGCACTGCAGTCGGGA AACTCCCAGGAATCGGTGACCGAG CAGGACTCGAAGGACTCAACCTAC TCATTGTCCTCCACCCTCACCCTGA GCAAGGCCGATTACGAGAAGCATA AGGTCTACGCCTGCGAAGTGACCC ACCAGGGCCTGAGCAGCCCAGTGA CGAAGTCCTTCAACCGGGGAGAAT GC

	GTTCCTCTTCCCGCCCAAGCCGAAGG ACACTCTGATGATTTCACGCACCCCG GAAGTCACTTGCGTGGTCGTGGACGT GTCGCACGAAGATCCCGAAGTGAAA TTCAATTGGTACGTGGATGGGGTCGA AGTGCACAACGCCAAGACCAAGCCT AGGGAAGAACAGTACAACTCTACGT ACCGGGTGGTGTCCGTGCTGACCGTG CTGCACCAGGACTGGCTGAACGGAA AGGAGTACAAGTGCAAAGTGTCAAA CAAGGCTCTCCCTGCCCCTATCGAAA AGACCATCAGCAAGGCCAAGGGTCA ACCTAGGGAGCCCCAGGTCTATACTT TGCCGCCTAGCCGGGAAGAAATGAC TAAGAACCAAGTGTCCCTGACTTGCC TTGTCAAGGGCTTTTATCCGTCCGAC ATCGCCGTGGAGTGGGAGTCCAACG GACAACCGGAGAACAACTACAAGAC CACCCCACCGGTGCTCGATTCCGATG GCTCCTTCTTCCTGTACTCCAAGCTG ACTGTGGACAAGTCAAGATGGCAGC AGGGAAACGTGTTCTCCTGCTCCGTG ATGCACGAAGCGCTGCACAACCATT ACACCCAGAAATCACTGTCACTTTCG CCGGGAAAA		
SEQ ID 1724	CAGATCACCTTGAAGGAGTCTGGGG GAGGCTTGGTACAGCCTGGCAGGTC CCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGATGATTATGCCATG CACTGGGTCCGGCAAGCTCCAGGGA AGGGGCTGGAGTGGGTCTCAGCTATT AGTGGTAGTGGTGGTAGCACATACT ACGCAGACTCCGTGAAGGGCCGGTT CACCATCTCCAGAGACAATTCCAAG AACACGCTGTATCTGCAAATGAACA GCCTGAGAGCCGAGGACACGGCCGT ATATTACTGTGCGAAAGATAACGATT TTTGGAGTGGGAAAGTCTTTGACTAC TGGGGCCAGGGCACCCTGGTCACCG TCTCCTCAGCATCCACCAAGGGGCCT TCCGTGTTCCCCCTGGCCCCTTCATC CAAGTCGACCTCTGGTGGAACCGCC GCACTCGGTTGCCTGGTCAAAGACTA CTTCCCCGAGCCCGTGACTGTCTCGT GGAACTCGGGCGCCCTCACATCCGG AGTGCATACCTTTCCCGCCGTGTTGC AGTCCAGCGGCCTGTACAGCCTGAG CTCCGTCGTGACAGTGCCGTCCTCCT CCCTTGGAACCCAGACCTATATCTGC AACGTCAATCACAAGCCCTCCAACA CCAAAGTGGACAAGAAGGTCGAACC CAAGTCCTGCGACAAGACTCACACCT GTCCGCCTTGTCCAGCCCCTGAGCTG CTGGGTGGTCCGTCCGTGTTCCTCTT	SEQ ID 1832	GACATCCAGATGACCCAGTCTCCA TCTTCTGTGTCTGCATCTGTGGGAG ACAGAGTCACCATCACTTGTCGGG CGAGTCAGAACATTCGCCACTGGT TAGTCTGGTATCAGCAAAAATTAG GGCAAGCCCCTAAACTCCTGATCT ATGCTGCGTCCAATTTGCAAAGTG GGGTCCCGTCAAGGTTCAGCGGCA GTGGATCTGGGACAGAATTCACTC TCACAATCAACAGCCTGCAGGCTG AAGATTTTGCAACCTATTACTGTCT ACAGCATAACAGTTACCCGTGGAC GTTCGGCCAAGGGACCAAGGTGGA AATCAAACGTACTGTGGCTGCTCC CTCCGTGTTCATTTTTCCTCCGTCG GACGAACAGCTGAAGTCCGGAACC GCGTCCGTGGTCTGTCTCCTGAACA ACTTCTATCCGCGCGAGGCGAAAG TGCAGTGGAAGGTCGACAACGCAC TGCAGTCGGGAAACTCCCAGGAAT CGGTGACCGAGCAGGACTCGAAGG ACTCAACCTACTCATTGTCCTCCAC CCTCACCCTGAGCAAGGCCGATTA CGAGAAGCATAAGGTCTACGCCTG CGAAGTGACCCACCAGGGCCTGAG CAGCCCAGTGACGAAGTCCTTCAA CCGGGGAGAATGC

	CCCGCCCAAGCCGAAGGACACTCTG ATGATTTCACGCACCCCGGAAGTCAC TTGCGTGGTCGTGGACGTGTCGCACG AAGATCCCGAAGTGAAATTCAATTG GTACGTGGATGGGGTCGAAGTGCAC AACGCCAAGACCAAGCCTAGGGAAG AACAGTACAACTCTACGTACCGGGT GGTGTCCGTGCTGACCGTGCTGCACC AGGACTGGCTGAACGGAAAGGAGTA CAAGTGCAAAGTGTCAAACAAGGCT CTCCCTGCCCCTATCGAAAAGACCAT CAGCAAGGCCAAGGGTCAACCTAGG GAGCCCCAGGTCTATACTTTGCCGCC TAGCCGGGAAGAAATGACTAAGAAC CAAGTGTCCCTGACTTGCCTTGTCAA GGGCTTTTATCCGTCCGACATCGCCG TGGAGTGGGAGTCCAACGGACAACC GGAGAACAACTACAAGACCACCCCA CCGGTGCTCGATTCCGATGGCTCCTT CTTCCTGTACTCCAAGCTGACTGTGG ACAAGTCAAGATGGCAGCAGGGAAA CGTGTTCTCCTGCTCCGTGATGCACG AAGCGCTGCACAACCATTACACCCA GAAATCACTGTCACTTTCGCCGGGAA AA		
SEQ ID 1725	GAAGTGCAGCTGGTGCAGTCTGGGG GAGGCTTGGTACAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTCAGTAGTTATAGCATG AACTGGGTCCGCCAGGCTCCAGGGA AGGGGCTGGAGTGGGTTTCATACATC AGTAGTACTAGTAGTACCATATACTA CGCAGACTCCGTGAAGGGCCGATTC ACCATCTCCAGAGACAATTCCAAGA ATATGCTGTTTCTACAAATGAACAGC CTGAGAGCTGAGGACACGGCTGTGT ATTACTGTGCGAAAGAAGGGGGCAG TGGCTGGCGCCACTACTTTGACTACT GGGGCCAGGGAACCCTGGTCACCGT CTCCTCAGCATCCACCAAGGGGCCTT CCGTGTTCCCCCTGGCCCCTTCATCC AAGTCGACCTCTGGTGGAACCGCCG CACTCGGTTGCCTGGTCAAAGACTAC TTCCCCGAGCCCGTGACTGTCTCGTG GAACTCGGGCGCCCTCACATCCGGA GTGCATACCTTTCCCGCCGTGTTGCA GTCCAGCGGCCTGTACAGCCTGAGCT CCGTCGTGACAGTGCCGTCCTCCTCC CTTGGAACCCAGACCTATATCTGCAA CGTCAATCACAAGCCCTCCAACACCA AAGTGGACAAGAAGGTCGAACCCAA GTCCTGCGACAAGACTCACACCTGTC CGCCTTGTCCAGCCCCTGAGCTGCTG GGTGGTCCGTCCGTGTTCCTCTTCCC	SEQ ID 1833	GAAATTGTGTTGACGCAGTCTCCA GACTTTCAGTCTGTGACTCCAAAGC AGAAAGTCACCATCACCTGCCGGG CCAGTCAGAGCATTGGTGGTAGCT TACACTGGTACCAGCAGAAACCAG GTCAGTCTCCAAAGCTCATCATCA AGTATGCTTCCCAGTCCTTCTCAGG GGTCCCCTCGAGGTTCAGTGGCAG TGGATCTGGGACAGATTTCACCCTC ACCATCGATAGCCTGGAGGCTGAA GATGCTGCAACGTACTATTGTCATC AGAGTATCAGTTTACCGCTCACTTT CGGCGGAGGGACCAAAGTGGATAT CAAACGTACTGTGGCTGCTCCCTCC GTGTTCATTTTTCCTCCGTCGGACG AACAGCTGAAGTCCGGAACCGCGT CCGTGGTCTGTCTCCTGAACAACTT CTATCCGCGCGAGGCGAAAGTGCA GTGGAAGGTCGACAACGCACTGCA GTCGGGAAACTCCCAGGAATCGGT GACCGAGCAGGACTCGAAGGACTC AACCTACTCATTGTCCTCCACCCTC ACCCTGAGCAAGGCCGATTACGAG AAGCATAAGGTCTACGCCTGCGAA GTGACCCACCAGGGCCTGAGCAGC CCAGTGACGAAGTCCTTCAACCGG GGAGAATGC

	GCCCAAGCCGAAGGACACTCTGATG ATTTCACGCACCCCGGAAGTCACTTG CGTGGTCGTGGACGTGTCGCACGAA GATCCCGAAGTGAAATTCAATTGGTA CGTGGATGGGGTCGAAGTGCACAAC GCCAAGACCAAGCCTAGGGAAGAAC AGTACAACTCTACGTACCGGGTGGTG TCCGTGCTGACCGTGCTGCACCAGGA CTGGCTGAACGGAAAGGAGTACAAG TGCAAAGTGTCAAACAAGGCTCTCCC TGCCCCTATCGAAAAGACCATCAGC AAGGCCAAGGGTCAACCTAGGGAGC CCCAGGTCTATACTTTGCCGCCTAGC CGGGAAGAAATGACTAAGAACCAAG TGTCCCTGACTTGCCTTGTCAAGGGC TTTTATCCGTCCGACATCGCCGTGGA GTGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCAAGCTGACTGTGGACAA GTCAAGATGGCAGCAGGGAAACGTG TTCTCCTGCTCCGTGATGCACGAAGC GCTGCACAACCATTACACCCAGAAA TCACTGTCACTTTCGCCGGGAAAA		
SEQ ID 1726	CAGGTCACCTTGAAGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTGTCCTGTGCAGCCTCTG GATTCACCTTCAGCAGCTATGCTATG CACTGGGTCCGCCAGGCTCCAGGCA AGGGGCTGGAGTGGGTGGCAGTTAT ATCATATGATGGAAGTAATAAATACT ACGCAGACTCCGTGAAGGGCCGATT CACCATCTCCAGAGACAATTCCAAG AACACGCTGTATCTGCAAATGAACA GCCTGAGAGCTGAGGACACGGCTGT GTATTACTGTGCGAGAGATTATTGTA GTAGTACCAGCTGCCAGAACTGGTTC GACCCCTGGGGCCAGGGCACCCTGG TCACCGTCTCCTCAGCATCCACCAAG GGGCCTTCCGTGTTCCCCCTGGCCCC TTCATCCAAGTCGACCTCTGGTGGAA CCGCCGCACTCGGTTGCCTGGTCAAA GACTACTTCCCCGAGCCCGTGACTGT CTCGTGGAACTCGGGCGCCCTCACAT CCGGAGTGCATACCTTTCCCGCCGTG TTGCAGTCCAGCGGCCTGTACAGCCT GAGCTCCGTCGTGACAGTGCCGTCCT CCTCCCTTGGAACCCAGACCTATATC TGCAACGTCAATCACAAGCCCTCCAA CACCAAAGTGGACAAGAAGGTCGAA CCCAAGTCCTGCGACAAGACTCACA CCTGTCCGCCTTGTCCAGCCCCTGAG CTGCTGGGTGGTCCGTCCGTGTTCCT	SEQ ID 1834	GAAACGACACTCACGCAGTCTCCA GGCACCCTGTCTTTGTCTCCAGGGG AAGGAGCCACCCTCTCCTGCAGGG CCAGTCAGAGTGTTACCAGCAACT ACTTAGCCTGGTACCAGCAGAAAC CTGGCCAGGCTCCCAGGCTCCTCAT CTATGGTGCATCCTACAGGGCCAC TGGCATCCCTGACAGGTTCAGCGG CAGTGGGTCTGGGACAGACTTCAC TCTCACCATCAGCAGACTGGAGCC TGAAGATTTTGCAGTGTATTACTGT CAGCAGTATGCTAGCTCAGTCACC TTCGGCCAAGGGACACGACTGGAG ATTAAACGTACTGTGGCTGCTCCCT CCGTGTTCATTTTTCCTCCGTCGGA CGAACAGCTGAAGTCCGGAACCGC GTCCGTGGTCTGTCTCCTGAACAAC TTCTATCCGCGCGAGGCGAAAGTG CAGTGGAAGGTCGACAACGCACTG CAGTCGGGAAACTCCCAGGAATCG GTGACCGAGCAGGACTCGAAGGAC TCAACCTACTCATTGTCCTCCACCC TCACCCTGAGCAAGGCCGATTACG AGAAGCATAAGGTCTACGCCTGCG AAGTGACCCACCAGGGCCTGAGCA GCCCAGTGACGAAGTCCTTCAACC GGGGAGAATGC

	CTTCCCGCCCAAGCCGAAGGACACTC TGATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGCA CGAAGATCCCGAAGTGAAATTCAAT TGGTACGTGGATGGGGTCGAAGTGC ACAACGCCAAGACCAAGCCTAGGGA AGAACAGTACAACTCTACGTACCGG GTGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGAG TACAAGTGCAAAGTGTCAAACAAGG CTCTCCCTGCCCCTATCGAAAAGACC ATCAGCAAGGCCAAGGGTCAACCTA GGGAGCCCCAGGTCTATACTTTGCCG CCTAGCCGGGAAGAAATGACTAAGA ACCAAGTGTCCCTGACTTGCCTTGTC AAGGGCTTTTATCCGTCCGACATCGC CGTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTCC TTCTTCCTGTACTCCAAGCTGACTGT GGACAAGTCAAGATGGCAGCAGGGA AACGTGTTCTCCTGCTCCGTGATGCA CGAAGCGCTGCACAACCATTACACC CAGAAATCACTGTCACTTTCGCCGGG AAAA		
SEQ ID 1727	CAGGTCCAGCTGGTGCAGTCTGGGG GAGGCTTGGTACAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTAGCAACTATGTCATG AGCTGGGTCCGCCAGGCTCCAGGGA AGGGGCTGGAGTGGGTCTCAGCTATT AGTGGTATTGGTGATACTACATACTA CGCGGACTCCGTGAAGGGCCGATTC ACCATCTCCAGAGACAACGCCAAGA ACACGCTGTATCTGCAAATGAACAGT CTGAGAGCCGAGGACACGGCTGTGT ATTACTGTGCAAGAGGGCGCGTGGC GGGGGATGCTTTTGATATCTGGGGCC AAGGGACAATGGTGACCGTCTCTTCA GCATCCACCAAGGGGCCTTCCGTGTT CCCCCTGGCCCCTTCATCCAAGTCGA CCTCTGGTGGAACCGCCGCACTCGGT TGCCTGGTCAAAGACTACTTCCCCGA GCCCGTGACTGTCTCGTGGAACTCGG GCGCCCTCACATCCGGAGTGCATACC TTTCCCGCCGTGTTGCAGTCCAGCGG CCTGTACAGCCTGAGCTCCGTCGTGA CAGTGCCGTCCTCCTCCCTTGGAACC CAGACCTATATCTGCAACGTCAATCA CAAGCCCTCCAACACCAAAGTGGAC AAGAAGGTCGAACCCAAGTCCTGCG ACAAGACTCACACCTGTCCGCCTTGT CCAGCCCCTGAGCTGCTGGGTGGTCC GTCCGTGTTCCTCTTCCCGCCCAAGC	SEQ ID 1835	GATGTTGTGATGACTCAGTCTCCAG CCACCCTGTCTGTGTCTCCAGGGGA AAGAGCCACCCTCTCCTGCAGGGC CAGTCAGAGTATTAGCAGCAACTT AGCCTGGTACCAGCAGAAACCTGG CCAGGCTCCCAGGCTCCTCATCTAT GGTGCCTCCACCAGGGCCACTGGT ATCCCAGCCAGGTTCAGTGGCAGT GGGTCTGGGACAGAGTTCACTCTC ACCATCAGCAGCCTGCAGTCTGAA GATTTTGCAGTTTATTACTGTCAGC AGTATAATAACTGGCCTAGAACGT TCGGCCAAGGGACCAAGCTGGAGA TCAAACGTACTGTGGCTGCTCCCTC CGTGTTCATTTTTCCTCCGTCGGAC GAACAGCTGAAGTCCGGAACCGCG TCCGTGGTCTGTCTCCTGAACAACT TCTATCCGCGCGAGGCGAAAGTGC AGTGGAAGGTCGACAACGCACTGC AGTCGGGAAACTCCCAGGAATCGG TGACCGAGCAGGACTCGAAGGACT CAACCTACTCATTGTCCTCCACCCT CACCCTGAGCAAGGCCGATTACGA GAAGCATAAGGTCTACGCCTGCGA AGTGACCCACCAGGGCCTGAGCAG CCCAGTGACGAAGTCCTTCAACCG GGGAGAATGC

	CGAAGGACACTCTGATGATTTCACGC ACCCCGGAAGTCACTTGCGTGGTCGT GGACGTGTCGCACGAAGATCCCGAA GTGAAATTCAATTGGTACGTGGATGG GGTCGAAGTGCACAACGCCAAGACC AAGCCTAGGGAAGAACAGTACAACT CTACGTACCGGGTGGTGTCCGTGCTG ACCGTGCTGCACCAGGACTGGCTGA ACGGAAAGGAGTACAAGTGCAAAGT GTCAAACAAGGCTCTCCCTGCCCCTA TCGAAAAGACCATCAGCAAGGCCAA GGGTCAACCTAGGGAGCCCCAGGTC TATACTTTGCCGCCTAGCCGGGAAGA AATGACTAAGAACCAAGTGTCCCTG ACTTGCCTTGTCAAGGGCTTTTATCC GTCCGACATCGCCGTGGAGTGGGAG TCCAACGGACAACCGGAGAACAACT ACAAGACCACCCCACCGGTGCTCGA TTCCGATGGCTCCTTCTTCCTGTACTC CAAGCTGACTGTGGACAAGTCAAGA TGGCAGCAGGGAAACGTGTTCTCCTG CTCCGTGATGCACGAAGCGCTGCAC AACCATTACACCCAGAAATCACTGTC ACTTTCGCCGGGAAAA		
SEQ ID 1728	CAGCTGCAGCTGCAGGAGTCGGGGG GAGGCTTGGTACAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTAGCAGCTATGCCATG AGCTGGGTCCGCCAGGCTCCAGGGA AGGGGCTGGAGTGGGTCTCAGCTATT AGTGGTAGTGGTGGTAGCACATACT ACGCAGACTCCGTGAAGGGCCGGTT CACCATCTCCAGAGACAATTCCAAG AACACGCTGTATCTGCAAATGAACA GCCTGAGAGCCGAGGACACGGCCGT ATATTACTGTGCGAAAGATCAAGGG GCAGCAGCTGGTACCCTGGGGTACTT TGACTACTGGGGCCAGGGAACCCTG GTGACCGTCTCCTCAGCATCCACCAA GGGGCCTTCCGTGTTCCCCCTGGCCC CTTCATCCAAGTCGACCTCTGGTGGA ACCGCCGCACTCGGTTGCCTGGTCAA AGACTACTTCCCCGAGCCCGTGACTG TCTCGTGGAACTCGGGCGCCCTCACA TCCGGAGTGCATACCTTTCCCGCCGT GTTGCAGTCCAGCGGCCTGTACAGCC TGAGCTCCGTCGTGACAGTGCCGTCC TCCTCCCTTGGAACCCAGACCTATAT CTGCAACGTCAATCACAAGCCCTCCA ACACCAAAGTGGACAAGAAGGTCGA ACCCAAGTCCTGCGACAAGACTCAC ACCTGTCCGCCTTGTCCAGCCCCTGA GCTGCTGGGTGGTCCGTCCGTGTTCC	SEQ ID 1836	GACATCCAGTTGACCCAGTCTCCA GACTCCCTGGCTGTGTCTCTGGGCG AGAGGGCCACCATCAACTGCAAGT CCAGCCAGAGTGTTTTATACAGCTC CAACAATAAGAACTACTTAGCTTG GTACCAGCAGAAACCAGGACAGCC TCCTAAGCTGCTCATTTACTGGGCA TCTGCCCGGGAATCCGGGGTCCCT GACCGATTCAGTGGCAGCGGGTCT GGGACAGATTTCACTCTCACCATC AACAGCCTGCAGGCTGAAGATGTG GCAGTTTATTACTGTCAGCAATTTT ATAGTCCTCCTCGGACGTTCGGCCA AGGGACCAAGGTGGAAATCAAACG TACTGTGGCTGCTCCCTCCGTGTTC ATTTTTCCTCCGTCGGACGAACAGC TGAAGTCCGGAACCGCGTCCGTGG TCTGTCTCCTGAACAACTTCTATCC GCGCGAGGCGAAAGTGCAGTGGAA GGTCGACAACGCACTGCAGTCGGG AAACTCCCAGGAATCGGTGACCGA GCAGGACTCGAAGGACTCAACCTA CTCATTGTCCTCCACCCTCACCCTG AGCAAGGCCGATTACGAGAAGCAT AAGGTCTACGCCTGCGAAGTGACC CACCAGGGCCTGAGCAGCCCAGTG ACGAAGTCCTTCAACCGGGGAGAA TGC

	TCTTCCCGCCCAAGCCGAAGGACACT CTGATGATTTCACGCACCCCGGAAGT CACTTGCGTGGTCGTGGACGTGTCGC ACGAAGATCCCGAAGTGAAATTCAA TTGGTACGTGGATGGGGTCGAAGTG CACAACGCCAAGACCAAGCCTAGGG AAGAACAGTACAACTCTACGTACCG GGTGGTGTCCGTGCTGACCGTGCTGC ACCAGGACTGGCTGAACGGAAAGGA GTACAAGTGCAAAGTGTCAAACAAG GCTCTCCCTGCCCCTATCGAAAAGAC CATCAGCAAGGCCAAGGGTCAACCT AGGGAGCCCCAGGTCTATACTTTGCC GCCTAGCCGGGAAGAAATGACTAAG AACCAAGTGTCCCTGACTTGCCTTGT CAAGGGCTTTTATCCGTCCGACATCG CCGTGGAGTGGGAGTCCAACGGACA ACCGGAGAACAACTACAAGACCACC CCACCGGTGCTCGATTCCGATGGCTC CTTCTTCCTGTACTCCAAGCTGACTG TGGACAAGTCAAGATGGCAGCAGGG AAACGTGTTCTCCTGCTCCGTGATGC ACGAAGCGCTGCACAACCATTACAC CCAGAAATCACTGTCACTTTCGCCGG GAAAA		
SEQ ID 1729	CAGGTGCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTCTCCTGCAAGGCTTCTG GATACACCTTCACCAGTTATGATATC AACTGGGTGCGACAGGCCACTGGAC AAGGGCTTGAGTGGATGGGATGGAT GAACCCTAACAGTGGTAACACAGGC TATGCACAGAAGTTCCAGGGCAGAG TCACCATGACCAGGAACACCTCCATA AGCACAGCCTACATGGAGCTGAGCA GCCTGAGATCTGAGGACACGGCCGT GTATTACTGTACGAGAGGAATCTATG ATAGTAGTGGTTCTTCCAATCCCTTT GACTCCTGGGGCCAGGGAACCCTGG TGACCGTCTCCTCAGCATCCACCAAG GGGCCTTCCGTGTTCCCCCTGGCCCC TTCATCCAAGTCGACCTCTGGTGGAA CCGCCGCACTCGGTTGCCTGGTCAAA GACTACTTCCCCGAGCCCGTGACTGT CTCGTGGAACTCGGGCGCCCTCACAT CCGGAGTGCATACCTTTCCCGCCGTG TTGCAGTCCAGCGGCCTGTACAGCCT GAGCTCCGTCGTGACAGTGCCGTCCT CCTCCCTTGGAACCCAGACCTATATC TGCAACGTCAATCACAAGCCCTCCAA CACCAAAGTGGACAAGAAGGTCGAA CCCAAGTCCTGCGACAAGACTCACA CCTGTCCGCCTTGTCCAGCCCCTGAG CTGCTGGGTGGTCCGTCCGTGTTCCT	SEQ ID 1837	GAAATTGTGTTGACACAGTCTCCA GGCACCCTGTCTTTGTCTCCAGGGG AAAGAGCCACCCTCTCCTGCAGGG CCAGTCAGAGTGTTAGCAGCAGCT ACTTAGCCTGGTACCAGCAGAAAC CTGGCCAGGCTCCCAGGCTCCTCAT CTATGGTGCATCCAGCAGGGCCAC TGGCATCCCAGACAGGTTCAGTGG CAGTGGGTCTGGGACAGACTTCAC TCTCACCATCAGCAGACTGGAGCC TGAAGATTTTGCAGTGTATTACTGT CAGCAGTATGGTAGCTCACCCCCG GGCACTTTCGGCGGAGGGACCAAA GTGGATATCAAACGTACTGTGGCT GCTCCCTCCGTGTTCATTTTTCCTC CGTCGGACGAACAGCTGAAGTCCG GAACCGCGTCCGTGGTCTGTCTCCT GAACAACTTCTATCCGCGCGAGGC GAAAGTGCAGTGGAAGGTCGACAA CGCACTGCAGTCGGGAAACTCCCA GGAATCGGTGACCGAGCAGGACTC GAAGGACTCAACCTACTCATTGTC CTCCACCCTCACCCTGAGCAAGGC CGATTACGAGAAGCATAAGGTCTA CGCCTGCGAAGTGACCCACCAGGG CCTGAGCAGCCCAGTGACGAAGTC CTTCAACCGGGGAGAATGC

	CTTCCCGCCCAAGCCGAAGGACACTC TGATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGCA CGAAGATCCCGAAGTGAAATTCAAT TGGTACGTGGATGGGGTCGAAGTGC ACAACGCCAAGACCAAGCCTAGGGA AGAACAGTACAACTCTACGTACCGG GTGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGAG TACAAGTGCAAAGTGTCAAACAAGG CTCTCCCTGCCCCTATCGAAAAGACC ATCAGCAAGGCCAAGGGTCAACCTA GGGAGCCCCAGGTCTATACTTTGCCG CCTAGCCGGGAAGAAATGACTAAGA ACCAAGTGTCCCTGACTTGCCTTGTC AAGGGCTTTTATCCGTCCGACATCGC CGTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTCC TTCTTCCTGTACTCCAAGCTGACTGT GGACAAGTCAAGATGGCAGCAGGGA AACGTGTTCTCCTGCTCCGTGATGCA CGAAGCGCTGCACAACCATTACACC CAGAAATCACTGTCACTTTCGCCGGG AAAA		
SEQ ID 1730	GAGGTGCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGATTTCCTGCGAGGCTTCTG GATACACCTTCACTGATTATGCTATA CATTGGGTGCGCCAGGCCCCCGGAC AAAGACTTGAGTGGATGGGATGGAT CAACGCTGGCGATGGTGGCACAAAA AGTTCACGGGAGTTCCAGGGCAGAG TCACCATTACCAGGGACACATCCGCG ACCACAGCCTACATGGAGGTGAGCA GTCTGAGATCTGAAGACACGGCTGTC TATTACTGTGCGAGAGGATATTGTAG TGGTGGTAGCTGCCCAGGAACGGAT TTTGACTACTGGGGCCAGGGAACCCT GGTCACCGTCTCCTCAGCATCCACCA AGGGGCCTTCCGTGTTCCCCCTGGCC CCTTCATCCAAGTCGACCTCTGGTGG AACCGCCGCACTCGGTTGCCTGGTCA AAGACTACTTCCCCGAGCCCGTGACT GTCTCGTGGAACTCGGGCGCCCTCAC ATCCGGAGTGCATACCTTTCCCGCCG TGTTGCAGTCCAGCGGCCTGTACAGC CTGAGCTCCGTCGTGACAGTGCCGTC CTCCTCCCTTGGAACCCAGACCTATA TCTGCAACGTCAATCACAAGCCCTCC AACACCAAAGTGGACAAGAAGGTCG AACCCAAGTCCTGCGACAAGACTCA CACCTGTCCGCCTTGTCCAGCCCCTG AGCTGCTGGGTGGTCCGTCCGTGTTC	SEQ ID 1838	GAAATTGTGCTGACTCAGTCTCCA GGCACCCTGTCTTTGTCTCCAGGGG AAAGAGCCACCCTCTCCTGCAGGG CCAGTCAGAGTTTAAGTACCAACT TAGCCTGGTACCAGCAGAAACCTG GCCAGGCTCCCAGGCTCCTCATCTA TGGTGCATCCACCAGGGCCACTGG TATCCCAGCCAGGTTCAGTGGCAG TGGGTCTGGCACAGAGTTCACTCTC ACCATCACCAGCCTGCAGTCTGAA GATTTTGCAGTTTATTACTGTCAGC AGTATCATAACTGGCCTCCGTACA CTTTTGGCCAGGGGACCAAGGTGG AGATCAAACGTACTGTGGCTGCTC CCTCCGTGTTCATTTTTCCTCCGTC GGACGAACAGCTGAAGTCCGGAAC CGCGTCCGTGGTCTGTCTCCTGAAC AACTTCTATCCGCGCGAGGCGAAA GTGCAGTGGAAGGTCGACAACGCA CTGCAGTCGGGAAACTCCCAGGAA TCGGTGACCGAGCAGGACTCGAAG GACTCAACCTACTCATTGTCCTCCA CCCTCACCCTGAGCAAGGCCGATT ACGAGAAGCATAAGGTCTACGCCT GCGAAGTGACCCACCAGGGCCTGA GCAGCCCAGTGACGAAGTCCTTCA ACCGGGGAGAATGC

	CTCTTCCCGCCCAAGCCGAAGGACAC TCTGATGATTTCACGCACCCCGGAAG TCACTTGCGTGGTCGTGGACGTGTCG CACGAAGATCCCGAAGTGAAATTCA ATTGGTACGTGGATGGGGTCGAAGT GCACAACGCCAAGACCAAGCCTAGG GAAGAACAGTACAACTCTACGTACC GGGTGGTGTCCGTGCTGACCGTGCTG CACCAGGACTGGCTGAACGGAAAGG AGTACAAGTGCAAAGTGTCAAACAA GGCTCTCCCTGCCCCTATCGAAAAGA CCATCAGCAAGGCCAAGGGTCAACC TAGGGAGCCCCAGGTCTATACTTTGC CGCCTAGCCGGGAAGAAATGACTAA GAACCAAGTGTCCCTGACTTGCCTTG TCAAGGGCTTTTATCCGTCCGACATC GCCGTGGAGTGGGAGTCCAACGGAC AACCGGAGAACAACTACAAGACCAC CCCACCGGTGCTCGATTCCGATGGCT CCTTCTTCCTGTACTCCAAGCTGACT GTGGACAAGTCAAGATGGCAGCAGG GAAACGTGTTCTCCTGCTCCGTGATG CACGAAGCGCTGCACAACCATTACA CCCAGAAATCACTGTCACTTTCGCCG GGAAAA		
SEQ ID 1731	CAGGTGCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTTTCCTGCAAGGCATCTG GATACACCTTCACCAGCTACTATATG CACTGGGTGCGACAGGCCCCTGGAC AAGGGCTTGAGTGGATGGGAATAAT CAACCCTAGTGGTGGTAGCACAAGC TACGCACAGAAGTTCCAGGGCAGAG TCACCATGACCAGGGACACGTCCAC GAGCACAGTCTACATGGAGCTGAGC AGCCTGAGATCTGAGGACACGGCCG TGTATTACTGTGCGAGAGATGGTGTA GGAGGGAGAGATGGCTACAATTTTG ACTACTGGGGCCAGGGAACCCTGGT CACCGTCTCCTCAGCATCCACCAAGG GGCCTTCCGTGTTCCCCCTGGCCCCT TCATCCAAGTCGACCTCTGGTGGAAC CGCCGCACTCGGTTGCCTGGTCAAAG ACTACTTCCCCGAGCCCGTGACTGTC TCGTGGAACTCGGGCGCCCTCACATC CGGAGTGCATACCTTTCCCGCCGTGT TGCAGTCCAGCGGCCTGTACAGCCTG AGCTCCGTCGTGACAGTGCCGTCCTC CTCCCTTGGAACCCAGACCTATATCT GCAACGTCAATCACAAGCCCTCCAA CACCAAAGTGGACAAGAAGGTCGAA CCCAAGTCCTGCGACAAGACTCACA CCTGTCCGCCTTGTCCAGCCCCTGAG CTGCTGGGTGGTCCGTCCGTGTTCCT	SEQ ID 1839	GACATCCAGATGACCCAGTCTCCTT CCACCCTGTCTGCATCTGTAGGAG ACAGAGTCACCATCACTTGCCGGG CCAGTCAGAGTATTAGTAGCTGGT TGGCCTGGTATCAGCAGAAACCAG GGAAAGCCCCTAAGCTCCTGATCT ATAAGGCGTCTAGTTTAGAAAGTG GGGTCCCATCAAGGTTCAGCGGCA GTGGATCTGGGACAGAATTCACTC TCACCATCAGCAGCCTGCAGCCTG ATGATTTTGCAACTTATTACTGCCA ACAGTATAATAGTTATTGGACGTTC GGCCAAGGGACCAAGGTGGAAATC AAACGTACTGTGGCTGCTCCCTCCG TGTTCATTTTTCCTCCGTCGGACGA ACAGCTGAAGTCCGGAACCGCGTC CGTGGTCTGTCTCCTGAACAACTTC TATCCGCGCGAGGCGAAAGTGCAG TGGAAGGTCGACAACGCACTGCAG TCGGGAAACTCCCAGGAATCGGTG ACCGAGCAGGACTCGAAGGACTCA ACCTACTCATTGTCCTCCACCCTCA CCCTGAGCAAGGCCGATTACGAGA AGCATAAGGTCTACGCCTGCGAAG TGACCCACCAGGGCCTGAGCAGCC CAGTGACGAAGTCCTTCAACCGGG GAGAATGC

	CTTCCCGCCCAAGCCGAAGGACACTC TGATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGCA CGAAGATCCCGAAGTGAAATTCAAT TGGTACGTGGATGGGGTCGAAGTGC ACAACGCCAAGACCAAGCCTAGGGA AGAACAGTACAACTCTACGTACCGG GTGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGAG TACAAGTGCAAAGTGTCAAACAAGG CTCTCCCTGCCCCTATCGAAAAGACC ATCAGCAAGGCCAAGGGTCAACCTA GGGAGCCCCAGGTCTATACTTTGCCG CCTAGCCGGGAAGAAATGACTAAGA ACCAAGTGTCCCTGACTTGCCTTGTC AAGGGCTTTTATCCGTCCGACATCGC CGTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTCC TTCTTCCTGTACTCCAAGCTGACTGT GGACAAGTCAAGATGGCAGCAGGGA AACGTGTTCTCCTGCTCCGTGATGCA CGAAGCGCTGCACAACCATTACACC CAGAAATCACTGTCACTTTCGCCGGG AAAA		
SEQ ID 1732	GAAGTGCAGCTGGTGCAGTCTGGGG GAGGCTTGGTCCAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCGTCAGTAGCAACTACATG AGCTGGGTCCGCCAGGCTCCAGGGA AGGGGCTGGAGTGGGTCTCAGTTATT TATAGCGGTGGTAGCACATACTACGC AGACTCCGTGAAGGGCCGATTCACC ATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTTCAAATGAACAGCCTG AGAGCTGAGGACACGGCTGTGTATT ACTGTGCGAGAGCCCCCCTAGCAGC AGATGGCTACTTTGACTACTGGGGCC AGGGAACCCTGGTCACCGTCTCCTCA GCATCCACCAAGGGGCCTTCCGTGTT CCCCCTGGCCCCTTCATCCAAGTCGA CCTCTGGTGGAACCGCCGCACTCGGT TGCCTGGTCAAAGACTACTTCCCCGA GCCCGTGACTGTCTCGTGGAACTCGG GCGCCCTCACATCCGGAGTGCATACC TTTCCCGCCGTGTTGCAGTCCAGCGG CCTGTACAGCCTGAGCTCCGTCGTGA CAGTGCCGTCCTCCTCCCTTGGAACC CAGACCTATATCTGCAACGTCAATCA CAAGCCCTCCAACACCAAAGTGGAC AAGAAGGTCGAACCCAAGTCCTGCG ACAAGACTCACACCTGTCCGCCTTGT CCAGCCCCTGAGCTGCTGGGTGGTCC GTCCGTGTTCCTCTTCCCGCCCAAGC	SEQ ID 1840	GAAACGACACTCACGCAGTCTCCA GGCACCCTGTCTTTGTCTCCAGGGG AAGGCGCCACCCTCTCCTGCAGGG CCAGTCACAGTGTTGGCGCCAACT ACATAGCCTGGTACCAGCAGAAAC CTGGCCAGGCTCCCAGGCTCCTTAT CCATACTGCATCCAAAAGGGCCAC TGGCGTCCCAGAGAGGTTCAGTGG CAGTGGGTCTGGGACAGACTTCAC TCTCAGTATCAGCAGACTGGAGCC TGAAGACTTTGCCGTGTATCACTGT CAGCAGTATGCTGCCGCACCGATT ACCTTCGGCCAAGGGACACGACTG GAGATTAAACGTACTGTGGCTGCT CCCTCCGTGTTCATTTTTCCTCCGT CGGACGAACAGCTGAAGTCCGGAA CCGCGTCCGTGGTCTGTCTCCTGAA CAACTTCTATCCGCGCGAGGCGAA AGTGCAGTGGAAGGTCGACAACGC ACTGCAGTCGGGAAACTCCCAGGA ATCGGTGACCGAGCAGGACTCGAA GGACTCAACCTACTCATTGTCCTCC ACCCTCACCCTGAGCAAGGCCGAT TACGAGAAGCATAAGGTCTACGCC TGCGAAGTGACCCACCAGGGCCTG AGCAGCCCAGTGACGAAGTCCTTC AACCGGGGAGAATGC

	CGAAGGACACTCTGATGATTTCACGC ACCCCGGAAGTCACTTGCGTGGTCGT GGACGTGTCGCACGAAGATCCCGAA GTGAAATTCAATTGGTACGTGGATGG GGTCGAAGTGCACAACGCCAAGACC AAGCCTAGGGAAGAACAGTACAACT CTACGTACCGGGTGGTGTCCGTGCTG ACCGTGCTGCACCAGGACTGGCTGA ACGGAAAGGAGTACAAGTGCAAAGT GTCAAACAAGGCTCTCCCTGCCCCTA TCGAAAAGACCATCAGCAAGGCCAA GGGTCAACCTAGGGAGCCCCAGGTC TATACTTTGCCGCCTAGCCGGGAAGA AATGACTAAGAACCAAGTGTCCCTG ACTTGCCTTGTCAAGGGCTTTTATCC GTCCGACATCGCCGTGGAGTGGGAG TCCAACGGACAACCGGAGAACAACT ACAAGACCACCCCACCGGTGCTCGA TTCCGATGGCTCCTTCTTCCTGTACTC CAAGCTGACTGTGGACAAGTCAAGA TGGCAGCAGGGAAACGTGTTCTCCTG CTCCGTGATGCACGAAGCGCTGCAC AACCATTACACCCAGAAATCACTGTC ACTTTCGCCGGGAAAA		
SEQ ID 1733	GAGGTCCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGTCCTC GGTGAAGGTCTCCTGCAAGGCTTCTG GAGGCACCTTCAGCAGCTATGCTATC AGCTGGGTGCGACAGGCCCCTGGAC AAGGGCTTGAGTGGATGGGAGGGAT CATCCCTATCTTTGGTACAGCAAACT ACGCACAGAAGTTCCAGGGCAGAGT CACGATTACCGCGGACGAATCCACG AGCACAGCCTACATGGAGCTGAGCA GCCTGAGATCTGAGGACACGGCCGT GTATTACTGTGCGAGAGCCCGGGGG CTACAGTACCTAATCTGGTACTTCGA TCTCTGGGGCCGTGGCACCCTGGTGA CCGTCTCCTCAGCATCCACCAAGGGG CCTTCCGTGTTCCCCCTGGCCCCTTC ATCCAAGTCGACCTCTGGTGGAACCG CCGCACTCGGTTGCCTGGTCAAAGAC TACTTCCCCGAGCCCGTGACTGTCTC GTGGAACTCGGGCGCCCTCACATCCG GAGTGCATACCTTTCCCGCCGTGTTG CAGTCCAGCGGCCTGTACAGCCTGA GCTCCGTCGTGACAGTGCCGTCCTCC TCCCTTGGAACCCAGACCTATATCTG CAACGTCAATCACAAGCCCTCCAAC ACCAAAGTGGACAAGAAGGTCGAAC CCAAGTCCTGCGACAAGACTCACAC CTGTCCGCCTTGTCCAGCCCCTGAGC TGCTGGGTGGTCCGTCCGTGTTCCTC	SEQ ID 1841	GAAATTGTGATGACACAGTCTCCA TCCTCCCTGTCTGCATCTGTGGGGG ACAGAGTCATCATCACTTGCCGGG CGAGTCAGGGCATTGCCAATTATTT AGCCTGGTATCAGCAGAAACCAGG GAAAGGTCCTAAACTCCTGATCTA TGCTTCATCTACTTTGCAATCAGGG GTCCCATCTCGGTTCAGTGGCAGTG GATCTGGGACAGATTTCACTCTCAC CATCAGCGGCCTGCAGCCTGAAGA TGTTGCAACTTATTACTGTCAGAAG TATAACAGTGTCCCTCTCACTTTCG GCGGAGGGACCAAAGTGGATATCA AACGTACTGTGGCTGCTCCCTCCGT GTTCATTTTTCCTCCGTCGGACGAA CAGCTGAAGTCCGGAACCGCGTCC GTGGTCTGTCTCCTGAACAACTTCT ATCCGCGCGAGGCGAAAGTGCAGT GGAAGGTCGACAACGCACTGCAGT CGGGAAACTCCCAGGAATCGGTGA CCGAGCAGGACTCGAAGGACTCAA CCTACTCATTGTCCTCCACCCTCAC CCTGAGCAAGGCCGATTACGAGAA GCATAAGGTCTACGCCTGCGAAGT GACCCACCAGGGCCTGAGCAGCCC AGTGACGAAGTCCTTCAACCGGGG AGAATGC

	TTCCCGCCCAAGCCGAAGGACACTCT GATGATTTCACGCACCCCGGAAGTCA CTTGCGTGGTCGTGGACGTGTCGCAC GAAGATCCCGAAGTGAAATTCAATT GGTACGTGGATGGGGTCGAAGTGCA CAACGCCAAGACCAAGCCTAGGGAA GAACAGTACAACTCTACGTACCGGG TGGTGTCCGTGCTGACCGTGCTGCAC CAGGACTGGCTGAACGGAAAGGAGT ACAAGTGCAAAGTGTCAAACAAGGC TCTCCCTGCCCCTATCGAAAAGACCA TCAGCAAGGCCAAGGGTCAACCTAG GGAGCCCCAGGTCTATACTTTGCCGC CTAGCCGGGAAGAAATGACTAAGAA CCAAGTGTCCCTGACTTGCCTTGTCA AGGGCTTTTATCCGTCCGACATCGCC GTGGAGTGGGAGTCCAACGGACAAC CGGAGAACAACTACAAGACCACCCC ACCGGTGCTCGATTCCGATGGCTCCT TCTTCCTGTACTCCAAGCTGACTGTG GACAAGTCAAGATGGCAGCAGGGAA ACGTGTTCTCCTGCTCCGTGATGCAC GAAGCGCTGCACAACCATTACACCC AGAAATCACTGTCACTTTCGCCGGGA AAA		
SEQ ID 1734	CAGGTCCAGCTGGTACAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTTTCCTGCAAGGCATCTG GATACACCTTCACCAGCTACTATATG CACTGGGTGCGACAGGCCCCTGGAC AAGGGCTTGAGTGGATGGGAATAAT CAACCCTAGTGGTGGTAGCACAAGC TACGCACAGAAGTTCCAGGGCAGAG TCACCATGACCAGGGACACGTCCAC GAGCACAGTCTACATGGAGCTGAGC AGCCTGAGATCTGAGGACACGGCCG TGTATTACTGTGCGAGCCCGGGTATG GTTCGGGGAGTTATTACTGCCCCGCT TGACTACTGGGGCCAGGGCACCCTG GTCACCGTCTCCTCAGCATCCACCAA GGGGCCTTCCGTGTTCCCCCTGGCCC CTTCATCCAAGTCGACCTCTGGTGGA ACCGCCGCACTCGGTTGCCTGGTCAA AGACTACTTCCCCGAGCCCGTGACTG TCTCGTGGAACTCGGGCGCCCTCACA TCCGGAGTGCATACCTTTCCCGCCGT GTTGCAGTCCAGCGGCCTGTACAGCC TGAGCTCCGTCGTGACAGTGCCGTCC TCCTCCCTTGGAACCCAGACCTATAT CTGCAACGTCAATCACAAGCCCTCCA ACACCAAAGTGGACAAGAAGGTCGA ACCCAAGTCCTGCGACAAGACTCAC ACCTGTCCGCCTTGTCCAGCCCCTGA GCTGCTGGGTGGTCCGTCCGTGTTCC	SEQ ID 1842	GATGTTGTGATGACTCAGTCTCCAG TCTCCCTGGCTGTGTCTCTGGGCGA GAGGGCCACCATCAACTGCAAGTC CAGCCAGAGTGTTTTATACAGAAC CAACAATAAGAACTACTTGGCTTG GTATCAGCAGAAACCAGGACAGCC TCCTAAGTTGCTCATTTACTGGGCA TCTACCCGGGAATCCGGGGTCCCT GACCGATTCAGTGGCAGCGGGTCT GGGACAGATTTCACTCTCACCATC AGCAGCCTGCAGCCTGAGGATGTG GCAGTGTACTACTGTCAGCAATATT ACAATCTTCCTCGATCTTTTGGCCA GGGGACCAAGCTGGAGATCAAACG TACTGTGGCTGCTCCCTCCGTGTTC ATTTTTCCTCCGTCGGACGAACAGC TGAAGTCCGGAACCGCGTCCGTGG TCTGTCTCCTGAACAACTTCTATCC GCGCGAGGCGAAAGTGCAGTGGAA GGTCGACAACGCACTGCAGTCGGG AAACTCCCAGGAATCGGTGACCGA GCAGGACTCGAAGGACTCAACCTA CTCATTGTCCTCCACCCTCACCCTG AGCAAGGCCGATTACGAGAAGCAT AAGGTCTACGCCTGCGAAGTGACC CACCAGGGCCTGAGCAGCCCAGTG ACGAAGTCCTTCAACCGGGGAGAA TGC

	TCTTCCCGCCCAAGCCGAAGGACACT CTGATGATTTCACGCACCCCGGAAGT CACTTGCGTGGTCGTGGACGTGTCGC ACGAAGATCCCGAAGTGAAATTCAA TTGGTACGTGGATGGGGTCGAAGTG CACAACGCCAAGACCAAGCCTAGGG AAGAACAGTACAACTCTACGTACCG GGTGGTGTCCGTGCTGACCGTGCTGC ACCAGGACTGGCTGAACGGAAAGGA GTACAAGTGCAAAGTGTCAAACAAG GCTCTCCCTGCCCCTATCGAAAAGAC CATCAGCAAGGCCAAGGGTCAACCT AGGGAGCCCCAGGTCTATACTTTGCC GCCTAGCCGGGAAGAAATGACTAAG AACCAAGTGTCCCTGACTTGCCTTGT CAAGGGCTTTTATCCGTCCGACATCG CCGTGGAGTGGGAGTCCAACGGACA ACCGGAGAACAACTACAAGACCACC CCACCGGTGCTCGATTCCGATGGCTC CTTCTTCCTGTACTCCAAGCTGACTG TGGACAAGTCAAGATGGCAGCAGGG AAACGTGTTCTCCTGCTCCGTGATGC ACGAAGCGCTGCACAACCATTACAC CCAGAAATCACTGTCACTTTCGCCGG GAAAA		
SEQ ID 1735	GAGGTCCAGCTGGTACAGTCTGGGG GAGGCCTGGTCAAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTCAGCAGCTATGCTATC AGCTGGGTGCGACAGGCCCCTGGAC AAGGGCTTGAGTGGATGGGAGGGAT CATCCCTATGTATGGTACAGCAAACT ACGCACAGAAGTTCCAGGGCAGAGT CACGATTACCGCGGACGAATCCACG AGCACAGCCTACATGGAACTGAGCA GCCTGAGATCTGAGGACACGGCCCT CTATTACTGTGCGAGAGAAGCTAAGT GGGGAATGTACTACTTTGACTACTGG GGCCAGGGCACCCTGGTCACCGTCTC CTCAGCATCCACCAAGGGGCCTTCCG TGTTCCCCCTGGCCCCTTCATCCAAG TCGACCTCTGGTGGAACCGCCGCACT CGGTTGCCTGGTCAAAGACTACTTCC CCGAGCCCGTGACTGTCTCGTGGAAC TCGGGCGCCCTCACATCCGGAGTGCA TACCTTTCCCGCCGTGTTGCAGTCCA GCGGCCTGTACAGCCTGAGCTCCGTC GTGACAGTGCCGTCCTCCTCCCTTGG AACCCAGACCTATATCTGCAACGTCA ATCACAAGCCCTCCAACACCAAAGT GGACAAGAAGGTCGAACCCAAGTCC TGCGACAAGACTCACACCTGTCCGCC TTGTCCAGCCCCTGAGCTGCTGGGTG GTCCGTCCGTGTTCCTCTTCCCGCCC	SEQ ID 1843	GATATTGTGATGACCCACACTCCA GACTCCCTGGCTGTGTCTCTGGGCG AGAGGGCCACCATCAACTGCAAGT CCAACCGGAGTGTTTTATACAGCC CCAACAATCAGAACTACTTAGGTT GGTACCAGCAGAAGCCAGGACAGC CTCCTAAGCTGCTCATTTACTGGGC ATCTACCCGGGACTCCGGGGCCCC TGACCGATTCAGTGGCAGCGGGTC TGGGACAGATTTCACTCTCACCATC AACAGCCTGCAGGCTGAAGATGTG GCAGTTTATTACTGTCAGCAATATG CAAGTACTCCATACACTTTTGGCCA GGGGACCAAGGTGGAGATCAAACG TACTGTGGCTGCTCCCTCCGTGTTC ATTTTTCCTCCGTCGGACGAACAGC TGAAGTCCGGAACCGCGTCCGTGG TCTGTCTCCTGAACAACTTCTATCC GCGCGAGGCGAAAGTGCAGTGGAA GGTCGACAACGCACTGCAGTCGGG AAACTCCCAGGAATCGGTGACCGA GCAGGACTCGAAGGACTCAACCTA CTCATTGTCCTCCACCCTCACCCTG AGCAAGGCCGATTACGAGAAGCAT AAGGTCTACGCCTGCGAAGTGACC CACCAGGGCCTGAGCAGCCCAGTG ACGAAGTCCTTCAACCGGGGAGAA TGC

	AAGCCGAAGGACACTCTGATGATTTC ACGCACCCCGGAAGTCACTTGCGTG GTCGTGGACGTGTCGCACGAAGATC CCGAAGTGAAATTCAATTGGTACGTG GATGGGGTCGAAGTGCACAACGCCA AGACCAAGCCTAGGGAAGAACAGTA CAACTCTACGTACCGGGTGGTGTCCG TGCTGACCGTGCTGCACCAGGACTGG CTGAACGGAAAGGAGTACAAGTGCA AAGTGTCAAACAAGGCTCTCCCTGCC CCTATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTATACTTTGCCGCCTAGCCGGG AAGAAATGACTAAGAACCAAGTGTC CCTGACTTGCCTTGTCAAGGGCTTTT ATCCGTCCGACATCGCCGTGGAGTGG GAGTCCAACGGACAACCGGAGAACA ACTACAAGACCACCCCACCGGTGCTC GATTCCGATGGCTCCTTCTTCCTGTA CTCCAAGCTGACTGTGGACAAGTCA AGATGGCAGCAGGGAAACGTGTTCT CCTGCTCCGTGATGCACGAAGCGCTG CACAACCATTACACCCAGAAATCACT GTCACTTTCGCCGGGAAAA		
SEQ ID 1736	GAGGTGCAGCTGGTGGAGTCCGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTCAGTAGCTATGCTATA CACTGGGTCCGCCAGGCTCCAGGCA AGGGGCTGGAGTGGGTGGCAATTAT ATCAGATGATGGAAGTAAGAGTTAC TACGCAGACTCCGTGCAGGGCCGATT CACCATCTCCAGAGACAATTCGAGG AACACAGTATATCTGCAAATGAACA GCCTGAGAGCTGAGGACACGGCTAT GTATTACTGTGCGAGAGACAGGGGA ACTAAATGGAACCAATTGAATGATG TTTTTGATATGTGGGGCCAAGGGACA ATGGTCACCGTCTCTTCAGCATCCAC CAAGGGGCCTTCCGTGTTCCCCCTGG CCCCTTCATCCAAGTCGACCTCTGGT GGAACCGCCGCACTCGGTTGCCTGGT CAAAGACTACTTCCCCGAGCCCGTGA CTGTCTCGTGGAACTCGGGCGCCCTC ACATCCGGAGTGCATACCTTTCCCGC CGTGTTGCAGTCCAGCGGCCTGTACA GCCTGAGCTCCGTCGTGACAGTGCCG TCCTCCTCCCTTGGAACCCAGACCTA TATCTGCAACGTCAATCACAAGCCCT CCAACACCAAAGTGGACAAGAAGGT CGAACCCAAGTCCTGCGACAAGACT CACACCTGTCCGCCTTGTCCAGCCCC TGAGCTGCTGGGTGGTCCGTCCGTGT	SEQ ID 1844	GATGTTGTGATGACTCAGTCTCCAG CCACCCTGTCTTTGTCTCCAGGGGA AAGAGCCACCCTCTCCTGCAGGGC CAGTGAGAGTGTTAATAGCAACTT CTTAGCCTGGTACCAGCAGAAACC TGGCCAGGCTCCCAGGCTCCTCATC TATGCTGCATCCACCAGGGCCACT GGTATCCCAGCCAGGTTCAGTGGC AGTGGGTCTGGGACAGAGTTCACT CTCATCATCACCAGCCTGCAGTCTG AAGATTTTGCAGTTTATTACTGTCA GCAGTATAATAACTGGCCGCTCAC TTTCGGCGGAGGGACCAAGCTGGA GATCAAACGTACTGTGGCTGCTCC CTCCGTGTTCATTTTTCCTCCGTCG GACGAACAGCTGAAGTCCGGAACC GCGTCCGTGGTCTGTCTCCTGAACA ACTTCTATCCGCGCGAGGCGAAAG TGCAGTGGAAGGTCGACAACGCAC TGCAGTCGGGAAACTCCCAGGAAT CGGTGACCGAGCAGGACTCGAAGG ACTCAACCTACTCATTGTCCTCCAC CCTCACCCTGAGCAAGGCCGATTA CGAGAAGCATAAGGTCTACGCCTG CGAAGTGACCCACCAGGGCCTGAG CAGCCCAGTGACGAAGTCCTTCAA CCGGGGAGAATGC

	TCCTCTTCCCGCCCAAGCCGAAGGAC ACTCTGATGATTTCACGCACCCCGGA AGTCACTTGCGTGGTCGTGGACGTGT CGCACGAAGATCCCGAAGTGAAATT CAATTGGTACGTGGATGGGGTCGAA GTGCACAACGCCAAGACCAAGCCTA GGGAAGAACAGTACAACTCTACGTA CCGGGTGGTGTCCGTGCTGACCGTGC TGCACCAGGACTGGCTGAACGGAAA GGAGTACAAGTGCAAAGTGTCAAAC AAGGCTCTCCCTGCCCCTATCGAAAA GACCATCAGCAAGGCCAAGGGTCAA CCTAGGGAGCCCCAGGTCTATACTTT GCCGCCTAGCCGGGAAGAAATGACT AAGAACCAAGTGTCCCTGACTTGCCT TGTCAAGGGCTTTTATCCGTCCGACA TCGCCGTGGAGTGGGAGTCCAACGG ACAACCGGAGAACAACTACAAGACC ACCCCACCGGTGCTCGATTCCGATGG CTCCTTCTTCCTGTACTCCAAGCTGA CTGTGGACAAGTCAAGATGGCAGCA GGGAAACGTGTTCTCCTGCTCCGTGA TGCACGAAGCGCTGCACAACCATTA CACCCAGAAATCACTGTCACTTTCGC CGGGAAAA		
SEQ ID 1737	CAGATGCAGCTGGTGCAATCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTCTCCTGCACGGCTTCTG GATACACCTTCACCAGTTCTGATATC AACTGGGTGCGACAGGCCACTGGAC AAGGGCTTGAGTGGATGGGATGGAT GAACCCTAACAGTGGTAACACCGGC TATGCAGAGAAGTTCCAGGGCAGGG TCACCATGACCAGCGACTCCTCCATA AGCACCGCCTACATGGAGTTGAGAA GCCTGACCACTGAGGACACGGCCGT ATATTACTGTGCGAGAGGTGGGGGT GCGAGCTATACTGACTCCTGGGGCCA GGGCACCCTGGTCACCGTCTCCTCAG CATCCACCAAGGGGCCTTCCGTGTTC CCCCTGGCCCCTTCATCCAAGTCGAC CTCTGGTGGAACCGCCGCACTCGGTT GCCTGGTCAAAGACTACTTCCCCGAG CCCGTGACTGTCTCGTGGAACTCGGG CGCCCTCACATCCGGAGTGCATACCT TTCCCGCCGTGTTGCAGTCCAGCGGC CTGTACAGCCTGAGCTCCGTCGTGAC AGTGCCGTCCTCCTCCCTTGGAACCC AGACCTATATCTGCAACGTCAATCAC AAGCCCTCCAACACCAAAGTGGACA AGAAGGTCGAACCCAAGTCCTGCGA CAAGACTCACACCTGTCCGCCTTGTC CAGCCCCTGAGCTGCTGGGTGGTCCG TCCGTGTTCCTCTTCCCGCCCAAGCC	SEQ ID 1845	GATGTTGTGATGACTCAGTCTCCAG CCACCCTGTCTTTGTCTCCAGGGGA AAGAGCCACCCTCTCCTGCAGGGC CAGTCAGAGTGTTAGCAGCTACTT AGCCTGGTACCAACAGAAACCTGG CCAGGCTCCCAGGCTCCTCATCTAT GATGCATCCAACAGGGCCACTGGC ATCCCAGCCAGGTTCAGTGGCAGT GGGTCTGGGACAGACTTCACTCTC ACCATCAGCAGCCTAGAGCCTGAA GATTTTGCAGTTTATTACTGTCAGC AGCGTAGCAACTGGTCGCTCACTTT CGGCGGAGGGACCAAGCTGGAGAT CAAACGTACTGTGGCTGCTCCCTCC GTGTTCATTTTTCCTCCGTCGGACG AACAGCTGAAGTCCGGAACCGCGT CCGTGGTCTGTCTCCTGAACAACTT CTATCCGCGCGAGGCGAAAGTGCA GTGGAAGGTCGACAACGCACTGCA GTCGGGAAACTCCCAGGAATCGGT GACCGAGCAGGACTCGAAGGACTC AACCTACTCATTGTCCTCCACCCTC ACCCTGAGCAAGGCCGATTACGAG AAGCATAAGGTCTACGCCTGCGAA GTGACCCACCAGGGCCTGAGCAGC CCAGTGACGAAGTCCTTCAACCGG GGAGAATGC

	GAAGGACACTCTGATGATTTCACGCA CCCCGGAAGTCACTTGCGTGGTCGTG GACGTGTCGCACGAAGATCCCGAAG TGAAATTCAATTGGTACGTGGATGGG GTCGAAGTGCACAACGCCAAGACCA AGCCTAGGGAAGAACAGTACAACTC TACGTACCGGGTGGTGTCCGTGCTGA CCGTGCTGCACCAGGACTGGCTGAA CGGAAAGGAGTACAAGTGCAAAGTG TCAAACAAGGCTCTCCCTGCCCCTAT CGAAAAGACCATCAGCAAGGCCAAG GGTCAACCTAGGGAGCCCCAGGTCT ATACTTTGCCGCCTAGCCGGGAAGA AATGACTAAGAACCAAGTGTCCCTG ACTTGCCTTGTCAAGGGCTTTTATCC GTCCGACATCGCCGTGGAGTGGGAG TCCAACGGACAACCGGAGAACAACT ACAAGACCACCCCACCGGTGCTCGA TTCCGATGGCTCCTTCTTCCTGTACTC CAAGCTGACTGTGGACAAGTCAAGA TGGCAGCAGGGAAACGTGTTCTCCTG CTCCGTGATGCACGAAGCGCTGCAC AACCATTACACCCAGAAATCACTGTC ACTTTCGCCGGGAAAA		
SEQ ID 1738	CAGGTCCAGCTGGTGCAGTCTGGGG GAGGCTTGGTACAGCCAGGGCGGTC CCTGAGACTCTCCTGTACAGCTTCTG GATTCACCTTTGGTGATTATGCTATG AGCTGGTTCCGCCAGGCTCCAGGGA AGGGGCTGGAGTGGGTAGGTTTCATT AGAAGCAAAGCTTATGGTGGGACAA CAGAATACGCCGCGTCTGTGAAAGG CAGATTCACCATCTCAAGAGATGATT CCAAAAGCATCGCCTATCTGCAAATG AACAGCCTGAAAACCGAGGACACAG CCGTGTATTACTGTACCGCTAAGGGG GGCTACGTCGGATACAGCTATGGAC CTTTTGGGGGCTACTGGGGCCAGGG AACCCTGGTCACCGTCTCCTCAGCAT CCACCAAGGGGCCTTCCGTGTTCCCC CTGGCCCCTTCATCCAAGTCGACCTC TGGTGGAACCGCCGCACTCGGTTGCC TGGTCAAAGACTACTTCCCCGAGCCC GTGACTGTCTCGTGGAACTCGGGCGC CCTCACATCCGGAGTGCATACCTTTC CCGCCGTGTTGCAGTCCAGCGGCCTG TACAGCCTGAGCTCCGTCGTGACAGT GCCGTCCTCCTCCCTTGGAACCCAGA CCTATATCTGCAACGTCAATCACAAG CCCTCCAACACCAAAGTGGACAAGA AGGTCGAACCCAAGTCCTGCGACAA GACTCACACCTGTCCGCCTTGTCCAG CCCCTGAGCTGCTGGGTGGTCCGTCC	SEQ ID 1846	GAAACGACACTCACGCAGTCTCCA GGCACCCTGTCTTTGTCTCCAGGGG AAAGAGCCACCCTCTCCTGCAGGG CCAGTCAGAGTGTTAGCAGCAGCT ACTTAGCCTGGTACCAACAGAAAC CTGGCCAGGCTCCCAGGCTCCTCAT CTATGGTGCTTCCACCAGGGCCACT GGCATCCCAGACAGGTTCAGTGGC AGTGGGTCTGGGACGGACTTCACT CTCACCATCGGCAGACTGGAGCCT GAAGATTTTGCAGTGTATTACTGTC AACACTATGGTCCCTCACGTCGGA TCACCTTCGGCCAAGGGACACGAC TGGAGATTAAACGTACTGTGGCTG CTCCCTCCGTGTTCATTTTTCCTCC GTCGGACGAACAGCTGAAGTCCGG AACCGCGTCCGTGGTCTGTCTCCTG AACAACTTCTATCCGCGCGAGGCG AAAGTGCAGTGGAAGGTCGACAAC GCACTGCAGTCGGGAAACTCCCAG GAATCGGTGACCGAGCAGGACTCG AAGGACTCAACCTACTCATTGTCCT CCACCCTCACCCTGAGCAAGGCCG ATTACGAGAAGCATAAGGTCTACG CCTGCGAAGTGACCCACCAGGGCC TGAGCAGCCCAGTGACGAAGTCCT TCAACCGGGGAGAATGC

	GTGTTCCTCTTCCCGCCCAAGCCGAA GGACACTCTGATGATTTCACGCACCC CGGAAGTCACTTGCGTGGTCGTGGAC GTGTCGCACGAAGATCCCGAAGTGA AATTCAATTGGTACGTGGATGGGGTC GAAGTGCACAACGCCAAGACCAAGC CTAGGGAAGAACAGTACAACTCTAC GTACCGGGTGGTGTCCGTGCTGACCG TGCTGCACCAGGACTGGCTGAACGG AAAGGAGTACAAGTGCAAAGTGTCA AACAAGGCTCTCCCTGCCCCTATCGA AAAGACCATCAGCAAGGCCAAGGGT CAACCTAGGGAGCCCCAGGTCTATA CTTTGCCGCCTAGCCGGGAAGAAAT GACTAAGAACCAAGTGTCCCTGACTT GCCTTGTCAAGGGCTTTTATCCGTCC GACATCGCCGTGGAGTGGGAGTCCA ACGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCCG ATGGCTCCTTCTTCCTGTACTCCAAG CTGACTGTGGACAAGTCAAGATGGC AGCAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACTT TCGCCGGGAAAA		
SEQ ID 1739	CAGGTGCAGCTGGTGCAGTCTGGGG GAGGCTTGGTACAGCCAGGGCGGTC CCTGAGACTCTCCTGTACAGCTTCTG GATTCACCTTTGGTGATTATGCTATG AGCTGGTTCCGCCAGGCTCCAGGGA AGGGGCTGGAGTGGGTAGGTTTCATT AGAAGCAAAGCTTATGGTGGGACAA CAGAATACGCCGCGTCTGTGAAAGG CAGATTCACCATCTCAAGAGATGATT CCAAAAGCATCGCCTATCTGCAAATG AACAGCCTGAAAACCGAGGACACAG CCGTGTATTACTGTACTAGAGGGGGG ACTATGGTTCGGGGTTTCGGATTTAA CTACTGGGGCCAGGGAACCCTGGTC ACCGTCTCCTCAGCATCCACCAAGGG GCCTTCCGTGTTCCCCCTGGCCCCTT CATCCAAGTCGACCTCTGGTGGAACC GCCGCACTCGGTTGCCTGGTCAAAGA CTACTTCCCCGAGCCCGTGACTGTCT CGTGGAACTCGGGCGCCCTCACATCC GGAGTGCATACCTTTCCCGCCGTGTT GCAGTCCAGCGGCCTGTACAGCCTG AGCTCCGTCGTGACAGTGCCGTCCTC CTCCCTTGGAACCCAGACCTATATCT GCAACGTCAATCACAAGCCCTCCAA CACCAAAGTGGACAAGAAGGTCGAA CCCAAGTCCTGCGACAAGACTCACA CCTGTCCGCCTTGTCCAGCCCCTGAG CTGCTGGGTGGTCCGTCCGTGTTCCT	SEQ ID 1847	GAAACGACACTCACGCAGTCTCCA GACACCCTGTCTGTGTCTCCAGGG GGAAGAGCCACCCTCTCCTGTAGG GCCAGTCAGAGCATTGGGAGCAAT TTAGCCTGGTACCAACAGAAACCT GGCCAGTCTCCCAGGCTCCTCATCT ATGATGCATCCACCAGGGCCACGG GAATCCCAGCCAGGTTCAGTGGCA GTGGGTCTGGGACAGAATTCACTC TCACCATCAGCAGCCTGGAGTCTG AAGATTTTGTACTTTATTACTGTCA GCAGCATGGTGAATGGCCCACCTT CGGCCAAGGGACACGACTGGAGAT TAAACGTACTGTGGCTGCTCCCTCC GTGTTCATTTTTCCTCCGTCGGACG AACAGCTGAAGTCCGGAACCGCGT CCGTGGTCTGTCTCCTGAACAACTT CTATCCGCGCGAGGCGAAAGTGCA GTGGAAGGTCGACAACGCACTGCA GTCGGGAAACTCCCAGGAATCGGT GACCGAGCAGGACTCGAAGGACTC AACCTACTCATTGTCCTCCACCCTC ACCCTGAGCAAGGCCGATTACGAG AAGCATAAGGTCTACGCCTGCGAA GTGACCCACCAGGGCCTGAGCAGC CCAGTGACGAAGTCCTTCAACCGG GGAGAATGC

	CTTCCCGCCCAAGCCGAAGGACACTC TGATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGCA CGAAGATCCCGAAGTGAAATTCAAT TGGTACGTGGATGGGGTCGAAGTGC ACAACGCCAAGACCAAGCCTAGGGA AGAACAGTACAACTCTACGTACCGG GTGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGAG TACAAGTGCAAAGTGTCAAACAAGG CTCTCCCTGCCCCTATCGAAAAGACC ATCAGCAAGGCCAAGGGTCAACCTA GGGAGCCCCAGGTCTATACTTTGCCG CCTAGCCGGGAAGAAATGACTAAGA ACCAAGTGTCCCTGACTTGCCTTGTC AAGGGCTTTTATCCGTCCGACATCGC CGTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTCC TTCTTCCTGTACTCCAAGCTGACTGT GGACAAGTCAAGATGGCAGCAGGGA AACGTGTTCTCCTGCTCCGTGATGCA CGAAGCGCTGCACAACCATTACACC CAGAAATCACTGTCACTTTCGCCGGG AAAA		
SEQ ID 1740	CAGGTGCAGCTACAGCAGTGGGGCG CAGGACTGTTGAAGCCTTCGGAGAC CCTGTCCCTCACCTGCGCTGTCTATG GTGGGTCCTTCAGTGGTTACTACTGG AGCTGGATCCGCCAGCCCCCAGGGA AGGGGCTGGAGTGGATTGGGGAAAT CAATCATAGTGGAAGCACCAACTAC AACCCGTCCCTCAAGAGTCGAGTCAC CATATCAGTAGACACGTCCAAGAAC CAGTTCTCCCTGAAGCTGAGCTCTGT GACCGCCGCGGACACGGCTGTGTATT ACTGTGCGAGAGCCCGGCGGGCTAT GATAGGGCCGCTTCCGCGACTTGTCG GGTACTTCGATCTCTGGGGCCGTGGA ACCCTGGTCACCGTCTCCTCAGCATC CACCAAGGGGCCTTCCGTGTTCCCCC TGGCCCCTTCATCCAAGTCGACCTCT GGTGGAACCGCCGCACTCGGTTGCCT GGTCAAAGACTACTTCCCCGAGCCCG TGACTGTCTCGTGGAACTCGGGCGCC CTCACATCCGGAGTGCATACCTTTCC CGCCGTGTTGCAGTCCAGCGGCCTGT ACAGCCTGAGCTCCGTCGTGACAGTG CCGTCCTCCTCCCTTGGAACCCAGAC CTATATCTGCAACGTCAATCACAAGC CCTCCAACACCAAAGTGGACAAGAA GGTCGAACCCAAGTCCTGCGACAAG ACTCACACCTGTCCGCCTTGTCCAGC CCCTGAGCTGCTGGGTGGTCCGTCCG	SEQ ID 1848	GATGTTGTGATGACTCAGTCTCCAG CCACCCTGTCTTTGTCTCCAGGGGA AAGAGCCACCCTCTCCTGCAGGGC CAGTCAGAGTGTCGGTAACTCCTT AGCCTGGTACCAGCAGAAGCCTGG CCAGGCTCCCCGGCTCCTCATCTAT GATGCATCCAACAGGGCCACTGGC ATCCCAGCCCGGTTCAGTGGCAGT GGGTCTGGGACAGACTTCACTCTC ACCATCACCAGCCTAGAGCCTGAA GATTTTGCAATTTATTACTGTCAAC AACGTGGCACCTGGCCTCCCCTCA CTTTCGGCGGAGGGACCAAGCTGG AGATCAAACGTACTGTGGCTGCTC CCTCCGTGTTCATTTTTCCTCCGTC GGACGAACAGCTGAAGTCCGGAAC CGCGTCCGTGGTCTGTCTCCTGAAC AACTTCTATCCGCGCGAGGCGAAA GTGCAGTGGAAGGTCGACAACGCA CTGCAGTCGGGAAACTCCCAGGAA TCGGTGACCGAGCAGGACTCGAAG GACTCAACCTACTCATTGTCCTCCA CCCTCACCCTGAGCAAGGCCGATT ACGAGAAGCATAAGGTCTACGCCT GCGAAGTGACCCACCAGGGCCTGA GCAGCCCAGTGACGAAGTCCTTCA ACCGGGGAGAATGC

	TGTTCCTCTTCCCGCCCAAGCCGAAG GACACTCTGATGATTTCACGCACCCC GGAAGTCACTTGCGTGGTCGTGGAC GTGTCGCACGAAGATCCCGAAGTGA AATTCAATTGGTACGTGGATGGGGTC GAAGTGCACAACGCCAAGACCAAGC CTAGGGAAGAACAGTACAACTCTAC GTACCGGGTGGTGTCCGTGCTGACCG TGCTGCACCAGGACTGGCTGAACGG AAAGGAGTACAAGTGCAAAGTGTCA AACAAGGCTCTCCCTGCCCCTATCGA AAAGACCATCAGCAAGGCCAAGGGT CAACCTAGGGAGCCCCAGGTCTATA CTTTGCCGCCTAGCCGGGAAGAAAT GACTAAGAACCAAGTGTCCCTGACTT GCCTTGTCAAGGGCTTTTATCCGTCC GACATCGCCGTGGAGTGGGAGTCCA ACGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCCG ATGGCTCCTTCTTCCTGTACTCCAAG CTGACTGTGGACAAGTCAAGATGGC AGCAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACTT TCGCCGGGAAAA		
SEQ ID 1741	CAGGTGCAGCTACAGCAGTGGGGCG CAGGACTGTTGAAGCCTTCGGAGAC CCTGTCCCTCACCTGCGCTGTCTATG GTGGGTCCTTCAGTGGTTACTACTGG AGCTGGATCCGCCAGCCCCCAGGGA AGGGGCTGGAGTGGATTGGGGAAAT CAATCATAGTGGAAGCACCAACTAC AACCCGTCCCTCAAGAGTCGAGTCAC CATATCAGTAGACACGTCCAAGAAC CAGTTCTCCCTGAAGCTGAGCTCTGT GACCGCCGCGGACACGGCTGTGTATT ACTGTGCGAGAGGCCGCCCCGCCCC ATCCTGGGTTAAAACCCGTAACTGGT TCGACCCCTGGGGCCAGGGAACCCT GGTCACCGTCTCCTCAGCATCCACCA AGGGGCCTTCCGTGTTCCCCCTGGCC CCTTCATCCAAGTCGACCTCTGGTGG AACCGCCGCACTCGGTTGCCTGGTCA AAGACTACTTCCCCGAGCCCGTGACT GTCTCGTGGAACTCGGGCGCCCTCAC ATCCGGAGTGCATACCTTTCCCGCCG TGTTGCAGTCCAGCGGCCTGTACAGC CTGAGCTCCGTCGTGACAGTGCCGTC CTCCTCCCTTGGAACCCAGACCTATA TCTGCAACGTCAATCACAAGCCCTCC AACACCAAAGTGGACAAGAAGGTCG AACCCAAGTCCTGCGACAAGACTCA CACCTGTCCGCCTTGTCCAGCCCCTG AGCTGCTGGGTGGTCCGTCCGTGTTC	SEQ ID 1849	GATGTTGTGATGACTCAGTCTCCAT CCTCCCTGTCTGCATCTGTAGGAGA CACAGTCACCATCACTTGCCGGGC CAGTCAGAGTATAACTAACTGGTT GGCCTGGTATCAGCAGAAACCAGG GAAAGCCCCCAAGCGCCTGATCTA TGGTGCGTCCAGTTTGCAGAGTGG GGTCCCATCAAGGTTCAGCGGCAG TGGATCTGGGACAGAATTCACTCT CACAATCAGCAGCCTGCAGCCTGA AGATTTTGCAACTTATTACTGTCAA CAGTATACTAATTACCCTCGTACGT TCGGCCAAGGGACCAAGCTGGAGA TCAAACGTACTGTGGCTGCTCCCTC CGTGTTCATTTTTCCTCCGTCGGAC GAACAGCTGAAGTCCGGAACCGCG TCCGTGGTCTGTCTCCTGAACAACT TCTATCCGCGCGAGGCGAAAGTGC AGTGGAAGGTCGACAACGCACTGC AGTCGGGAAACTCCCAGGAATCGG TGACCGAGCAGGACTCGAAGGACT CAACCTACTCATTGTCCTCCACCCT CACCCTGAGCAAGGCCGATTACGA GAAGCATAAGGTCTACGCCTGCGA AGTGACCCACCAGGGCCTGAGCAG CCCAGTGACGAAGTCCTTCAACCG GGGAGAATGC

	CTCTTCCCGCCCAAGCCGAAGGACAC TCTGATGATTTCACGCACCCCGGAAG TCACTTGCGTGGTCGTGGACGTGTCG CACGAAGATCCCGAAGTGAAATTCA ATTGGTACGTGGATGGGGTCGAAGT GCACAACGCCAAGACCAAGCCTAGG GAAGAACAGTACAACTCTACGTACC GGGTGGTGTCCGTGCTGACCGTGCTG CACCAGGACTGGCTGAACGGAAAGG AGTACAAGTGCAAAGTGTCAAACAA GGCTCTCCCTGCCCCTATCGAAAAGA CCATCAGCAAGGCCAAGGGTCAACC TAGGGAGCCCCAGGTCTATACTTTGC CGCCTAGCCGGGAAGAAATGACTAA GAACCAAGTGTCCCTGACTTGCCTTG TCAAGGGCTTTTATCCGTCCGACATC GCCGTGGAGTGGGAGTCCAACGGAC AACCGGAGAACAACTACAAGACCAC CCCACCGGTGCTCGATTCCGATGGCT CCTTCTTCCTGTACTCCAAGCTGACT GTGGACAAGTCAAGATGGCAGCAGG GAAACGTGTTCTCCTGCTCCGTGATG CACGAAGCGCTGCACAACCATTACA CCCAGAAATCACTGTCACTTTCGCCG GGAAAA		
SEQ ID 1742	CAGGTACAGCTGCAGCAGTCAGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCAACAGTGCT GCTTGGAACTGGATCAGGCAGTCCCC ATCGAGAGGCCTTGAGTGGCTGGGA AGGACATACTACAGGTCCAAGTGGT ATAATGATTATGCAGTATCTGTGAAA AGTCGAATAACCATCAACCCAGACA CATCCAAGAACCAGTTCTCCCTGCAG CTGAACTCTGTGACTCCCGAGGACAC GGCTGTGTATTACTGTGCAAGAGAG GCTAGCAGTGGCTGGAACTGGGGCC AGGGAACCCTGGTCACCGTCTCCTCA GCATCCACCAAGGGGCCTTCCGTGTT CCCCCTGGCCCCTTCATCCAAGTCGA CCTCTGGTGGAACCGCCGCACTCGGT TGCCTGGTCAAAGACTACTTCCCCGA GCCCGTGACTGTCTCGTGGAACTCGG GCGCCCTCACATCCGGAGTGCATACC TTTCCCGCCGTGTTGCAGTCCAGCGG CCTGTACAGCCTGAGCTCCGTCGTGA CAGTGCCGTCCTCCTCCCTTGGAACC CAGACCTATATCTGCAACGTCAATCA CAAGCCCTCCAACACCAAAGTGGAC AAGAAGGTCGAACCCAAGTCCTGCG ACAAGACTCACACCTGTCCGCCTTGT CCAGCCCCTGAGCTGCTGGGTGGTCC GTCCGTGTTCCTCTTCCCGCCCAAGC	SEQ ID 1850	GACATCCAGATGACCCAGTCTCCTT CCACCCTGTCTGCATCTGTAGGAG ACAGAGTCACCATCACTTGTCGGG CCAGGCAGAGCATCAGTAACCGGT TGGCCTGGTATCAGCAGAAACCAG GGAGAGCCCCTAATGTCCTGATCT ATAAGGCGTCTACTTTAGCAAATG GGGTCCCATCAAGGTTCAGCGGCA GTGGATCTGGGACAGAATTCACTC TCACCATCAGCAGCCTGCAGCCTG ATGACTTTGCAACTTATTACTGCCA ACAGTATCAAAGTTACTGGACGTT CGGCCCAGGGACCAAGGTGGAAAT CAAACGTACTGTGGCTGCTCCCTCC GTGTTCATTTTTCCTCCGTCGGACG AACAGCTGAAGTCCGGAACCGCGT CCGTGGTCTGTCTCCTGAACAACTT CTATCCGCGCGAGGCGAAAGTGCA GTGGAAGGTCGACAACGCACTGCA GTCGGGAAACTCCCAGGAATCGGT GACCGAGCAGGACTCGAAGGACTC AACCTACTCATTGTCCTCCACCCTC ACCCTGAGCAAGGCCGATTACGAG AAGCATAAGGTCTACGCCTGCGAA GTGACCCACCAGGGCCTGAGCAGC CCAGTGACGAAGTCCTTCAACCGG GGAGAATGC

	CGAAGGACACTCTGATGATTTCACGC ACCCCGGAAGTCACTTGCGTGGTCGT GGACGTGTCGCACGAAGATCCCGAA GTGAAATTCAATTGGTACGTGGATGG GGTCGAAGTGCACAACGCCAAGACC AAGCCTAGGGAAGAACAGTACAACT CTACGTACCGGGTGGTGTCCGTGCTG ACCGTGCTGCACCAGGACTGGCTGA ACGGAAAGGAGTACAAGTGCAAAGT GTCAAACAAGGCTCTCCCTGCCCCTA TCGAAAAGACCATCAGCAAGGCCAA GGGTCAACCTAGGGAGCCCCAGGTC TATACTTTGCCGCCTAGCCGGGAAGA AATGACTAAGAACCAAGTGTCCCTG ACTTGCCTTGTCAAGGGCTTTTATCC GTCCGACATCGCCGTGGAGTGGGAG TCCAACGGACAACCGGAGAACAACT ACAAGACCACCCCACCGGTGCTCGA TTCCGATGGCTCCTTCTTCCTGTACTC CAAGCTGACTGTGGACAAGTCAAGA TGGCAGCAGGGAAACGTGTTCTCCTG CTCCGTGATGCACGAAGCGCTGCAC AACCATTACACCCAGAAATCACTGTC ACTTTCGCCGGGAAAA		
SEQ ID 1743	CAGGTGCAGCTGCAGGAGTCCGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCAACAATGCT GCTTGGAACTGGATCAGGCAGTCCCC ATCGAGAGGCCTTGAGTGGCTGGGA AGGACATTCTACAGGTCCAAGTGGT ATAATGACTATGCAGTTTCTGTGAAA AGTCGACTAACCGTCAACCCAGACA CATCCAAGAACCAGTTCTCCCTGCGG TTGAACTCTGTGAGTCCCGAGGACAC GGCTGTGTATTACTGTGCAAGAGGG GGAAGATATACCAAGGGAGGGTACT TTGACGACTGGGGCCAGGGAACCCT GGTGACCGTCTCCTCAGCATCCACCA AGGGGCCTTCCGTGTTCCCCCTGGCC CCTTCATCCAAGTCGACCTCTGGTGG AACCGCCGCACTCGGTTGCCTGGTCA AAGACTACTTCCCCGAGCCCGTGACT GTCTCGTGGAACTCGGGCGCCCTCAC ATCCGGAGTGCATACCTTTCCCGCCG TGTTGCAGTCCAGCGGCCTGTACAGC CTGAGCTCCGTCGTGACAGTGCCGTC CTCCTCCCTTGGAACCCAGACCTATA TCTGCAACGTCAATCACAAGCCCTCC AACACCAAAGTGGACAAGAAGGTCG AACCCAAGTCCTGCGACAAGACTCA CACCTGTCCGCCTTGTCCAGCCCCTG AGCTGCTGGGTGGTCCGTCCGTGTTC	SEQ ID 1851	GACATCCAGTTGACCCAGTCTCCA GCCACCCTGTCTTTGTCTCCAGGGG AAAGAGCCACCCTCTCCTGCAAGG CCAGTCAGAGTGTTAGTAGCTACTT AGCCTGGTACCAACAGAAACTTGG CCAGGCTCCCAGGCTCCTCATCTAT GATGCATCCAACAGGGCCACTGGC ATCCCAGCCAGGTTCAGTGCCAGT GGGTCTGGGACAGACTTCACTCTC ACCATCAGCAGCCTGCAGCCTGAA GATGTTGCAACTTATTACTGTCAAA AGTATAACAGTCCCCCTCGGACGT TCGGCCAGGGGACCAAGGTGGAAA TCAAACGTACTGTGGCTGCTCCCTC CGTGTTCATTTTTCCTCCGTCGGAC GAACAGCTGAAGTCCGGAACCGCG TCCGTGGTCTGTCTCCTGAACAACT TCTATCCGCGCGAGGCGAAAGTGC AGTGGAAGGTCGACAACGCACTGC AGTCGGGAAACTCCCAGGAATCGG TGACCGAGCAGGACTCGAAGGACT CAACCTACTCATTGTCCTCCACCCT CACCCTGAGCAAGGCCGATTACGA GAAGCATAAGGTCTACGCCTGCGA AGTGACCCACCAGGGCCTGAGCAG CCCAGTGACGAAGTCCTTCAACCG GGGAGAATGC

	CTCTTCCCGCCCAAGCCGAAGGACAC TCTGATGATTTCACGCACCCCGGAAG TCACTTGCGTGGTCGTGGACGTGTCG CACGAAGATCCCGAAGTGAAATTCA ATTGGTACGTGGATGGGGTCGAAGT GCACAACGCCAAGACCAAGCCTAGG GAAGAACAGTACAACTCTACGTACC GGGTGGTGTCCGTGCTGACCGTGCTG CACCAGGACTGGCTGAACGGAAAGG AGTACAAGTGCAAAGTGTCAAACAA GGCTCTCCCTGCCCCTATCGAAAAGA CCATCAGCAAGGCCAAGGGTCAACC TAGGGAGCCCCAGGTCTATACTTTGC CGCCTAGCCGGGAAGAAATGACTAA GAACCAAGTGTCCCTGACTTGCCTTG TCAAGGGCTTTTATCCGTCCGACATC GCCGTGGAGTGGGAGTCCAACGGAC AACCGGAGAACAACTACAAGACCAC CCCACCGGTGCTCGATTCCGATGGCT CCTTCTTCCTGTACTCCAAGCTGACT GTGGACAAGTCAAGATGGCAGCAGG GAAACGTGTTCTCCTGCTCCGTGATG CACGAAGCGCTGCACAACCATTACA CCCAGAAATCACTGTCACTTTCGCCG GGAAAA		
SEQ ID 1744	CAGGTCACCTTGAAGGAGTCTGGTCC TACGCTGGTGAAACCCACACAGACC CTCACGCTGACCTGCACCTTCTCTGG GTTCTCACTCAGCACTAGTGGAGTGG GTGTGGGCTGGATCCGTCAGCCCCCA GGAAAGGCCCTGGAGTGGCTTGCAC TCATTTATTGGGATGATGATAAGCGC TACAGCCCATCTCTGAAGAGCAGGCT CACCATCACCAAGGACACCTCCAAA AACCAGGTGGTCCTTACAATGACCA ACATGGACCCTGTGGACACAGCCAC ATATTACTGTGCACACAGATTGGATA GCAGTGGCCGTGGTGGTTACTTTGAC TACTGGGGCCAGGGCACCCTGGTCA CCGTCTCCTCAGCATCCACCAAGGGG CCTTCCGTGTTCCCCCTGGCCCCTTC ATCCAAGTCGACCTCTGGTGGAACCG CCGCACTCGGTTGCCTGGTCAAAGAC TACTTCCCCGAGCCCGTGACTGTCTC GTGGAACTCGGGCGCCCTCACATCCG GAGTGCATACCTTTCCCGCCGTGTTG CAGTCCAGCGGCCTGTACAGCCTGA GCTCCGTCGTGACAGTGCCGTCCTCC TCCCTTGGAACCCAGACCTATATCTG CAACGTCAATCACAAGCCCTCCAAC ACCAAAGTGGACAAGAAGGTCGAAC CCAAGTCCTGCGACAAGACTCACAC CTGTCCGCCTTGTCCAGCCCCTGAGC TGCTGGGTGGTCCGTCCGTGTTCCTC	SEQ ID 1852	GAAACGACACTCACGCAGTCTCCA GGCACCCTGTCTTTGTCTCCAGGGG AAAGGGTCAGCCTTTCCTGCAGGG CCAGTCAGAATGTTTACAGCAATTT CTTAGCCTGGTATCAACAGAGACC TGGCCAGGCTCCCAGTCTCCTCATC TATGGTGCCTCCAGCAGGGCCGCT GGCGTCCCAGACAGGTTCAGTGGC AGTGGGTCTGGGACAGACTTCGCT CTCACCATCAGCAGAGTGGAGCCT GAAGATTTTGCAGTCTATTACTGTC AACAATATGGAACCTCACCGATCA CCTTCGGCCAAGGGACACGACTGG AGATTAAACGTACTGTGGCTGCTC CCTCCGTGTTCATTTTTCCTCCGTC GGACGAACAGCTGAAGTCCGGAAC CGCGTCCGTGGTCTGTCTCCTGAAC AACTTCTATCCGCGCGAGGCGAAA GTGCAGTGGAAGGTCGACAACGCA CTGCAGTCGGGAAACTCCCAGGAA TCGGTGACCGAGCAGGACTCGAAG GACTCAACCTACTCATTGTCCTCCA CCCTCACCCTGAGCAAGGCCGATT ACGAGAAGCATAAGGTCTACGCCT GCGAAGTGACCCACCAGGGCCTGA GCAGCCCAGTGACGAAGTCCTTCA ACCGGGGAGAATGC

	TTCCCGCCCAAGCCGAAGGACACTCT GATGATTTCACGCACCCCGGAAGTCA CTTGCGTGGTCGTGGACGTGTCGCAC GAAGATCCCGAAGTGAAATTCAATT GGTACGTGGATGGGGTCGAAGTGCA CAACGCCAAGACCAAGCCTAGGGAA GAACAGTACAACTCTACGTACCGGG TGGTGTCCGTGCTGACCGTGCTGCAC CAGGACTGGCTGAACGGAAAGGAGT ACAAGTGCAAAGTGTCAAACAAGGC TCTCCCTGCCCCTATCGAAAAGACCA TCAGCAAGGCCAAGGGTCAACCTAG GGAGCCCCAGGTCTATACTTTGCCGC CTAGCCGGGAAGAAATGACTAAGAA CCAAGTGTCCCTGACTTGCCTTGTCA AGGGCTTTTATCCGTCCGACATCGCC GTGGAGTGGGAGTCCAACGGACAAC CGGAGAACAACTACAAGACCACCCC ACCGGTGCTCGATTCCGATGGCTCCT TCTTCCTGTACTCCAAGCTGACTGTG GACAAGTCAAGATGGCAGCAGGGAA ACGTGTTCTCCTGCTCCGTGATGCAC GAAGCGCTGCACAACCATTACACCC AGAAATCACTGTCACTTTCGCCGGGA AAA		
SEQ ID 1745	GAGGTGCAGCTGGTGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTACAGCCTCTG GATTCACCTTCAGTAGCTATGGCATG CACTGGGTCCGCCAGGCTCCAGGCA AGGGGCTGGAGTGGGTGGCAGTTAT ATCATATGATGGAAGTAATAAATACT ATGCAGACTCCGTGAAGGGCCGATT CACCATCTCCAGAGACAATTCCAAG AACACGCTGTATCTGCAAATGAACA GCCTGAGAGCTGAGGACACGGCTGT GTATTACTGTGCGAAAGAGTTGGTGG GTACCAGCTCTCCTTATTACTACTAC TACTACGGTATGGACGTCTGGGGCCA AGGGACAATGGTCACCGTCTCTTCAG CATCCACCAAGGGGCCTTCCGTGTTC CCCCTGGCCCCTTCATCCAAGTCGAC CTCTGGTGGAACCGCCGCACTCGGTT GCCTGGTCAAAGACTACTTCCCCGAG CCCGTGACTGTCTCGTGGAACTCGGG CGCCCTCACATCCGGAGTGCATACCT TTCCCGCCGTGTTGCAGTCCAGCGGC CTGTACAGCCTGAGCTCCGTCGTGAC AGTGCCGTCCTCCTCCCTTGGAACCC AGACCTATATCTGCAACGTCAATCAC AAGCCCTCCAACACCAAAGTGGACA AGAAGGTCGAACCCAAGTCCTGCGA CAAGACTCACACCTGTCCGCCTTGTC CAGCCCCTGAGCTGCTGGGTGGTCCG	SEQ ID 1853	GAAATTGTGCTGACTCAGTCTCCAC GCTCCTCACCCGTCACCCTTGGACA GCCGGCCTCCATCTCCTGTAGGTCT AGTCAAAGTCTCGAACACGGTGAT GGAAACACGTACTTGAGTTGGCTT CAGCAGAGGCCAGGCCAGCCTCCA AGACTCCTGATTTATAAGGTTTCTA ACCGGTTGTCTGGGGTCCCAGACA GATTCAGTGGCAGTGGGGCAGGGA CTGATTTCACACTGAAAATCAGCA GGGTGGAAGCTGAGGATGTCGGGG TTTATTACTGCATGCAAGGTATATA CTGGCCTCGAACCTTCGGCCAAGG GACACGACTGGAGATTAAACGTAC TGTGGCTGCTCCCTCCGTGTTCATT TTTCCTCCGTCGGACGAACAGCTG AAGTCCGGAACCGCGTCCGTGGTC TGTCTCCTGAACAACTTCTATCCGC GCGAGGCGAAAGTGCAGTGGAAG GTCGACAACGCACTGCAGTCGGGA AACTCCCAGGAATCGGTGACCGAG CAGGACTCGAAGGACTCAACCTAC TCATTGTCCTCCACCCTCACCCTGA GCAAGGCCGATTACGAGAAGCATA AGGTCTACGCCTGCGAAGTGACCC ACCAGGGCCTGAGCAGCCCAGTGA CGAAGTCCTTCAACCGGGGAGAAT GC

	TCCGTGTTCCTCTTCCCGCCCAAGCC GAAGGACACTCTGATGATTTCACGCA CCCCGGAAGTCACTTGCGTGGTCGTG GACGTGTCGCACGAAGATCCCGAAG TGAAATTCAATTGGTACGTGGATGGG GTCGAAGTGCACAACGCCAAGACCA AGCCTAGGGAAGAACAGTACAACTC TACGTACCGGGTGGTGTCCGTGCTGA CCGTGCTGCACCAGGACTGGCTGAA CGGAAAGGAGTACAAGTGCAAAGTG TCAAACAAGGCTCTCCCTGCCCCTAT CGAAAAGACCATCAGCAAGGCCAAG GGTCAACCTAGGGAGCCCCAGGTCT ATACTTTGCCGCCTAGCCGGGAAGA AATGACTAAGAACCAAGTGTCCCTG ACTTGCCTTGTCAAGGGCTTTTATCC GTCCGACATCGCCGTGGAGTGGGAG TCCAACGGACAACCGGAGAACAACT ACAAGACCACCCCACCGGTGCTCGA TTCCGATGGCTCCTTCTTCCTGTACTC CAAGCTGACTGTGGACAAGTCAAGA TGGCAGCAGGGAAACGTGTTCTCCTG CTCCGTGATGCACGAAGCGCTGCAC AACCATTACACCCAGAAATCACTGTC ACTTTCGCCGGGAAAA		
SEQ ID 1746	CAGCTGCAGCTGCAGGAGTCGGGGG GAGGCTTGGTCCAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCGTCAGTAGCAACTACATG AGCTGGGTCCGCCAGGCTCCAGGGA AGGGGCTGGAGTGGGTCTCAGTTATT TATAGCGGTGGTAGCACATACTACGC AGACTCCGTGAAGGGCAGATTCACC ATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTTCAAATGAACAGCCTG AGAGCCGAGGACACGGCTGTGTATT ACTGTGCGAGAGACTATTACTATGGT TCGGGGAGTTCTCCCTGGGGCCAGG GAACCCTGGTCACCGTCTCCTCAGCA TCCACCAAGGGGCCTTCCGTGTTCCC CCTGGCCCCTTCATCCAAGTCGACCT CTGGTGGAACCGCCGCACTCGGTTGC CTGGTCAAAGACTACTTCCCCGAGCC CGTGACTGTCTCGTGGAACTCGGGCG CCCTCACATCCGGAGTGCATACCTTT CCCGCCGTGTTGCAGTCCAGCGGCCT GTACAGCCTGAGCTCCGTCGTGACAG TGCCGTCCTCCTCCCTTGGAACCCAG ACCTATATCTGCAACGTCAATCACAA GCCCTCCAACACCAAAGTGGACAAG AAGGTCGAACCCAAGTCCTGCGACA AGACTCACACCTGTCCGCCTTGTCCA GCCCCTGAGCTGCTGGGTGGTCCGTC CGTGTTCCTCTTCCCGCCCAAGCCGA	SEQ ID 1854	GAAACGACACTCACGCAGTCTCCA GTCACCCTGTCTTTGTCTCCAGGGG ACAGAGCCACCCTCTCTTGCAGGG CCAGTCAGAGTGTTAGCAGCACCT CCTTAGCCTGGTACCAGCACAAAC CTGGCCAGGCTCCCAGGCTCCTCAT CTATGGTGCATCCAGGAGGGCCAC TGGCATCCCAGACAGGTTCAGTGG CAGTGGGTCTGGGACAGACTTCAC TCTCACCATCAACAGACTGGAGCC TGAAGATTTTGCAGTGTATTACTGT CAGCACTATGGTAGTTCACCTCCA ATCACCTTCGGCCAAGGGACACGA CTGGAGATTAAACGTACTGTGGCT GCTCCCTCCGTGTTCATTTTTCCTC CGTCGGACGAACAGCTGAAGTCCG GAACCGCGTCCGTGGTCTGTCTCCT GAACAACTTCTATCCGCGCGAGGC GAAAGTGCAGTGGAAGGTCGACAA CGCACTGCAGTCGGGAAACTCCCA GGAATCGGTGACCGAGCAGGACTC GAAGGACTCAACCTACTCATTGTC CTCCACCCTCACCCTGAGCAAGGC CGATTACGAGAAGCATAAGGTCTA CGCCTGCGAAGTGACCCACCAGGG CCTGAGCAGCCCAGTGACGAAGTC CTTCAACCGGGGAGAATGC

	AGGACACTCTGATGATTTCACGCACC CCGGAAGTCACTTGCGTGGTCGTGGA CGTGTCGCACGAAGATCCCGAAGTG AAATTCAATTGGTACGTGGATGGGGT CGAAGTGCACAACGCCAAGACCAAG CCTAGGGAAGAACAGTACAACTCTA CGTACCGGGTGGTGTCCGTGCTGACC GTGCTGCACCAGGACTGGCTGAACG GAAAGGAGTACAAGTGCAAAGTGTC AAACAAGGCTCTCCCTGCCCCTATCG AAAAGACCATCAGCAAGGCCAAGGG TCAACCTAGGGAGCCCCAGGTCTATA CTTTGCCGCCTAGCCGGGAAGAAAT GACTAAGAACCAAGTGTCCCTGACTT GCCTTGTCAAGGGCTTTTATCCGTCC GACATCGCCGTGGAGTGGGAGTCCA ACGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCCG ATGGCTCCTTCTTCCTGTACTCCAAG CTGACTGTGGACAAGTCAAGATGGC AGCAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACTT TCGCCGGGAAAA		
SEQ ID 1747	CAGGTGCAGCTACAGCAGTGGGGCG CAGGACTGTTGAAGCCTTCGGAGAC CCTGTCCCTCACCTGCGCTGTCTATG GTGGGTCCTTCAGTGGTTACTACTGG AGCTGGATCCGCCAGCCCCCAGGGA AGGGGCTGGAGTGGATTGGGGAAAT CAATCATAGTGGAAGCACCAACTAC AACCCGTCCCTCAAGAGTCGAGTCAC CATATCAGTAGACACGTCCAAGAAC CAGTTCTCCCTGAAGCTGAGCTCTGT GACCGCCGCGGACACGGCTGTGTATT ACTGTGCGAGAGGCCGGCCATATTGT AGTAGTACCAGCTGCTACCCAGAGT GGTTCGACCCCTGGGGCCAGGGAAC CCTGGTCACCGTCTCCTCAGCATCCA CCAAGGGGCCTTCCGTGTTCCCCCTG GCCCCTTCATCCAAGTCGACCTCTGG TGGAACCGCCGCACTCGGTTGCCTGG TCAAAGACTACTTCCCCGAGCCCGTG ACTGTCTCGTGGAACTCGGGCGCCCT CACATCCGGAGTGCATACCTTTCCCG CCGTGTTGCAGTCCAGCGGCCTGTAC AGCCTGAGCTCCGTCGTGACAGTGCC GTCCTCCTCCCTTGGAACCCAGACCT ATATCTGCAACGTCAATCACAAGCCC TCCAACACCAAAGTGGACAAGAAGG TCGAACCCAAGTCCTGCGACAAGAC TCACACCTGTCCGCCTTGTCCAGCCC CTGAGCTGCTGGGTGGTCCGTCCGTG	SEQ ID 1855	GAAACGACACTCACGCAGTCTCCA GCCACCCTGTCTGTGTCTCCAGGGG AAAGAGCCACCCTCTCCTGCAGGG CCAGTCAGAGTGTTGGCAGCAAAT TAGCCTGGTACCAGCAGAAACCTG GCCAGGCTCCCAGGCTCCTCATCTA TGGTGCATCCACCAGGGCCACTGG TGTCCCAGTCCGGTTCAGTGGCAGT GGGTCTGGGACAGAATTCACTCTC ACCATCAGCAGCCTGCAGTCTGAA GATTTTGCAGTTTATTACTGTCAGC AGTATAATAACTGGCCCCCGATCA CCTTCGGCCAAGGGACACGACTGG AGATTAAACGTACTGTGGCTGCTC CCTCCGTGTTCATTTTTCCTCCGTC GGACGAACAGCTGAAGTCCGGAAC CGCGTCCGTGGTCTGTCTCCTGAAC AACTTCTATCCGCGCGAGGCGAAA GTGCAGTGGAAGGTCGACAACGCA CTGCAGTCGGGAAACTCCCAGGAA TCGGTGACCGAGCAGGACTCGAAG GACTCAACCTACTCATTGTCCTCCA CCCTCACCCTGAGCAAGGCCGATT ACGAGAAGCATAAGGTCTACGCCT GCGAAGTGACCCACCAGGGCCTGA GCAGCCCAGTGACGAAGTCCTTCA ACCGGGGAGAATGC

	TTCCTCTTCCCGCCCAAGCCGAAGGA CACTCTGATGATTTCACGCACCCCGG AAGTCACTTGCGTGGTCGTGGACGTG TCGCACGAAGATCCCGAAGTGAAAT TCAATTGGTACGTGGATGGGGTCGA AGTGCACAACGCCAAGACCAAGCCT AGGGAAGAACAGTACAACTCTACGT ACCGGGTGGTGTCCGTGCTGACCGTG CTGCACCAGGACTGGCTGAACGGAA AGGAGTACAAGTGCAAAGTGTCAAA CAAGGCTCTCCCTGCCCCTATCGAAA AGACCATCAGCAAGGCCAAGGGTCA ACCTAGGGAGCCCCAGGTCTATACTT TGCCGCCTAGCCGGGAAGAAATGAC TAAGAACCAAGTGTCCCTGACTTGCC TTGTCAAGGGCTTTTATCCGTCCGAC ATCGCCGTGGAGTGGGAGTCCAACG GACAACCGGAGAACAACTACAAGAC CACCCCACCGGTGCTCGATTCCGATG GCTCCTTCTTCCTGTACTCCAAGCTG ACTGTGGACAAGTCAAGATGGCAGC AGGGAAACGTGTTCTCCTGCTCCGTG ATGCACGAAGCGCTGCACAACCATT ACACCCAGAAATCACTGTCACTTTCG CCGGGAAAA		
SEQ ID 1748	CAGGTCACCTTGAAGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTCAGTAGCTATGGCATG CACTGGGTCCGCCAGGCTCCAGGCA AGGGGCTGGAGTGGGTGGCAGTTAT ATCATATGATGGAAGTAATAAATACT ATGCAGACTCCGTGAAGGGCCGATT CACCATCTCCAGAGACAATTCCAAG AACACGCTGTATCTGCAAATGAACA GCCTGAGAGCTGAGGACACGGCTGT GTATTACTGTGCGAAATTAAGGGGTA TAGATTACTATGATAGTAGTGGTTAC CAACGGGGGTTTGACTACTGGGGCC AGGGAACCCTGGTCACCGTCTCCTCA GCATCCACCAAGGGGCCTTCCGTGTT CCCCCTGGCCCCTTCATCCAAGTCGA CCTCTGGTGGAACCGCCGCACTCGGT TGCCTGGTCAAAGACTACTTCCCCGA GCCCGTGACTGTCTCGTGGAACTCGG GCGCCCTCACATCCGGAGTGCATACC TTTCCCGCCGTGTTGCAGTCCAGCGG CCTGTACAGCCTGAGCTCCGTCGTGA CAGTGCCGTCCTCCTCCCTTGGAACC CAGACCTATATCTGCAACGTCAATCA CAAGCCCTCCAACACCAAAGTGGAC AAGAAGGTCGAACCCAAGTCCTGCG ACAAGACTCACACCTGTCCGCCTTGT CCAGCCCCTGAGCTGCTGGGTGGTCC	SEQ ID 1856	GAAATTGTGTTGACGCAGTCTCCA CTCTCCCTGCCCGTCACCCCTGGAG AGCCGGCCTCCATCTCCTGCAGGTC TAGTCAGAGCCTCCTGCATAGTAA TGGATACAACTATTTGGATTGGTAC CTGCAGAAGCCAGGGCAGTCTCCA CAGCTCCTGATCTATTTGGGTTCTA ATCGGGCCTCCGGGGTCCCTGACA GGTTCAGTGGCAGTGGATCAGGCA CAGATTTTACACTGAAAATCAGCA GAGTGGAGGCTGAGGATGTTGGGG TGTATTACTGCATGCAAACTCTTCA AACTCCGCTCACTTTCGGCGGAGG GACCAAAGTGGATATCAAACGTAC TGTGGCTGCTCCCTCCGTGTTCATT TTTCCTCCGTCGGACGAACAGCTG AAGTCCGGAACCGCGTCCGTGGTC TGTCTCCTGAACAACTTCTATCCGC GCGAGGCGAAAGTGCAGTGGAAG GTCGACAACGCACTGCAGTCGGGA AACTCCCAGGAATCGGTGACCGAG CAGGACTCGAAGGACTCAACCTAC TCATTGTCCTCCACCCTCACCCTGA GCAAGGCCGATTACGAGAAGCATA AGGTCTACGCCTGCGAAGTGACCC ACCAGGGCCTGAGCAGCCCAGTGA CGAAGTCCTTCAACCGGGGAGAAT GC

	GTCCGTGTTCCTCTTCCCGCCCAAGC CGAAGGACACTCTGATGATTTCACGC ACCCCGGAAGTCACTTGCGTGGTCGT GGACGTGTCGCACGAAGATCCCGAA GTGAAATTCAATTGGTACGTGGATGG GGTCGAAGTGCACAACGCCAAGACC AAGCCTAGGGAAGAACAGTACAACT CTACGTACCGGGTGGTGTCCGTGCTG ACCGTGCTGCACCAGGACTGGCTGA ACGGAAAGGAGTACAAGTGCAAAGT GTCAAACAAGGCTCTCCCTGCCCCTA TCGAAAAGACCATCAGCAAGGCCAA GGGTCAACCTAGGGAGCCCCAGGTC TATACTTTGCCGCCTAGCCGGGAAGA AATGACTAAGAACCAAGTGTCCCTG ACTTGCCTTGTCAAGGGCTTTTATCC GTCCGACATCGCCGTGGAGTGGGAG TCCAACGGACAACCGGAGAACAACT ACAAGACCACCCCACCGGTGCTCGA TTCCGATGGCTCCTTCTTCCTGTACTC CAAGCTGACTGTGGACAAGTCAAGA TGGCAGCAGGGAAACGTGTTCTCCTG CTCCGTGATGCACGAAGCGCTGCAC AACCATTACACCCAGAAATCACTGTC ACTTTCGCCGGGAAAA		
SEQ ID 1749	CAGGTGCAGCTGCAGGAGTCCGGCC CAGGACTGGTGAAGCCTTCGGAGAC CCTGTCCCTCACCTGCACTGTCTCTG GTGGCTCCATCAGTAGTTACTACTGG AGCTGGATCCGGCAGCCCCCAGGGA AGGGACTGGAGTGGATTGGCTATAT CTATTACACTGGGAGCACCAACTACA ACCCCTCCCTCAAGAGCCGAGTCACC ATATCAGTAGACACGTCCAAGAACC AGTTCTCCCTGAAGCTGAGCTCTGTG ACCACTGCGGACACGGCCGTGTATTA CTGTGCGAGAGGTGGGAGGGGGGAT GGGGCCGCTTTTGACATCTGGGGCCA AGGGACAATGGTCACCGTCTCTTCAG CATCCACCAAGGGGCCTTCCGTGTTC CCCCTGGCCCCTTCATCCAAGTCGAC CTCTGGTGGAACCGCCGCACTCGGTT GCCTGGTCAAAGACTACTTCCCCGAG CCCGTGACTGTCTCGTGGAACTCGGG CGCCCTCACATCCGGAGTGCATACCT TTCCCGCCGTGTTGCAGTCCAGCGGC CTGTACAGCCTGAGCTCCGTCGTGAC AGTGCCGTCCTCCTCCCTTGGAACCC AGACCTATATCTGCAACGTCAATCAC AAGCCCTCCAACACCAAAGTGGACA AGAAGGTCGAACCCAAGTCCTGCGA CAAGACTCACACCTGTCCGCCTTGTC CAGCCCCTGAGCTGCTGGGTGGTCCG TCCGTGTTCCTCTTCCCGCCCAAGCC	SEQ ID 1857	GATGTTGTGATGACTCAGTCTCCAG ACTCCCTGGCTGTGTCTCTGGGCGA GAGGGCCACCATCAACTGCAAGTC CAGCCAGAGTGTTTTATACAGCTCC AACAATAAGAACTACTTAGCTTGG TACCAGCAGAAACCAGGACAGCCT CCTAAGCTGCTCATTTACTGGGCAT CTACCCGGGAATCCGGGGTCCCTG ACCGATTCAGTGGCAGCGGGTCTG GGACAGATTTCACTCTCACCATCA GCAGCCTGCAGGCTGAAGATGTGG CAGTTTATTACTGTCAGCAATATTA TAGTAGTACTCCGTACACTTTTGGC CAGGGGACCAAGCTGGAGATCAAA CGTACTGTGGCTGCTCCCTCCGTGT TCATTTTTCCTCCGTCGGACGAACA GCTGAAGTCCGGAACCGCGTCCGT GGTCTGTCTCCTGAACAACTTCTAT CCGCGCGAGGCGAAAGTGCAGTGG AAGGTCGACAACGCACTGCAGTCG GGAAACTCCCAGGAATCGGTGACC GAGCAGGACTCGAAGGACTCAACC TACTCATTGTCCTCCACCCTCACCC TGAGCAAGGCCGATTACGAGAAGC ATAAGGTCTACGCCTGCGAAGTGA CCCACCAGGGCCTGAGCAGCCCAG TGACGAAGTCCTTCAACCGGGGAG AATGC

	GAAGGACACTCTGATGATTTCACGCA CCCCGGAAGTCACTTGCGTGGTCGTG GACGTGTCGCACGAAGATCCCGAAG TGAAATTCAATTGGTACGTGGATGGG GTCGAAGTGCACAACGCCAAGACCA AGCCTAGGGAAGAACAGTACAACTC TACGTACCGGGTGGTGTCCGTGCTGA CCGTGCTGCACCAGGACTGGCTGAA CGGAAAGGAGTACAAGTGCAAAGTG TCAAACAAGGCTCTCCCTGCCCCTAT CGAAAAGACCATCAGCAAGGCCAAG GGTCAACCTAGGGAGCCCCAGGTCT ATACTTTGCCGCCTAGCCGGGAAGA AATGACTAAGAACCAAGTGTCCCTG ACTTGCCTTGTCAAGGGCTTTTATCC GTCCGACATCGCCGTGGAGTGGGAG TCCAACGGACAACCGGAGAACAACT ACAAGACCACCCCACCGGTGCTCGA TTCCGATGGCTCCTTCTTCCTGTACTC CAAGCTGACTGTGGACAAGTCAAGA TGGCAGCAGGGAAACGTGTTCTCCTG CTCCGTGATGCACGAAGCGCTGCAC AACCATTACACCCAGAAATCACTGTC ACTTTCGCCGGGAAAA		
SEQ ID 1750	CAGGTGCAGCTGGTGCAATCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCGTCTG GATTCACCTTCAGCAGCTCTGCCATG CACTGGGTCCGCCAGGCTCCAGGCA AGGGACTGGAGTGGGTGGCAATGAT TTGGCATGATGAGAGTAAGAAATAC TATGCAGACTCCGTGAAGGGCCGATT CACTATCTCCAGAGACAATTCCAAGA ACACGCTGTATCTGCAAATGAACAG CCTGAGAGCTGAGGACACGGCTGTG TATTACTGTGCGAGACCCCCCGACGG TGGTAACTCCGGTCGCTGGTACTTCG ATCTCTGGGGCCGTGGCACCCTGGTC ACCGTCTCCTCAGCATCCACCAAGGG GCCTTCCGTGTTCCCCCTGGCCCCTT CATCCAAGTCGACCTCTGGTGGAACC GCCGCACTCGGTTGCCTGGTCAAAGA CTACTTCCCCGAGCCCGTGACTGTCT CGTGGAACTCGGGCGCCCTCACATCC GGAGTGCATACCTTTCCCGCCGTGTT GCAGTCCAGCGGCCTGTACAGCCTG AGCTCCGTCGTGACAGTGCCGTCCTC CTCCCTTGGAACCCAGACCTATATCT GCAACGTCAATCACAAGCCCTCCAA CACCAAAGTGGACAAGAAGGTCGAA CCCAAGTCCTGCGACAAGACTCACA CCTGTCCGCCTTGTCCAGCCCCTGAG CTGCTGGGTGGTCCGTCCGTGTTCCT	SEQ ID 1858	GATATTGTGATGACCCACACTCCCC TCTCTCTGTCCGTCACCCCTGGACA GCCGGCCTCCATCTCCTGCAAGTCT AGTCAGAGCCTCCTGGGTGGTGAT GGAAAGACCTATTTGTATTGGTAC CTGCAGAAGCCAGGCCAGCCTCCA CAGCTCCTGCTCTATGAAGTTTCCA ACCGATTCTCTGGAGTGCCAGATA GGTTCAGTGGCAGCGGGGCAGCGA CAGATTTCACACTGAAAATCAGCA GGGTGGAAGCTGAGGATGTCGGGG TTTATTACTGCATGCAATCTACACA ATTTCCGTGGACGTTCGGCCAAGG GACCAAGGTGGAGATCAAACGTAC TGTGGCTGCTCCCTCCGTGTTCATT TTTCCTCCGTCGGACGAACAGCTG AAGTCCGGAACCGCGTCCGTGGTC TGTCTCCTGAACAACTTCTATCCGC GCGAGGCGAAAGTGCAGTGGAAG GTCGACAACGCACTGCAGTCGGGA AACTCCCAGGAATCGGTGACCGAG CAGGACTCGAAGGACTCAACCTAC TCATTGTCCTCCACCCTCACCCTGA GCAAGGCCGATTACGAGAAGCATA AGGTCTACGCCTGCGAAGTGACCC ACCAGGGCCTGAGCAGCCCAGTGA CGAAGTCCTTCAACCGGGGAGAAT GC

	CTTCCCGCCCAAGCCGAAGGACACTC TGATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGCA CGAAGATCCCGAAGTGAAATTCAAT TGGTACGTGGATGGGGTCGAAGTGC ACAACGCCAAGACCAAGCCTAGGGA AGAACAGTACAACTCTACGTACCGG GTGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGAG TACAAGTGCAAAGTGTCAAACAAGG CTCTCCCTGCCCCTATCGAAAAGACC ATCAGCAAGGCCAAGGGTCAACCTA GGGAGCCCCAGGTCTATACTTTGCCG CCTAGCCGGGAAGAAATGACTAAGA ACCAAGTGTCCCTGACTTGCCTTGTC AAGGGCTTTTATCCGTCCGACATCGC CGTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTCC TTCTTCCTGTACTCCAAGCTGACTGT GGACAAGTCAAGATGGCAGCAGGGA AACGTGTTCTCCTGCTCCGTGATGCA CGAAGCGCTGCACAACCATTACACC CAGAAATCACTGTCACTTTCGCCGGG AAAA		
SEQ ID 1751	CAGATGCAGCTGGTGCAATCTGGGG GAGGCTTGGTACAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTAGCAGCTATGCCATG AGCTGGGTCCGCCAGGCTCCAGGGA AGGGGCTGGAGTGGGTCTCAGCTATT AGTGGTAGTGGTGGTAGCACATACT ACGCAGACTCCGTGAAGGGCCGGTT CACCATCTCCAGAGACAATTCCAAG AACACGCTGTATCTGCAAATGAACA GCCTGAGAGCCGAGGACACGGCCGT ATATTACTGTGCGAAAGACAAGAAC GTCCGAAAACATGACTACGGTGACC ACCCCTACGGGGGGTACTTTGACTAC TGGGGCCAGGGCACCCTGGTGACCG TCTCCTCAGCATCCACCAAGGGGCCT TCCGTGTTCCCCCTGGCCCCTTCATC CAAGTCGACCTCTGGTGGAACCGCC GCACTCGGTTGCCTGGTCAAAGACTA CTTCCCCGAGCCCGTGACTGTCTCGT GGAACTCGGGCGCCCTCACATCCGG AGTGCATACCTTTCCCGCCGTGTTGC AGTCCAGCGGCCTGTACAGCCTGAG CTCCGTCGTGACAGTGCCGTCCTCCT CCCTTGGAACCCAGACCTATATCTGC AACGTCAATCACAAGCCCTCCAACA CCAAAGTGGACAAGAAGGTCGAACC CAAGTCCTGCGACAAGACTCACACCT GTCCGCCTTGTCCAGCCCCTGAGCTG	SEQ ID 1859	GAAACGACACTCACGCAGTCTCCA GGCACCCTGTCTTTGTCTGCAGGGG AAAGAGCCACCCTCTCCTGCAGGG CCAGTCAGAGTGTTAGCAGCAGCT ACTTAGCCTGGTACCAGCAGAAAC CTGGCCAGGCTCCCAGGCTCCTCAT CTATGCTGCATCCTACAGGGCCACT GGCATCCCAGACAGGTTCAGTGGC CGTGGGTCTGGGACAGAGTTCACT CTCACCATCAGCAGCCTGCAGTCT GAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCCTCCCA TCACCTTCGGCCAAGGGACACGAC TGGAGATTAAACGTACTGTGGCTG CTCCCTCCGTGTTCATTTTTCCTCC GTCGGACGAACAGCTGAAGTCCGG AACCGCGTCCGTGGTCTGTCTCCTG AACAACTTCTATCCGCGCGAGGCG AAAGTGCAGTGGAAGGTCGACAAC GCACTGCAGTCGGGAAACTCCCAG GAATCGGTGACCGAGCAGGACTCG AAGGACTCAACCTACTCATTGTCCT CCACCCTCACCCTGAGCAAGGCCG ATTACGAGAAGCATAAGGTCTACG CCTGCGAAGTGACCCACCAGGGCC TGAGCAGCCCAGTGACGAAGTCCT TCAACCGGGGAGAATGC

	CTGGGTGGTCCGTCCGTGTTCCTCTT CCCGCCCAAGCCGAAGGACACTCTG ATGATTTCACGCACCCCGGAAGTCAC TTGCGTGGTCGTGGACGTGTCGCACG AAGATCCCGAAGTGAAATTCAATTG GTACGTGGATGGGGTCGAAGTGCAC AACGCCAAGACCAAGCCTAGGGAAG AACAGTACAACTCTACGTACCGGGT GGTGTCCGTGCTGACCGTGCTGCACC AGGACTGGCTGAACGGAAAGGAGTA CAAGTGCAAAGTGTCAAACAAGGCT CTCCCTGCCCCTATCGAAAAGACCAT CAGCAAGGCCAAGGGTCAACCTAGG GAGCCCCAGGTCTATACTTTGCCGCC TAGCCGGGAAGAAATGACTAAGAAC CAAGTGTCCCTGACTTGCCTTGTCAA GGGCTTTTATCCGTCCGACATCGCCG TGGAGTGGGAGTCCAACGGACAACC GGAGAACAACTACAAGACCACCCCA CCGGTGCTCGATTCCGATGGCTCCTT CTTCCTGTACTCCAAGCTGACTGTGG ACAAGTCAAGATGGCAGCAGGGAAA CGTGTTCTCCTGCTCCGTGATGCACG AAGCGCTGCACAACCATTACACCCA GAAATCACTGTCACTTTCGCCGGGAA AA		
SEQ ID 1752	GAGGTCCAGCTGGTACAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTTTCCTGCAAGGCTTCTG GATACACCTTCACTAGCTATGCTATG CATTGGGTGCGCCAGGCCCCCGGAC AAAGGCTTGAGTGGATGGGATGGAT CAACGCTGGCAATGGTAACACAAAA TATTCACAGAAGTTCCAGGGCAGAG TCACCATTACCAGGGACACATCCGCG AGCACAGCCTACATGGAGCTGAGCA GCCTGAGATCTGAAGACACGGCTGT GTATTACTGTGCGAGAGTGGCGGGA GCTACTTCCCTATGGTACTGGGGCCA GGGCACCCTGGTCACCGTCTCCTCAG CATCCACCAAGGGGCCTTCCGTGTTC CCCCTGGCCCCTTCATCCAAGTCGAC CTCTGGTGGAACCGCCGCACTCGGTT GCCTGGTCAAAGACTACTTCCCCGAG CCCGTGACTGTCTCGTGGAACTCGGG CGCCCTCACATCCGGAGTGCATACCT TTCCCGCCGTGTTGCAGTCCAGCGGC CTGTACAGCCTGAGCTCCGTCGTGAC AGTGCCGTCCTCCTCCCTTGGAACCC AGACCTATATCTGCAACGTCAATCAC AAGCCCTCCAACACCAAAGTGGACA AGAAGGTCGAACCCAAGTCCTGCGA CAAGACTCACACCTGTCCGCCTTGTC CAGCCCCTGAGCTGCTGGGTGGTCCG TCCGTGTTCCTCTTCCCGCCCAAGCC	SEQ ID 1860	GATGTTGTGATGACTCAGTCTCCAG CCACCCTGTCTGTGTCTCCAGGGGA AAGAGCCACCCTCTCCTGCAGGGC CAGTCAGAGTGTTAGCAGCAACTT AGCCTGGTACCAGCAGAAACCTGG CCAGGCTCCCAGGCTCCTCATCTAT GATGCATCCACCAGGGCCACTGGT ATCCCAGCCAGGTTCAGTGGCAGT GGGTCTGGGACAGAGTTCACTCTC ACCATCAGCAGCCTGCAGTCTGAA GATTTTGCAGTTTATTACTGTCAGC ACTATAATAACTGGCCTCATACCTT CGGCCAAGGGACCAAGCTGGAGAT CAAACGTACTGTGGCTGCTCCCTCC GTGTTCATTTTTCCTCCGTCGGACG AACAGCTGAAGTCCGGAACCGCGT CCGTGGTCTGTCTCCTGAACAACTT CTATCCGCGCGAGGCGAAAGTGCA GTGGAAGGTCGACAACGCACTGCA GTCGGGAAACTCCCAGGAATCGGT GACCGAGCAGGACTCGAAGGACTC AACCTACTCATTGTCCTCCACCCTC ACCCTGAGCAAGGCCGATTACGAG AAGCATAAGGTCTACGCCTGCGAA GTGACCCACCAGGGCCTGAGCAGC CCAGTGACGAAGTCCTTCAACCGG GGAGAATGC

	GAAGGACACTCTGATGATTTCACGCA CCCCGGAAGTCACTTGCGTGGTCGTG GACGTGTCGCACGAAGATCCCGAAG TGAAATTCAATTGGTACGTGGATGGG GTCGAAGTGCACAACGCCAAGACCA AGCCTAGGGAAGAACAGTACAACTC TACGTACCGGGTGGTGTCCGTGCTGA CCGTGCTGCACCAGGACTGGCTGAA CGGAAAGGAGTACAAGTGCAAAGTG TCAAACAAGGCTCTCCCTGCCCCTAT CGAAAAGACCATCAGCAAGGCCAAG GGTCAACCTAGGGAGCCCCAGGTCT ATACTTTGCCGCCTAGCCGGGAAGA AATGACTAAGAACCAAGTGTCCCTG ACTTGCCTTGTCAAGGGCTTTTATCC GTCCGACATCGCCGTGGAGTGGGAG TCCAACGGACAACCGGAGAACAACT ACAAGACCACCCCACCGGTGCTCGA TTCCGATGGCTCCTTCTTCCTGTACTC CAAGCTGACTGTGGACAAGTCAAGA TGGCAGCAGGGAAACGTGTTCTCCTG CTCCGTGATGCACGAAGCGCTGCAC AACCATTACACCCAGAAATCACTGTC ACTTTCGCCGGGAAAA		
SEQ ID 1753	CAGGTACAGCTGCAGCAGTCAGGTC CAGGACTGGTGAAGCCCTCGCAGAG CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCAACAGTGCT GCTTGGAACTGGATCAGGCAGTCCCC ATCGAGAGGCCTTGAGTGGCTGGGA AGGACATACTACAGGTCCAAGTGGT ATAATGATTATGCAGTATCTGTGAAG AGTCGAATAACCATCAAACCAGACA CATCCAAGAACCAGTTCTCCCTGCAG CTGAACTCTGTGACTCCCGAGGACAC GGCTGTGTATTACTGTACAAGGCTAG CTAATTCCGACGGTGTGGACGTCTGG GGCCAAGGGACAATGGTCACCGTCT CCTCAGCATCCACCAAGGGGCCTTCC GTGTTCCCCCTGGCCCCTTCATCCAA GTCGACCTCTGGTGGAACCGCCGCAC TCGGTTGCCTGGTCAAAGACTACTTC CCCGAGCCCGTGACTGTCTCGTGGAA CTCGGGCGCCCTCACATCCGGAGTGC ATACCTTTCCCGCCGTGTTGCAGTCC AGCGGCCTGTACAGCCTGAGCTCCGT CGTGACAGTGCCGTCCTCCTCCCTTG GAACCCAGACCTATATCTGCAACGTC AATCACAAGCCCTCCAACACCAAAG TGGACAAGAAGGTCGAACCCAAGTC CTGCGACAAGACTCACACCTGTCCGC CTTGTCCAGCCCCTGAGCTGCTGGGT GGTCCGTCCGTGTTCCTCTTCCCGCC	SEQ ID 1861	GAAACGACACTCACGCAGTCTCCA GGCACCCTGTCTTTGTCTCCAGGGG AAAGAGCCACCCTCTCCTGCAGGG CCAGTCAGAGTGTTAGCAGCAACT CCTTAGCCTGGTACCAGCAGAAAC CTGGCCAGGCTCCCAGGCTCCTCAT CTATGGTGCATCCAGCAGGGCCTC TGGCATCCCAGACAGGTTCAATGG CAGTGGGTCTGGGACAGACTTCAC TCTCACCATCAATAGGCTGGAGCC TGAAGACTTTGCAGTGTATTACTGT CAGCAGTATGGTAACTCACAGACC TTCGGCCAAGGGACACGACTGGAG ATTAAACGTACTGTGGCTGCTCCCT CCGTGTTCATTTTTCCTCCGTCGGA CGAACAGCTGAAGTCCGGAACCGC GTCCGTGGTCTGTCTCCTGAACAAC TTCTATCCGCGCGAGGCGAAAGTG CAGTGGAAGGTCGACAACGCACTG CAGTCGGGAAACTCCCAGGAATCG GTGACCGAGCAGGACTCGAAGGAC TCAACCTACTCATTGTCCTCCACCC TCACCCTGAGCAAGGCCGATTACG AGAAGCATAAGGTCTACGCCTGCG AAGTGACCCACCAGGGCCTGAGCA GCCCAGTGACGAAGTCCTTCAACC GGGGAGAATGC

	CAAGCCGAAGGACACTCTGATGATTT CACGCACCCCGGAAGTCACTTGCGTG GTCGTGGACGTGTCGCACGAAGATC CCGAAGTGAAATTCAATTGGTACGTG GATGGGGTCGAAGTGCACAACGCCA AGACCAAGCCTAGGGAAGAACAGTA CAACTCTACGTACCGGGTGGTGTCCG TGCTGACCGTGCTGCACCAGGACTGG CTGAACGGAAAGGAGTACAAGTGCA AAGTGTCAAACAAGGCTCTCCCTGCC CCTATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTATACTTTGCCGCCTAGCCGGG AAGAAATGACTAAGAACCAAGTGTC CCTGACTTGCCTTGTCAAGGGCTTTT ATCCGTCCGACATCGCCGTGGAGTGG GAGTCCAACGGACAACCGGAGAACA ACTACAAGACCACCCCACCGGTGCTC GATTCCGATGGCTCCTTCTTCCTGTA CTCCAAGCTGACTGTGGACAAGTCA AGATGGCAGCAGGGAAACGTGTTCT CCTGCTCCGTGATGCACGAAGCGCTG CACAACCATTACACCCAGAAATCACT GTCACTTTCGCCGGGAAAA		
SEQ ID 1754	CAGGTACAGCTGCAGCAGTCAGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCGACAGTGCT GTTTGGACCTGGATCAGGCAGTCCCC ATCGAGAGGCCTTGAGTGGCTGGGA AGGACATACTACAAGTCGAAGTGGT ATAATGATTATGCAGCATCTGTGAAA AGTCGAATAACCATCAACCCAGACA CATCCAAGAACCAGTTCTCCCTGCAC CTGAACTCTGTGACTCCCGAGGACAC GGCTGTGTATTACTGTGCAAGAGGTG TAACCCGGACCTTTGACTACTGGGGC CAGGGGACCACGGTCACCGTCTCCTC AGCATCCACCAAGGGGCCTTCCGTGT TCCCCCTGGCCCCTTCATCCAAGTCG ACCTCTGGTGGAACCGCCGCACTCGG TTGCCTGGTCAAAGACTACTTCCCCG AGCCCGTGACTGTCTCGTGGAACTCG GGCGCCCTCACATCCGGAGTGCATAC CTTTCCCGCCGTGTTGCAGTCCAGCG GCCTGTACAGCCTGAGCTCCGTCGTG ACAGTGCCGTCCTCCTCCCTTGGAAC CCAGACCTATATCTGCAACGTCAATC ACAAGCCCTCCAACACCAAAGTGGA CAAGAAGGTCGAACCCAAGTCCTGC GACAAGACTCACACCTGTCCGCCTTG TCCAGCCCCTGAGCTGCTGGGTGGTC CGTCCGTGTTCCTCTTCCCGCCCAAG	SEQ ID 1862	GATGTTGTGATGACTCAGTCTCCAG CCACCCTGTCTGTGTCTCCAGGGGA AAGAGCCACCCTCTCCTGCAGGGC CAGTCAGAGTGTTAGCAGCAACTT AGCCTGGTACCAGCAGAAACCTGG CCAGGCTCCCAGGCTCCTCATCTAT GGTGCATCCACCAGGGCCACTGGT ATCCCAGCCAGGTTCAGTGGCAGT GGGTCTGGGACAGAGTTCACTCTC ACCATCAGCAGCCTGCAGTCTGAA GATTTTGCAGTTTATTACTGTCAGC AGTATAATAACTGGCCCCGGACGT TCGGCCAAGGGACCAAGCTGGAGA TCAAACGTACTGTGGCTGCTCCCTC CGTGTTCATTTTTCCTCCGTCGGAC GAACAGCTGAAGTCCGGAACCGCG TCCGTGGTCTGTCTCCTGAACAACT TCTATCCGCGCGAGGCGAAAGTGC AGTGGAAGGTCGACAACGCACTGC AGTCGGGAAACTCCCAGGAATCGG TGACCGAGCAGGACTCGAAGGACT CAACCTACTCATTGTCCTCCACCCT CACCCTGAGCAAGGCCGATTACGA GAAGCATAAGGTCTACGCCTGCGA AGTGACCCACCAGGGCCTGAGCAG CCCAGTGACGAAGTCCTTCAACCG GGGAGAATGC

	CCGAAGGACACTCTGATGATTTCACG CACCCCGGAAGTCACTTGCGTGGTCG TGGACGTGTCGCACGAAGATCCCGA AGTGAAATTCAATTGGTACGTGGATG GGGTCGAAGTGCACAACGCCAAGAC CAAGCCTAGGGAAGAACAGTACAAC TCTACGTACCGGGTGGTGTCCGTGCT GACCGTGCTGCACCAGGACTGGCTG AACGGAAAGGAGTACAAGTGCAAAG TGTCAAACAAGGCTCTCCCTGCCCCT ATCGAAAAGACCATCAGCAAGGCCA AGGGTCAACCTAGGGAGCCCCAGGT CTATACTTTGCCGCCTAGCCGGGAAG AAATGACTAAGAACCAAGTGTCCCT GACTTGCCTTGTCAAGGGCTTTTATC CGTCCGACATCGCCGTGGAGTGGGA GTCCAACGGACAACCGGAGAACAAC TACAAGACCACCCCACCGGTGCTCG ATTCCGATGGCTCCTTCTTCCTGTACT CCAAGCTGACTGTGGACAAGTCAAG ATGGCAGCAGGGAAACGTGTTCTCCT GCTCCGTGATGCACGAAGCGCTGCA CAACCATTACACCCAGAAATCACTGT CACTTTCGCCGGGAAAA		
SEQ ID 1755	CAGCTGCAGCTGCAGGAGTCGGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCAACAGTGCT GCTTGGAACTGGATCAGGCAGTCCCC ATCGAGAGGCCTTGAGTGGCTGGGA AGGACATACTACAGGTCCAAGTGGT ATAATGATTATGCAGTATCTGTGAAA AGTCGAATAACCATCAACCCAGACA CATCCAAGAACCAGTTCTCCCTGCAG CTGAACTCTGTGACTCCCGAGGACAC GGCTGTGTATTACTGTGCAGAAGGCA ATGGGCCGTTCGACCCCTGGGGCCA GGGAACCCTGGTGACCGTCTCCTCAG CATCCACCAAGGGGCCTTCCGTGTTC CCCCTGGCCCCTTCATCCAAGTCGAC CTCTGGTGGAACCGCCGCACTCGGTT GCCTGGTCAAAGACTACTTCCCCGAG CCCGTGACTGTCTCGTGGAACTCGGG CGCCCTCACATCCGGAGTGCATACCT TTCCCGCCGTGTTGCAGTCCAGCGGC CTGTACAGCCTGAGCTCCGTCGTGAC AGTGCCGTCCTCCTCCCTTGGAACCC AGACCTATATCTGCAACGTCAATCAC AAGCCCTCCAACACCAAAGTGGACA AGAAGGTCGAACCCAAGTCCTGCGA CAAGACTCACACCTGTCCGCCTTGTC CAGCCCCTGAGCTGCTGGGTGGTCCG TCCGTGTTCCTCTTCCCGCCCAAGCC	SEQ ID 1863	GATGTTGTGATGACTCAGTCTCCAC TCTCCCTGCCCGTCACCCTTGGACA GCCGGCCTCCATCTCCTGCAGGTCT AGTCAAAGCCTCGTATACAGTGAT GGAAACACCTACTTGAATTGGTTTC AGCAGAGGCCAGGCCAATCTCCAA GGCGCCTAATTTATAAGGTTTCTAA CCGGGACTCTGGGGTCCCAGACAG ATTCAGCGGCAGTGGGTCAGGCAC TGATTTCACACTGAAAATCAGCAG GGTGGAGGCTGAGGATGTTGGGGT TTATTACTGCATGCAAGGTACACAT TGGCCTCGGACTTTCGGCGGAGGG ACCAAGCTGGAGATCAAACGTACT GTGGCTGCTCCCTCCGTGTTCATTT TTCCTCCGTCGGACGAACAGCTGA AGTCCGGAACCGCGTCCGTGGTCT GTCTCCTGAACAACTTCTATCCGCG CGAGGCGAAAGTGCAGTGGAAGGT CGACAACGCACTGCAGTCGGGAAA CTCCCAGGAATCGGTGACCGAGCA GGACTCGAAGGACTCAACCTACTC ATTGTCCTCCACCCTCACCCTGAGC AAGGCCGATTACGAGAAGCATAAG GTCTACGCCTGCGAAGTGACCCAC CAGGGCCTGAGCAGCCCAGTGACG AAGTCCTTCAACCGGGGAGAATGC

	GAAGGACACTCTGATGATTTCACGCA CCCCGGAAGTCACTTGCGTGGTCGTG GACGTGTCGCACGAAGATCCCGAAG TGAAATTCAATTGGTACGTGGATGGG GTCGAAGTGCACAACGCCAAGACCA AGCCTAGGGAAGAACAGTACAACTC TACGTACCGGGTGGTGTCCGTGCTGA CCGTGCTGCACCAGGACTGGCTGAA CGGAAAGGAGTACAAGTGCAAAGTG TCAAACAAGGCTCTCCCTGCCCCTAT CGAAAAGACCATCAGCAAGGCCAAG GGTCAACCTAGGGAGCCCCAGGTCT ATACTTTGCCGCCTAGCCGGGAAGA AATGACTAAGAACCAAGTGTCCCTG ACTTGCCTTGTCAAGGGCTTTTATCC GTCCGACATCGCCGTGGAGTGGGAG TCCAACGGACAACCGGAGAACAACT ACAAGACCACCCCACCGGTGCTCGA TTCCGATGGCTCCTTCTTCCTGTACTC CAAGCTGACTGTGGACAAGTCAAGA TGGCAGCAGGGAAACGTGTTCTCCTG CTCCGTGATGCACGAAGCGCTGCAC AACCATTACACCCAGAAATCACTGTC ACTTTCGCCGGGAAAA		
SEQ ID 1756	CAGATCACCTTGAAGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGTAGCCTCTG GATTCACCTTCAGTACCTATCCCATG CACTGGGTCCGCCAGGCTCCAGGCA AGGGGCTGGAGTGGGTGGCAGTTAT ATCATATGATGGACGTAATGAATACT ACGCAGACTCCGTGAAGGGCCGATT CACCATCTCCAGAGACAATTCCAAA AACACGCTGTATCTGCAAATGAACA GTCTGCGAGCTGAAGACACGGCTGT CTATTATTGTGCGACTCGGGATACAC CTTTGGTTGGGGTTTCGATATACTGG GGCCAGGGCACCCTGGTCACCGTCTC CTCAGCATCCACCAAGGGGCCTTCCG TGTTCCCCCTGGCCCCTTCATCCAAG TCGACCTCTGGTGGAACCGCCGCACT CGGTTGCCTGGTCAAAGACTACTTCC CCGAGCCCGTGACTGTCTCGTGGAAC TCGGGCGCCCTCACATCCGGAGTGCA TACCTTTCCCGCCGTGTTGCAGTCCA GCGGCCTGTACAGCCTGAGCTCCGTC GTGACAGTGCCGTCCTCCTCCCTTGG AACCCAGACCTATATCTGCAACGTCA ATCACAAGCCCTCCAACACCAAAGT GGACAAGAAGGTCGAACCCAAGTCC TGCGACAAGACTCACACCTGTCCGCC TTGTCCAGCCCCTGAGCTGCTGGGTG GTCCGTCCGTGTTCCTCTTCCCGCCC	SEQ ID 1864	GACATCCAGATGACCCAGTCTCCTT CCACCCTGTCTGCATCTGTAGGAG ACAGAGTCACCATCACTTGCCGGG CCAGTCAGAGTATTAGTAGGTGGT TGGCCTGGTATCAGCAGAAGCCAG GGAAAGCCCCTAAGCTCCTGATCT ATAAGGCGTCTACTATAAAAAGTG GGGTCCCATCAAGATTCAGCGCCA GTGGATCTGGGACAGAATTCACTC TCACCATCAGCAGCCTGCAGCCTG AAGATTTTGCAACTTATTACTGCCA ACACTATAAAAGTGATTCCCGGAC GTTCGGCCAAGGGACCAAGGTGGA AATCAAACGTACTGTGGCTGCTCC CTCCGTGTTCATTTTTCCTCCGTCG GACGAACAGCTGAAGTCCGGAACC GCGTCCGTGGTCTGTCTCCTGAACA ACTTCTATCCGCGCGAGGCGAAAG TGCAGTGGAAGGTCGACAACGCAC TGCAGTCGGGAAACTCCCAGGAAT CGGTGACCGAGCAGGACTCGAAGG ACTCAACCTACTCATTGTCCTCCAC CCTCACCCTGAGCAAGGCCGATTA CGAGAAGCATAAGGTCTACGCCTG CGAAGTGACCCACCAGGGCCTGAG CAGCCCAGTGACGAAGTCCTTCAA CCGGGGAGAATGC

	AAGCCGAAGGACACTCTGATGATTTC ACGCACCCCGGAAGTCACTTGCGTG GTCGTGGACGTGTCGCACGAAGATC CCGAAGTGAAATTCAATTGGTACGTG GATGGGGTCGAAGTGCACAACGCCA AGACCAAGCCTAGGGAAGAACAGTA CAACTCTACGTACCGGGTGGTGTCCG TGCTGACCGTGCTGCACCAGGACTGG CTGAACGGAAAGGAGTACAAGTGCA AAGTGTCAAACAAGGCTCTCCCTGCC CCTATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTATACTTTGCCGCCTAGCCGGG AAGAAATGACTAAGAACCAAGTGTC CCTGACTTGCCTTGTCAAGGGCTTTT ATCCGTCCGACATCGCCGTGGAGTGG GAGTCCAACGGACAACCGGAGAACA ACTACAAGACCACCCCACCGGTGCTC GATTCCGATGGCTCCTTCTTCCTGTA CTCCAAGCTGACTGTGGACAAGTCA AGATGGCAGCAGGGAAACGTGTTCT CCTGCTCCGTGATGCACGAAGCGCTG CACAACCATTACACCCAGAAATCACT GTCACTTTCGCCGGGAAAA		
SEQ ID 1757	CAGATGCAGCTGGTGCAATCTGGGG GAGGCCTGGTCAAGGCTGGGGGGTC CCTGAGACTCTCCTGTTCAGCCTCTG GATTCACCTTCAGTAGCTATGCTATG CACTGGGTCCGCCAGGCTCCAGGGA AGGGACTGGAATATGTTTCAGCTATT AGTAGTAATGGGGGTAGCACATACT ACGCAGACTCAGTGAAGGGCAGATT CACCATCTCCAGAGACAATTCCAAG AACACGCTGTATCTTCAAATGAGCAG TCTGAGAGCTGAGGACACGGCTGTG TATTACTGTGTGAATCGGGCGGGTTA CGGTGACTACAGACACTTCCAGCACT GGGGCCAGGGCACCCTGGTCACCGT CTCCTCAGCATCCACCAAGGGGCCTT CCGTGTTCCCCCTGGCCCCTTCATCC AAGTCGACCTCTGGTGGAACCGCCG CACTCGGTTGCCTGGTCAAAGACTAC TTCCCCGAGCCCGTGACTGTCTCGTG GAACTCGGGCGCCCTCACATCCGGA GTGCATACCTTTCCCGCCGTGTTGCA GTCCAGCGGCCTGTACAGCCTGAGCT CCGTCGTGACAGTGCCGTCCTCCTCC CTTGGAACCCAGACCTATATCTGCAA CGTCAATCACAAGCCCTCCAACACCA AAGTGGACAAGAAGGTCGAACCCAA GTCCTGCGACAAGACTCACACCTGTC CGCCTTGTCCAGCCCCTGAGCTGCTG GGTGGTCCGTCCGTGTTCCTCTTCCC	SEQ ID 1865	GATGTTGTGATGACTCAGTCTCCAT CCTCCCTCGCTGCATCTGTTGGAGA CAGAATTACCATCACTTGCCGGCC AAGTCAGGACATAGGCACTTATTT AAATTGGTATCAACAGAAGGCAGG GGAAGCCCCTAAGCTCCTCATCTAT GCTGCCTCCAATCTGCACAGTGGC GTCTCATCAAGGTTCAGAGGCGTT GGGTCTGGGACACAATTCACTCTC ACCATCAGCAGTCTGCAACCTGAG GATTTTGCAACTTACTACTGTCATC AGAGTTACGGTCCTCGGACATTCG GCCAAGGGACCAAGCTGGAGATCA AACGTACTGTGGCTGCTCCCTCCGT GTTCATTTTTCCTCCGTCGGACGAA CAGCTGAAGTCCGGAACCGCGTCC GTGGTCTGTCTCCTGAACAACTTCT ATCCGCGCGAGGCGAAAGTGCAGT GGAAGGTCGACAACGCACTGCAGT CGGGAAACTCCCAGGAATCGGTGA CCGAGCAGGACTCGAAGGACTCAA CCTACTCATTGTCCTCCACCCTCAC CCTGAGCAAGGCCGATTACGAGAA GCATAAGGTCTACGCCTGCGAAGT GACCCACCAGGGCCTGAGCAGCCC AGTGACGAAGTCCTTCAACCGGGG AGAATGC

	GCCCAAGCCGAAGGACACTCTGATG ATTTCACGCACCCCGGAAGTCACTTG CGTGGTCGTGGACGTGTCGCACGAA GATCCCGAAGTGAAATTCAATTGGTA CGTGGATGGGGTCGAAGTGCACAAC GCCAAGACCAAGCCTAGGGAAGAAC AGTACAACTCTACGTACCGGGTGGTG TCCGTGCTGACCGTGCTGCACCAGGA CTGGCTGAACGGAAAGGAGTACAAG TGCAAAGTGTCAAACAAGGCTCTCCC TGCCCCTATCGAAAAGACCATCAGC AAGGCCAAGGGTCAACCTAGGGAGC CCCAGGTCTATACTTTGCCGCCTAGC CGGGAAGAAATGACTAAGAACCAAG TGTCCCTGACTTGCCTTGTCAAGGGC TTTTATCCGTCCGACATCGCCGTGGA GTGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCAAGCTGACTGTGGACAA GTCAAGATGGCAGCAGGGAAACGTG TTCTCCTGCTCCGTGATGCACGAAGC GCTGCACAACCATTACACCCAGAAA TCACTGTCACTTTCGCCGGGAAAA		
SEQ ID 1758	GAGGTGCAGCTGGTGCAGTCTGGGG GAGGCGTGGTCCAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCGTCTG GATTCACCTTCAGTAGCTATGGCATG CACTGGGTCCGCCAGGCTCCAGGCA AGGGGCTGGAGTGGGTGGCATTTAT ATCATATGATGGAAGTAATAAATACT ACGCAGACTCCGTGAAGGGCCGATT CACCATCTCCAGAGACAATTCCAAG AACACGCTGTATCTGCAAATGAACA GCCTGAGAGCCGAGGACACGGCCGT ATATTACTGTGCGACAACAGGGGAC CGCTTCCAAGAGTTTGACTACTGGGG CCAGGGAACCCTGGTCACCGTCTCCT CAGCATCCACCAAGGGGCCTTCCGTG TTCCCCCTGGCCCCTTCATCCAAGTC GACCTCTGGTGGAACCGCCGCACTCG GTTGCCTGGTCAAAGACTACTTCCCC GAGCCCGTGACTGTCTCGTGGAACTC GGGCGCCCTCACATCCGGAGTGCAT ACCTTTCCCGCCGTGTTGCAGTCCAG CGGCCTGTACAGCCTGAGCTCCGTCG TGACAGTGCCGTCCTCCTCCCTTGGA ACCCAGACCTATATCTGCAACGTCAA TCACAAGCCCTCCAACACCAAAGTG GACAAGAAGGTCGAACCCAAGTCCT GCGACAAGACTCACACCTGTCCGCCT TGTCCAGCCCCTGAGCTGCTGGGTGG TCCGTCCGTGTTCCTCTTCCCGCCCA	SEQ ID 1866	GAAACGACACTCACGCAGTCTCCA GCCACCCTGTCTGTGTCTCCAGGGG AAAGAGCCACCCTCTCCTGCAGGG CCAGTCAGAGTGTTAGCAGCAACT TAGCCTGGTACCAGCAGAAACCTG GCCAGGCTCCCAGGCTCCTCATCTA TGGTGCATCCACCAGGGCCACTGG CATCCCAGCCAGGTTCAGTGGCAG TGGGTCTGGGACAGAGTTCACTCT CACCATCAGCAGCCTGCAGTCTGA AGATTTTGCAGTTTATTACTGTCAG CAGTATAATAACTGGCCTCCGATC ACCTTCGGCCAAGGGACACGACTG GAGATTAAACGTACTGTGGCTGCT CCCTCCGTGTTCATTTTTCCTCCGT CGGACGAACAGCTGAAGTCCGGAA CCGCGTCCGTGGTCTGTCTCCTGAA CAACTTCTATCCGCGCGAGGCGAA AGTGCAGTGGAAGGTCGACAACGC ACTGCAGTCGGGAAACTCCCAGGA ATCGGTGACCGAGCAGGACTCGAA GGACTCAACCTACTCATTGTCCTCC ACCCTCACCCTGAGCAAGGCCGAT TACGAGAAGCATAAGGTCTACGCC TGCGAAGTGACCCACCAGGGCCTG AGCAGCCCAGTGACGAAGTCCTTC AACCGGGGAGAATGC

	AGCCGAAGGACACTCTGATGATTTCA CGCACCCCGGAAGTCACTTGCGTGGT CGTGGACGTGTCGCACGAAGATCCC GAAGTGAAATTCAATTGGTACGTGG ATGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTAC AACTCTACGTACCGGGTGGTGTCCGT GCTGACCGTGCTGCACCAGGACTGG CTGAACGGAAAGGAGTACAAGTGCA AAGTGTCAAACAAGGCTCTCCCTGCC CCTATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTATACTTTGCCGCCTAGCCGGG AAGAAATGACTAAGAACCAAGTGTC CCTGACTTGCCTTGTCAAGGGCTTTT ATCCGTCCGACATCGCCGTGGAGTGG GAGTCCAACGGACAACCGGAGAACA ACTACAAGACCACCCCACCGGTGCTC GATTCCGATGGCTCCTTCTTCCTGTA CTCCAAGCTGACTGTGGACAAGTCA AGATGGCAGCAGGGAAACGTGTTCT CCTGCTCCGTGATGCACGAAGCGCTG CACAACCATTACACCCAGAAATCACT GTCACTTTCGCCGGGAAAA		
SEQ ID 1759	CAGATGCAGCTGGTGCAGTCTGGGG GAGTCTTGCTTCAGCCAGGGCGGTCC CTGAGACTCTCCTGTACAGCTTCTGG ATTCACCTTTGCTGCTTATAATATCA ACTGGTTCCGCCAGGGTCCTGGGGG GGGGCTGGAGTGGGTAGGTTTCATTA GAGCCAACGCTGATAGTGGGACAAC AGAGTACGCCGCGTCTGTGAAAGGC AGATTCTTCATCTCAAGAGATGATTC CAGAAGCACCGCCTACCTGCAAATG ACTAGCCTTAAAACCGAGGACACAG CCGTTTATTACTGTGCCAGAGATGAT CGGGGTCGGGGAGATGACTTTGACT ACTGGGGCCAGGGCACCCTGGTCAC CGTCTCCTCAGCATCCACCAAGGGGC CTTCCGTGTTCCCCCTGGCCCCTTCAT CCAAGTCGACCTCTGGTGGAACCGCC GCACTCGGTTGCCTGGTCAAAGACTA CTTCCCCGAGCCCGTGACTGTCTCGT GGAACTCGGGCGCCCTCACATCCGG AGTGCATACCTTTCCCGCCGTGTTGC AGTCCAGCGGCCTGTACAGCCTGAG CTCCGTCGTGACAGTGCCGTCCTCCT CCCTTGGAACCCAGACCTATATCTGC AACGTCAATCACAAGCCCTCCAACA CCAAAGTGGACAAGAAGGTCGAACC CAAGTCCTGCGACAAGACTCACACCT GTCCGCCTTGTCCAGCCCCTGAGCTG CTGGGTGGTCCGTCCGTGTTCCTCTT	SEQ ID 1867	GATGTTGTGATGACTCAGTCTCCAG GCACCCTGTCTTTGTCTCCAGGGGA AAGAGCCACCCTCTCCTGCAGGGC CAGTCAGAGTGTTAGCAGCAGCTA CTTAGCCTGGTACCAGCAGAAACC TGGCCAGGCTCCCAGGCTCCTCATC TATGGTGCATCCAGCAGGGCCACT GGCATCCCAGACAGGTTCAGTGGC AGTGGGTCTGGGACAGACTTCACT CTCACCATCAGCAGACTGGAGCCT GAAGATTTTGCAGTGTATTACTGTC AGCAGTATGGTAGCTCAGGGTACA CTTTTGGCCAGGGGACCAAGCTGG AGATCAAACGTACTGTGGCTGCTC CCTCCGTGTTCATTTTTCCTCCGTC GGACGAACAGCTGAAGTCCGGAAC CGCGTCCGTGGTCTGTCTCCTGAAC AACTTCTATCCGCGCGAGGCGAAA GTGCAGTGGAAGGTCGACAACGCA CTGCAGTCGGGAAACTCCCAGGAA TCGGTGACCGAGCAGGACTCGAAG GACTCAACCTACTCATTGTCCTCCA CCCTCACCCTGAGCAAGGCCGATT ACGAGAAGCATAAGGTCTACGCCT GCGAAGTGACCCACCAGGGCCTGA GCAGCCCAGTGACGAAGTCCTTCA ACCGGGGAGAATGC

	CCCGCCCAAGCCGAAGGACACTCTG ATGATTTCACGCACCCCGGAAGTCAC TTGCGTGGTCGTGGACGTGTCGCACG AAGATCCCGAAGTGAAATTCAATTG GTACGTGGATGGGGTCGAAGTGCAC AACGCCAAGACCAAGCCTAGGGAAG AACAGTACAACTCTACGTACCGGGT GGTGTCCGTGCTGACCGTGCTGCACC AGGACTGGCTGAACGGAAAGGAGTA CAAGTGCAAAGTGTCAAACAAGGCT CTCCCTGCCCCTATCGAAAAGACCAT CAGCAAGGCCAAGGGTCAACCTAGG GAGCCCCAGGTCTATACTTTGCCGCC TAGCCGGGAAGAAATGACTAAGAAC CAAGTGTCCCTGACTTGCCTTGTCAA GGGCTTTTATCCGTCCGACATCGCCG TGGAGTGGGAGTCCAACGGACAACC GGAGAACAACTACAAGACCACCCCA CCGGTGCTCGATTCCGATGGCTCCTT CTTCCTGTACTCCAAGCTGACTGTGG ACAAGTCAAGATGGCAGCAGGGAAA CGTGTTCTCCTGCTCCGTGATGCACG AAGCGCTGCACAACCATTACACCCA GAAATCACTGTCACTTTCGCCGGGAA AA		
SEQ ID 1760	CAGGTGCAGCTGGTGCAATCTGGGG GAGGCTTGGTACAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTAGCAGCTATGGCATG ACGTGGGTCCGCCAGGCTCCAGGGA AGGGGCTGGAGTGGGTCTCAACTATT AGTGGTAATGGTGTTGGCACATACTA CCCAGACTCCGTGAAGGACCGGTTC ACCATCTCCAGAGACAGTTCCAAGA ACACGGTGTATCTGCAAATGAACAG CCTGAGAGCCGAGGACACGGCCGTA TATTACTGTGTGAAACATGGTAGGGC CGGAATAAACTGGTACTTCGATCTCT GGGGCCGTGGCACCCTGGTGACCGT CTCCTCAGCATCCACCAAGGGGCCTT CCGTGTTCCCCCTGGCCCCTTCATCC AAGTCGACCTCTGGTGGAACCGCCG CACTCGGTTGCCTGGTCAAAGACTAC TTCCCCGAGCCCGTGACTGTCTCGTG GAACTCGGGCGCCCTCACATCCGGA GTGCATACCTTTCCCGCCGTGTTGCA GTCCAGCGGCCTGTACAGCCTGAGCT CCGTCGTGACAGTGCCGTCCTCCTCC CTTGGAACCCAGACCTATATCTGCAA CGTCAATCACAAGCCCTCCAACACCA AAGTGGACAAGAAGGTCGAACCCAA GTCCTGCGACAAGACTCACACCTGTC CGCCTTGTCCAGCCCCTGAGCTGCTG GGTGGTCCGTCCGTGTTCCTCTTCCC	SEQ ID 1868	GAAACGACACTCACGCAGTCTCCA GGCACCCTGTCTTTGTCTCCAGGGG AAAGAGCCACCCTCTCCTGCAGGG CCAGTCAGAGTGTTAGCAGCAGCT ACTTAGCCTGGTACCAGCAGAAAC CTGGCCAGGCTCCCAGGCTCCTCAT CTATGGTGCATCCAGCAGGGCCAC TGGCATCCCAGACAGGTTCAGTGG CAGTGGGTCTGGGACAGACTTCAC TCTCACCATCAGCAGACTGGAGCC TGAAGATTTTGCAGTGTATTACTGT CAGCAGTATGGTAGCTCGTTCGGC CAAGGGACACGACTGGAGATTAAA CGTACTGTGGCTGCTCCCTCCGTGT TCATTTTTCCTCCGTCGGACGAACA GCTGAAGTCCGGAACCGCGTCCGT GGTCTGTCTCCTGAACAACTTCTAT CCGCGCGAGGCGAAAGTGCAGTGG AAGGTCGACAACGCACTGCAGTCG GGAAACTCCCAGGAATCGGTGACC GAGCAGGACTCGAAGGACTCAACC TACTCATTGTCCTCCACCCTCACCC TGAGCAAGGCCGATTACGAGAAGC ATAAGGTCTACGCCTGCGAAGTGA CCCACCAGGGCCTGAGCAGCCCAG TGACGAAGTCCTTCAACCGGGGAG AATGC

	GCCCAAGCCGAAGGACACTCTGATG ATTTCACGCACCCCGGAAGTCACTTG CGTGGTCGTGGACGTGTCGCACGAA GATCCCGAAGTGAAATTCAATTGGTA CGTGGATGGGGTCGAAGTGCACAAC GCCAAGACCAAGCCTAGGGAAGAAC AGTACAACTCTACGTACCGGGTGGTG TCCGTGCTGACCGTGCTGCACCAGGA CTGGCTGAACGGAAAGGAGTACAAG TGCAAAGTGTCAAACAAGGCTCTCCC TGCCCCTATCGAAAAGACCATCAGC AAGGCCAAGGGTCAACCTAGGGAGC CCCAGGTCTATACTTTGCCGCCTAGC CGGGAAGAAATGACTAAGAACCAAG TGTCCCTGACTTGCCTTGTCAAGGGC TTTTATCCGTCCGACATCGCCGTGGA GTGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCAAGCTGACTGTGGACAA GTCAAGATGGCAGCAGGGAAACGTG TTCTCCTGCTCCGTGATGCACGAAGC GCTGCACAACCATTACACCCAGAAA TCACTGTCACTTTCGCCGGGAAAA		
SEQ ID 1761	CAGGTACAGCTGCAGCAGTCAGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCAACAGTGCT GCTTGGAACTGGATCAGGCAGTCCCC ATCGAGAGGCCTTGAGTGGCTGGGA AGGACATACTACAGGTCCAAGTGGT ATAATGATTATGCAGTATCTGTGAAA AGTCGAATAACCATCAACCCAGACA CATCCAAGAACCAGTTCTCCCTGCAG CTGAACTCTGTGACTCCCGAGGACAC GGCTGTGTATTACTGTGCAAGAGGG GGAGGGCTTTGGGCTTTTGATATCTG GGGCCAAGGGACCACGGTCACCGTC TCCTCAGCATCCACCAAGGGGCCTTC CGTGTTCCCCCTGGCCCCTTCATCCA AGTCGACCTCTGGTGGAACCGCCGC ACTCGGTTGCCTGGTCAAAGACTACT TCCCCGAGCCCGTGACTGTCTCGTGG AACTCGGGCGCCCTCACATCCGGAGT GCATACCTTTCCCGCCGTGTTGCAGT CCAGCGGCCTGTACAGCCTGAGCTCC GTCGTGACAGTGCCGTCCTCCTCCCT TGGAACCCAGACCTATATCTGCAACG TCAATCACAAGCCCTCCAACACCAA AGTGGACAAGAAGGTCGAACCCAAG TCCTGCGACAAGACTCACACCTGTCC GCCTTGTCCAGCCCCTGAGCTGCTGG GTGGTCCGTCCGTGTTCCTCTTCCCG	SEQ ID 1869	GAAATTGTGTTGACACAGTCTCCTT CCACCCTGTCTGCATCTGTAGGGG ACAGAGTCACCATCACTTGCCGGG CCAGTCAGAGTATTAGTAGCTGCTT GGCCTGGTATCAGCAGAAACCAGG GAAAGCCCCTAAGCTCCTGATCTA TGCTGCATCCACTTTGCAAAGTGG GGTCCCATCAAGGTTCAGCGGCAG TGGATCTGGGACAGAATTCACTCT CACAATCAGCACCCTGCAGCCTGA AGATTTTGCAACTTATTACTGTCAA CAGCTTAATAGTTACCCTCAGACGT TCGGCCAAGGGACCAAAGTGGATA TCAAACGTACTGTGGCTGCTCCCTC CGTGTTCATTTTTCCTCCGTCGGAC GAACAGCTGAAGTCCGGAACCGCG TCCGTGGTCTGTCTCCTGAACAACT TCTATCCGCGCGAGGCGAAAGTGC AGTGGAAGGTCGACAACGCACTGC AGTCGGGAAACTCCCAGGAATCGG TGACCGAGCAGGACTCGAAGGACT CAACCTACTCATTGTCCTCCACCCT CACCCTGAGCAAGGCCGATTACGA GAAGCATAAGGTCTACGCCTGCGA AGTGACCCACCAGGGCCTGAGCAG CCCAGTGACGAAGTCCTTCAACCG GGGAGAATGC

	CCCAAGCCGAAGGACACTCTGATGA TTTCACGCACCCCGGAAGTCACTTGC GTGGTCGTGGACGTGTCGCACGAAG ATCCCGAAGTGAAATTCAATTGGTAC GTGGATGGGGTCGAAGTGCACAACG CCAAGACCAAGCCTAGGGAAGAACA GTACAACTCTACGTACCGGGTGGTGT CCGTGCTGACCGTGCTGCACCAGGAC TGGCTGAACGGAAAGGAGTACAAGT GCAAAGTGTCAAACAAGGCTCTCCCT GCCCCTATCGAAAAGACCATCAGCA AGGCCAAGGGTCAACCTAGGGAGCC CCAGGTCTATACTTTGCCGCCTAGCC GGGAAGAAATGACTAAGAACCAAGT GTCCCTGACTTGCCTTGTCAAGGGCT TTTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAGA ACAACTACAAGACCACCCCACCGGT GCTCGATTCCGATGGCTCCTTCTTCC TGTACTCCAAGCTGACTGTGGACAAG TCAAGATGGCAGCAGGGAAACGTGT TCTCCTGCTCCGTGATGCACGAAGCG CTGCACAACCATTACACCCAGAAATC ACTGTCACTTTCGCCGGGAAAA		
SEQ ID 1762	GAGGTCCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTCTCCTGCAAGGCTTCTG GATACACCTTCACCGGCTACTATATG CACTGGGTGCGACAGGCCCCTGGAC AAGGGCTTGAGTGGATGGGATGGAT CAACCCTAACAGTGGTGGCACAAAC TATGCACAGAAGTTTCAGGGCAGGG TCACCATGACCAGGGACACGTCCATC AGCACAGCCTACATGGAGCTGAGCA GGCTGAGATCTGACGACACGGCCGT GTATTACTGTGCGAGAGACAAGATC GGCAGCTGTCCTTACTGGGGCCAGG GAACCCTGGTCACCGTCTCCTCAGCA TCCACCAAGGGGCCTTCCGTGTTCCC CCTGGCCCCTTCATCCAAGTCGACCT CTGGTGGAACCGCCGCACTCGGTTGC CTGGTCAAAGACTACTTCCCCGAGCC CGTGACTGTCTCGTGGAACTCGGGCG CCCTCACATCCGGAGTGCATACCTTT CCCGCCGTGTTGCAGTCCAGCGGCCT GTACAGCCTGAGCTCCGTCGTGACAG TGCCGTCCTCCTCCCTTGGAACCCAG ACCTATATCTGCAACGTCAATCACAA GCCCTCCAACACCAAAGTGGACAAG AAGGTCGAACCCAAGTCCTGCGACA AGACTCACACCTGTCCGCCTTGTCCA GCCCCTGAGCTGCTGGGTGGTCCGTC CGTGTTCCTCTTCCCGCCCAAGCCGA	SEQ ID 1870	GATATTGTGATGACCCACACTCCA CTCTCTCTGTCCGTCACCCCTGGAC AGCCGGCCTCCATCTCCTGCAAGTC TAGTCAGAGCCTCCTGCATAGTGA TGGAAAGACCTATTTGTATTGGTAC CTGCAGAAGCCAGGCCAGCCTCCA CAGCTCCTGATCTATGAAGTTTCCA ACCGGTTCTCTGGAGTGCCAGATA GGTTCAGTGGCAGCGGGTCAGGGA CAGATTTCACACTGAAAATCAGCC GGGTGGAGGCTGAGGATGTTGGGG TTTATTACTGCATGCAAAGTATACA GCTTCCGCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAACGTAC TGTGGCTGCTCCCTCCGTGTTCATT TTTCCTCCGTCGGACGAACAGCTG AAGTCCGGAACCGCGTCCGTGGTC TGTCTCCTGAACAACTTCTATCCGC GCGAGGCGAAAGTGCAGTGGAAG GTCGACAACGCACTGCAGTCGGGA AACTCCCAGGAATCGGTGACCGAG CAGGACTCGAAGGACTCAACCTAC TCATTGTCCTCCACCCTCACCCTGA GCAAGGCCGATTACGAGAAGCATA AGGTCTACGCCTGCGAAGTGACCC ACCAGGGCCTGAGCAGCCCAGTGA CGAAGTCCTTCAACCGGGGAGAAT GC

	AGGACACTCTGATGATTTCACGCACC CCGGAAGTCACTTGCGTGGTCGTGGA CGTGTCGCACGAAGATCCCGAAGTG AAATTCAATTGGTACGTGGATGGGGT CGAAGTGCACAACGCCAAGACCAAG CCTAGGGAAGAACAGTACAACTCTA CGTACCGGGTGGTGTCCGTGCTGACC GTGCTGCACCAGGACTGGCTGAACG GAAAGGAGTACAAGTGCAAAGTGTC AAACAAGGCTCTCCCTGCCCCTATCG AAAAGACCATCAGCAAGGCCAAGGG TCAACCTAGGGAGCCCCAGGTCTATA CTTTGCCGCCTAGCCGGGAAGAAAT GACTAAGAACCAAGTGTCCCTGACTT GCCTTGTCAAGGGCTTTTATCCGTCC GACATCGCCGTGGAGTGGGAGTCCA ACGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCCG ATGGCTCCTTCTTCCTGTACTCCAAG CTGACTGTGGACAAGTCAAGATGGC AGCAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACTT TCGCCGGGAAAA		
SEQ ID 1763	CAGGTCACCTTGAAGGAGTCTGGTCC TACGCTGGTGAAACCCACACAGACC CTCACGCTGACCTGCACCTTCTCTGG GTTCTCACTCAGCACTAGTGGAGTGG GTGTGGGCTGGATCCGTCAGCCCCCA GGAAAGGCCCTGGAGTGGCTTGCAC TCATTTATTGGGATGATGATAAGCGC TACAGCCCATCTCTGAAGAGCAGGCT CACCATCACCAAGGACACCTCCAAA AACCAGGTGGTCCTTACAATGACCA ACATGGACCCTGTGGACACAGCCAC ATATTACTGTGCACACAGACCGGATA GCAGCAGTCAATGTTTTGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTC CTCAGCATCCACCAAGGGGCCTTCCG TGTTCCCCCTGGCCCCTTCATCCAAG TCGACCTCTGGTGGAACCGCCGCACT CGGTTGCCTGGTCAAAGACTACTTCC CCGAGCCCGTGACTGTCTCGTGGAAC TCGGGCGCCCTCACATCCGGAGTGCA TACCTTTCCCGCCGTGTTGCAGTCCA GCGGCCTGTACAGCCTGAGCTCCGTC GTGACAGTGCCGTCCTCCTCCCTTGG AACCCAGACCTATATCTGCAACGTCA ATCACAAGCCCTCCAACACCAAAGT GGACAAGAAGGTCGAACCCAAGTCC TGCGACAAGACTCACACCTGTCCGCC TTGTCCAGCCCCTGAGCTGCTGGGTG GTCCGTCCGTGTTCCTCTTCCCGCCC	SEQ ID 1871	GATGTTGTGATGACTCAGTCTCCAG GCACCCTGTCTTTGTCTCCAGGGGA AAGAGCCACCCTCTCCTGCAGGGC CAGTCAGAGTGTTAGCAGCAGCTA CTTAGCCTGGTACCAGCAGAAACC TGGCCAGGCTCCCAGGCTCCTCATC TATGGTGCATCCAGCAGGGCCACT GGCATCCCAGACAGGTTCAGTGGC AGTGGGTCTGGGACAGACTTCACT CTCACCATCAGCAGACTGGAGCCT GAAGATTTTGCAGTGTATTACTGTC AGCAGTATAATAACTGGCCTCTCA CTTTCGGCGGAGGGACCAAGCTGG AGATCAAACGTACTGTGGCTGCTC CCTCCGTGTTCATTTTTCCTCCGTC GGACGAACAGCTGAAGTCCGGAAC CGCGTCCGTGGTCTGTCTCCTGAAC AACTTCTATCCGCGCGAGGCGAAA GTGCAGTGGAAGGTCGACAACGCA CTGCAGTCGGGAAACTCCCAGGAA TCGGTGACCGAGCAGGACTCGAAG GACTCAACCTACTCATTGTCCTCCA CCCTCACCCTGAGCAAGGCCGATT ACGAGAAGCATAAGGTCTACGCCT GCGAAGTGACCCACCAGGGCCTGA GCAGCCCAGTGACGAAGTCCTTCA ACCGGGGAGAATGC

	AAGCCGAAGGACACTCTGATGATTTC ACGCACCCCGGAAGTCACTTGCGTG GTCGTGGACGTGTCGCACGAAGATC CCGAAGTGAAATTCAATTGGTACGTG GATGGGGTCGAAGTGCACAACGCCA AGACCAAGCCTAGGGAAGAACAGTA CAACTCTACGTACCGGGTGGTGTCCG TGCTGACCGTGCTGCACCAGGACTGG CTGAACGGAAAGGAGTACAAGTGCA AAGTGTCAAACAAGGCTCTCCCTGCC CCTATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTATACTTTGCCGCCTAGCCGGG AAGAAATGACTAAGAACCAAGTGTC CCTGACTTGCCTTGTCAAGGGCTTTT ATCCGTCCGACATCGCCGTGGAGTGG GAGTCCAACGGACAACCGGAGAACA ACTACAAGACCACCCCACCGGTGCTC GATTCCGATGGCTCCTTCTTCCTGTA CTCCAAGCTGACTGTGGACAAGTCA AGATGGCAGCAGGGAAACGTGTTCT CCTGCTCCGTGATGCACGAAGCGCTG CACAACCATTACACCCAGAAATCACT GTCACTTTCGCCGGGAAAA		
SEQ ID 1764	CAGGTCACCTTGAAGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTCAGTAGCTATGCTATG CACTGGGTCCGCCAGGCTCCAGGCA AGGGGCTGGAGTGGGTGGCAGTTAT ATCATATGATGGAAGTAATAAATACT ACGCAGACTCCGTGAAGGGCCGATT CACCATCTCCAGAGACAATTCCAAG AACACGCTGTATCTGCAAATGAACA GCCTGAGAGCTGAGGACACGGCTGT GTATTACTGTGCGAGAAGCAGTGGCT GGTCACTGCCTGAAGACTACTGGGG CCAGGGAACCCTGGTCACCGTCTCCT CAGCATCCACCAAGGGGCCTTCCGTG TTCCCCCTGGCCCCTTCATCCAAGTC GACCTCTGGTGGAACCGCCGCACTCG GTTGCCTGGTCAAAGACTACTTCCCC GAGCCCGTGACTGTCTCGTGGAACTC GGGCGCCCTCACATCCGGAGTGCAT ACCTTTCCCGCCGTGTTGCAGTCCAG CGGCCTGTACAGCCTGAGCTCCGTCG TGACAGTGCCGTCCTCCTCCCTTGGA ACCCAGACCTATATCTGCAACGTCAA TCACAAGCCCTCCAACACCAAAGTG GACAAGAAGGTCGAACCCAAGTCCT GCGACAAGACTCACACCTGTCCGCCT TGTCCAGCCCCTGAGCTGCTGGGTGG TCCGTCCGTGTTCCTCTTCCCGCCCA	SEQ ID 1872	GACATCCAGTTGACCCAGTCTCCC GACTCCCTGGCTGTGTCTCTGGGCG AGAGGGCCACCATCAACTGCACGT CCAGCCAGAGTGTTTTATACAGCTC CAACAATAAGAACTACATAGCTTG GTACCAGCAGAAACCAGGACAGCC TCCTAAGCTGCTCATTTACTGGGCA TCTACCCGGGAATCCGGGGTCCCT GACCGATTCAGTGGCAGCGGGTCT GGGACAGATTTCACTCTCACCATC AGCAGCCTGCAGGCTGAAGATGTG GCAGTTTATTACTGTCAGCAATATT ATTATATTCCTCGGACGTTCGGCCA AGGGACCAAGGTGGAAATCAAACG TACTGTGGCTGCTCCCTCCGTGTTC ATTTTTCCTCCGTCGGACGAACAGC TGAAGTCCGGAACCGCGTCCGTGG TCTGTCTCCTGAACAACTTCTATCC GCGCGAGGCGAAAGTGCAGTGGAA GGTCGACAACGCACTGCAGTCGGG AAACTCCCAGGAATCGGTGACCGA GCAGGACTCGAAGGACTCAACCTA CTCATTGTCCTCCACCCTCACCCTG AGCAAGGCCGATTACGAGAAGCAT AAGGTCTACGCCTGCGAAGTGACC CACCAGGGCCTGAGCAGCCCAGTG ACGAAGTCCTTCAACCGGGGAGAA TGC

	AGCCGAAGGACACTCTGATGATTTCA CGCACCCCGGAAGTCACTTGCGTGGT CGTGGACGTGTCGCACGAAGATCCC GAAGTGAAATTCAATTGGTACGTGG ATGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTAC AACTCTACGTACCGGGTGGTGTCCGT GCTGACCGTGCTGCACCAGGACTGG CTGAACGGAAAGGAGTACAAGTGCA AAGTGTCAAACAAGGCTCTCCCTGCC CCTATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTATACTTTGCCGCCTAGCCGGG AAGAAATGACTAAGAACCAAGTGTC CCTGACTTGCCTTGTCAAGGGCTTTT ATCCGTCCGACATCGCCGTGGAGTGG GAGTCCAACGGACAACCGGAGAACA ACTACAAGACCACCCCACCGGTGCTC GATTCCGATGGCTCCTTCTTCCTGTA CTCCAAGCTGACTGTGGACAAGTCA AGATGGCAGCAGGGAAACGTGTTCT CCTGCTCCGTGATGCACGAAGCGCTG CACAACCATTACACCCAGAAATCACT GTCACTTTCGCCGGGAAAA		
SEQ ID 1765	CAGGTCCAGCTGGTACAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTCTCCTGCAAGGTTTCCG GATACACCCTCACTGAATTATCCATG CACTGGGTGCGACAGGCTCCTGGAA AAGGGCTTGAGTGGATGGGAGGTTT TGATCCTGAAGATGGTGAAACAATCT ACGCACAGAAGTTCCAGGGCAGAGT CACCATGACCGAGGACACATCTACA GACACAGCCTACATGGAGCTGAGCA GCCTGAGATCTGAGGACACGGCCGT GTATTACTGTGCAACGGATGTGAACC CGGAGCTACTGGGGGCGGGATTTGA CTACTGGGGCCAGGGCACCCTGGTC ACCGTCTCCTCAGCATCCACCAAGGG GCCTTCCGTGTTCCCCCTGGCCCCTT CATCCAAGTCGACCTCTGGTGGAACC GCCGCACTCGGTTGCCTGGTCAAAGA CTACTTCCCCGAGCCCGTGACTGTCT CGTGGAACTCGGGCGCCCTCACATCC GGAGTGCATACCTTTCCCGCCGTGTT GCAGTCCAGCGGCCTGTACAGCCTG AGCTCCGTCGTGACAGTGCCGTCCTC CTCCCTTGGAACCCAGACCTATATCT GCAACGTCAATCACAAGCCCTCCAA CACCAAAGTGGACAAGAAGGTCGAA CCCAAGTCCTGCGACAAGACTCACA CCTGTCCGCCTTGTCCAGCCCCTGAG CTGCTGGGTGGTCCGTCCGTGTTCCT	SEQ ID 1873	GATGTTGTGATGACTCAGTCTCCAC TCTCCCTGCCCGTCACCCCTGGAGA GCCGGCCTCCATCTCCTGCAGGTCT AGTCAGAGCCTCCTGCATAGTAAT GGATACAACTATTTGGATTGGTAC CTGCAGAAGCCAGGGCAGTCTCCA CAGCTCCTGATCTATTTGGGTTCTA ATCGGGCCCCCGGGGTCCCTGACA GGTTCAGTGGCAGTGGATCAGGCA CAGATTTTACACTGAAAATCAGCA GAGTGGAGGCTGAGGATGTTGGGG TTTATTACTGCATGCAAGCTCTACA AACTCGGACATTCGGCCAAGGGAC CAAGCTGGAGATCAAACGTACTGT GGCTGCTCCCTCCGTGTTCATTTTT CCTCCGTCGGACGAACAGCTGAAG TCCGGAACCGCGTCCGTGGTCTGTC TCCTGAACAACTTCTATCCGCGCGA GGCGAAAGTGCAGTGGAAGGTCGA CAACGCACTGCAGTCGGGAAACTC CCAGGAATCGGTGACCGAGCAGGA CTCGAAGGACTCAACCTACTCATT GTCCTCCACCCTCACCCTGAGCAA GGCCGATTACGAGAAGCATAAGGT CTACGCCTGCGAAGTGACCCACCA GGGCCTGAGCAGCCCAGTGACGAA GTCCTTCAACCGGGGAGAATGC

	CTTCCCGCCCAAGCCGAAGGACACTC TGATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGCA CGAAGATCCCGAAGTGAAATTCAAT TGGTACGTGGATGGGGTCGAAGTGC ACAACGCCAAGACCAAGCCTAGGGA AGAACAGTACAACTCTACGTACCGG GTGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGAG TACAAGTGCAAAGTGTCAAACAAGG CTCTCCCTGCCCCTATCGAAAAGACC ATCAGCAAGGCCAAGGGTCAACCTA GGGAGCCCCAGGTCTATACTTTGCCG CCTAGCCGGGAAGAAATGACTAAGA ACCAAGTGTCCCTGACTTGCCTTGTC AAGGGCTTTTATCCGTCCGACATCGC CGTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTCC TTCTTCCTGTACTCCAAGCTGACTGT GGACAAGTCAAGATGGCAGCAGGGA AACGTGTTCTCCTGCTCCGTGATGCA CGAAGCGCTGCACAACCATTACACC CAGAAATCACTGTCACTTTCGCCGGG AAAA		
SEQ ID 1766	CAGGTCACCTTGAAGGAGTCTGGGG GAGGCTTGGTCCAGCCTGGAGGGTC CCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTCAGTGACCAGTACATG GACTGGGTCCGCCAGGCTCCAGGGA AGGGGCTGGAGTGGGTTGGCCGTGT TAGAAACAAAGCTAACAGTTACACC ACAGAATACGCCGCGTCTGTGAAAG GCAGATTCACCATCTCAAGAGATGAT TCAAAGAACTCACTGTATCTGCAAAT GAATAGTCTGAACACCGAGGACACG GCCATGTATTTCTGTGCTAGTAGTCT CAATAGTGGGGGCTACCGATGCTTCC ATCACTGGGGCCAGGGCACCCTGGT GACCGTCTCCTCAGCATCCACCAAGG GGCCTTCCGTGTTCCCCCTGGCCCCT TCATCCAAGTCGACCTCTGGTGGAAC CGCCGCACTCGGTTGCCTGGTCAAAG ACTACTTCCCCGAGCCCGTGACTGTC TCGTGGAACTCGGGCGCCCTCACATC CGGAGTGCATACCTTTCCCGCCGTGT TGCAGTCCAGCGGCCTGTACAGCCTG AGCTCCGTCGTGACAGTGCCGTCCTC CTCCCTTGGAACCCAGACCTATATCT GCAACGTCAATCACAAGCCCTCCAA CACCAAAGTGGACAAGAAGGTCGAA CCCAAGTCCTGCGACAAGACTCACA CCTGTCCGCCTTGTCCAGCCCCTGAG CTGCTGGGTGGTCCGTCCGTGTTCCT	SEQ ID 1874	GAAACGACACTCACGCAGTCTCCA GGCACCCTGTCTTTGTCTCCAGGGG AAAGAGCCACCCTCTCCTGCAGGG CCAGTCAGAGTCTTACCAGCAGCT ACTTAGCCTGGTACCAGCAGAAAC CTGGCCAGGCTCCCAGACTCCTCAT CTATCGTGCATCCAGCAGGGCCAC TGGCATCCCAGACCGGTTCAGTGG CAGTGGGTCTGGGACAGACTTCAC TCTCACCATCAGCAGACTGGAGCC TGAAGATTTTGCAGTTTATTACTGT CAGCAGTATGGTAGTTCACCTAAC ACCTTCGGCCAAGGGACACGACTG GAGATTAAACGTACTGTGGCTGCT CCCTCCGTGTTCATTTTTCCTCCGT CGGACGAACAGCTGAAGTCCGGAA CCGCGTCCGTGGTCTGTCTCCTGAA CAACTTCTATCCGCGCGAGGCGAA AGTGCAGTGGAAGGTCGACAACGC ACTGCAGTCGGGAAACTCCCAGGA ATCGGTGACCGAGCAGGACTCGAA GGACTCAACCTACTCATTGTCCTCC ACCCTCACCCTGAGCAAGGCCGAT TACGAGAAGCATAAGGTCTACGCC TGCGAAGTGACCCACCAGGGCCTG AGCAGCCCAGTGACGAAGTCCTTC AACCGGGGAGAATGC

	CTTCCCGCCCAAGCCGAAGGACACTC TGATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGCA CGAAGATCCCGAAGTGAAATTCAAT TGGTACGTGGATGGGGTCGAAGTGC ACAACGCCAAGACCAAGCCTAGGGA AGAACAGTACAACTCTACGTACCGG GTGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGAG TACAAGTGCAAAGTGTCAAACAAGG CTCTCCCTGCCCCTATCGAAAAGACC ATCAGCAAGGCCAAGGGTCAACCTA GGGAGCCCCAGGTCTATACTTTGCCG CCTAGCCGGGAAGAAATGACTAAGA ACCAAGTGTCCCTGACTTGCCTTGTC AAGGGCTTTTATCCGTCCGACATCGC CGTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTCC TTCTTCCTGTACTCCAAGCTGACTGT GGACAAGTCAAGATGGCAGCAGGGA AACGTGTTCTCCTGCTCCGTGATGCA CGAAGCGCTGCACAACCATTACACC CAGAAATCACTGTCACTTTCGCCGGG AAAA		
SEQ ID 1767	CAGGTCCAGCTGGTGCAGTCTGGGG GAGGCTTGGTCCAGCCTGGGGGGTC CCTGAGACTCTCCTGTTCAGCCTCTG GATTCACCTTCAGTAGCTATGCTATG CACTGGGTCCGCCAGGCTCCAGGGA AGGGACTGGAATATGTTTCAGCTATT AGTAGTAATGGGGGTAGCACATACT ACGCAGACTCAGTGAAGGGCAGATT CACCATCTCCAGAGACAATTCCAAG AACACGCTGTATCTTCAAATGAGCAG TCTGAGAGCTGAGGACACGGCTGTG TATTACTGTGTGAAAGCGCCGAGGG GTGTAGTACCAGCTGCTATGCGGGG GGGCTACTGGGGCCAGGGAACCCTG GTCACCGTCTCCTCAGCATCCACCAA GGGGCCTTCCGTGTTCCCCCTGGCCC CTTCATCCAAGTCGACCTCTGGTGGA ACCGCCGCACTCGGTTGCCTGGTCAA AGACTACTTCCCCGAGCCCGTGACTG TCTCGTGGAACTCGGGCGCCCTCACA TCCGGAGTGCATACCTTTCCCGCCGT GTTGCAGTCCAGCGGCCTGTACAGCC TGAGCTCCGTCGTGACAGTGCCGTCC TCCTCCCTTGGAACCCAGACCTATAT CTGCAACGTCAATCACAAGCCCTCCA ACACCAAAGTGGACAAGAAGGTCGA ACCCAAGTCCTGCGACAAGACTCAC ACCTGTCCGCCTTGTCCAGCCCCTGA GCTGCTGGGTGGTCCGTCCGTGTTCC	SEQ ID 1875	GAAATTGTGTTGACACAGTCTCCA CTCTCCCTGCCCGTCACCCTTGGAC AGCCGGCCTCCATCTCCTGCAGGTC TAGTCAAAGCCTCGTACACAGTAA TGGACACACCTACTTGAGTTGGTTT CAGCAGAGGCCAGGCCAATCTCCA AGGCGCCTCATTTATGAGGTTTCTA ACCGGGACTCTGGTGTCCCAGACA GATTCAGCGGCAGTGGGTCAGGCA CTGATTTCACACTAAGAATCAGCA GGGTGGAGGCTGAGGATGTTGGGG TTTATTACTGCTTGCAAGGAACACA CTGGCCCCCCCTCACTGTCGGCGG AGGGACCAAAGTGGATATCAAACG TACTGTGGCTGCTCCCTCCGTGTTC ATTTTTCCTCCGTCGGACGAACAGC TGAAGTCCGGAACCGCGTCCGTGG TCTGTCTCCTGAACAACTTCTATCC GCGCGAGGCGAAAGTGCAGTGGAA GGTCGACAACGCACTGCAGTCGGG AAACTCCCAGGAATCGGTGACCGA GCAGGACTCGAAGGACTCAACCTA CTCATTGTCCTCCACCCTCACCCTG AGCAAGGCCGATTACGAGAAGCAT AAGGTCTACGCCTGCGAAGTGACC CACCAGGGCCTGAGCAGCCCAGTG ACGAAGTCCTTCAACCGGGGAGAA TGC

	TCTTCCCGCCCAAGCCGAAGGACACT CTGATGATTTCACGCACCCCGGAAGT CACTTGCGTGGTCGTGGACGTGTCGC ACGAAGATCCCGAAGTGAAATTCAA TTGGTACGTGGATGGGGTCGAAGTG CACAACGCCAAGACCAAGCCTAGGG AAGAACAGTACAACTCTACGTACCG GGTGGTGTCCGTGCTGACCGTGCTGC ACCAGGACTGGCTGAACGGAAAGGA GTACAAGTGCAAAGTGTCAAACAAG GCTCTCCCTGCCCCTATCGAAAAGAC CATCAGCAAGGCCAAGGGTCAACCT AGGGAGCCCCAGGTCTATACTTTGCC GCCTAGCCGGGAAGAAATGACTAAG AACCAAGTGTCCCTGACTTGCCTTGT CAAGGGCTTTTATCCGTCCGACATCG CCGTGGAGTGGGAGTCCAACGGACA ACCGGAGAACAACTACAAGACCACC CCACCGGTGCTCGATTCCGATGGCTC CTTCTTCCTGTACTCCAAGCTGACTG TGGACAAGTCAAGATGGCAGCAGGG AAACGTGTTCTCCTGCTCCGTGATGC ACGAAGCGCTGCACAACCATTACAC CCAGAAATCACTGTCACTTTCGCCGG GAAAA		
SEQ ID 1768	CAGGTGCAGCTGCAGGAGTCGGGGG GAGGCTTGGTACAGCCAGGGCGGTC CCTGAGACTCTCCTGTACAGCTTCTG GATTCACCTTTGGTGATTATGCTATG AGCTGGTTCCGCCAGGCTCCAGGGA AGGGGCTGGAGTGGGTAGGTTTCATT AGAAGCAAAGCTTATGGTGGGACAA CAGAATACGCCGCGTCTGTGAAAGG CAGATTCACCATCTCAAGAGATGATT CCAAAAGCATCGCCTATCTGCAAATG AACAGCCTGAAAACCGAGGACACAG CCGTGTATTACTGTACTAGATTGGTG GGCAATAGTGGGAGCTACTATCCGTT TGGGTACTGGGGCCAGGGAACCCTG GTGACCGTCTCCTCAGCATCCACCAA GGGGCCTTCCGTGTTCCCCCTGGCCC CTTCATCCAAGTCGACCTCTGGTGGA ACCGCCGCACTCGGTTGCCTGGTCAA AGACTACTTCCCCGAGCCCGTGACTG TCTCGTGGAACTCGGGCGCCCTCACA TCCGGAGTGCATACCTTTCCCGCCGT GTTGCAGTCCAGCGGCCTGTACAGCC TGAGCTCCGTCGTGACAGTGCCGTCC TCCTCCCTTGGAACCCAGACCTATAT CTGCAACGTCAATCACAAGCCCTCCA ACACCAAAGTGGACAAGAAGGTCGA ACCCAAGTCCTGCGACAAGACTCAC ACCTGTCCGCCTTGTCCAGCCCCTGA GCTGCTGGGTGGTCCGTCCGTGTTCC	SEQ ID 1876	GATGTTGTGATGACTCAGTCTCCAG CCACCCTGTCTTTGTCTCCAGGGGA AAGAGCCACCCTCTCCTGCAGGGC CAGTCAGAGTGTTGGCAGCGACTT AGCCTGGTACCAGCAGAAACCTGG CCAGGCTCCCAGGCTCCTCATCTAC CGTGCATCCACCAGGGCCGCTGGT ATCCCAGCCAGGTTCAGTGGCAGT GGGTCTGGGACAGACTTCACTCTC ACCATCAGCAGACTGGAGCCTGAA GATTTTGCAGTGTTTTACTGTCAGC AGTATGGTAGATCACCGTACACTT CTGGCCAGGGGACCAAGCTGGAGA TCAAACGTACTGTGGCTGCTCCCTC CGTGTTCATTTTTCCTCCGTCGGAC GAACAGCTGAAGTCCGGAACCGCG TCCGTGGTCTGTCTCCTGAACAACT TCTATCCGCGCGAGGCGAAAGTGC AGTGGAAGGTCGACAACGCACTGC AGTCGGGAAACTCCCAGGAATCGG TGACCGAGCAGGACTCGAAGGACT CAACCTACTCATTGTCCTCCACCCT CACCCTGAGCAAGGCCGATTACGA GAAGCATAAGGTCTACGCCTGCGA AGTGACCCACCAGGGCCTGAGCAG CCCAGTGACGAAGTCCTTCAACCG GGGAGAATGC

	TCTTCCCGCCCAAGCCGAAGGACACT CTGATGATTTCACGCACCCCGGAAGT CACTTGCGTGGTCGTGGACGTGTCGC ACGAAGATCCCGAAGTGAAATTCAA TTGGTACGTGGATGGGGTCGAAGTG CACAACGCCAAGACCAAGCCTAGGG AAGAACAGTACAACTCTACGTACCG GGTGGTGTCCGTGCTGACCGTGCTGC ACCAGGACTGGCTGAACGGAAAGGA GTACAAGTGCAAAGTGTCAAACAAG GCTCTCCCTGCCCCTATCGAAAAGAC CATCAGCAAGGCCAAGGGTCAACCT AGGGAGCCCCAGGTCTATACTTTGCC GCCTAGCCGGGAAGAAATGACTAAG AACCAAGTGTCCCTGACTTGCCTTGT CAAGGGCTTTTATCCGTCCGACATCG CCGTGGAGTGGGAGTCCAACGGACA ACCGGAGAACAACTACAAGACCACC CCACCGGTGCTCGATTCCGATGGCTC CTTCTTCCTGTACTCCAAGCTGACTG TGGACAAGTCAAGATGGCAGCAGGG AAACGTGTTCTCCTGCTCCGTGATGC ACGAAGCGCTGCACAACCATTACAC CCAGAAATCACTGTCACTTTCGCCGG GAAAA		
SEQ ID 1769	CAGGTGCAGCTACAGCAGTGGGGCG CAGGACTGTTGAAGCCTTCGGAGAC CCTGTCCCTCACCTGCGCTGTCTATG GTGGGTCCTTCAGTGGTTACTACTGG AGCTGGATCCGCCAGCCCCCAGGGA AGGGGCTGGAGTGGATTGGGGAAAT CAATCATAGTGGAAGCACCAACTAC AACCCGTCCCTCAAGAGTCGAGTCAC CATATCAGTAGACACGTCCAAGAAC CAGTTCTCCCTGAAGCTGAGCTCGGT GACCGCCGCGGACACGGCTGTGTATT ACTGTGCGAGAGGCCGGTCCCTTCCC TACCGGGGGTTGGCTCCTAGATCTTT CGGAGGATACTACTTTGACTACTGGG GCCAGGGAACCCTGGTCACCGTCTCC TCAGCATCCACCAAGGGGCCTTCCGT GTTCCCCCTGGCCCCTTCATCCAAGT CGACCTCTGGTGGAACCGCCGCACTC GGTTGCCTGGTCAAAGACTACTTCCC CGAGCCCGTGACTGTCTCGTGGAACT CGGGCGCCCTCACATCCGGAGTGCAT ACCTTTCCCGCCGTGTTGCAGTCCAG CGGCCTGTACAGCCTGAGCTCCGTCG TGACAGTGCCGTCCTCCTCCCTTGGA ACCCAGACCTATATCTGCAACGTCAA TCACAAGCCCTCCAACACCAAAGTG GACAAGAAGGTCGAACCCAAGTCCT GCGACAAGACTCACACCTGTCCGCCT TGTCCAGCCCCTGAGCTGCTGGGTGG	SEQ ID 1877	GATATTGTGATGACCCACACTCCA GACTCCCTGGCTGTGTCTCTGGGCG AGAGGGCCACCATCAACTGCAAGT CCAGCCAGAGTGTTTTATACAGCTC CAACAATAAGAACTACTTAGCTTG GTACCAGCAGAAACCAGGACAGCC TCCTAAGCTGCTCATTTACTGGGCA TCTACCCGGGAATCCGGGGTCCCT GACCGATTCAGTGGCAGCGGGTCT GGGACAGATTTCACTCTCACCATC AGCAGCCTGCAGGCTGAAGATGTG GCAGTTTATTACTGTCAGCAATATT ATAGTACTCCGCTCACTTTCGGCGG AGGGACCAAGGTGGAGATCAAACG TACTGTGGCTGCTCCCTCCGTGTTC ATTTTTCCTCCGTCGGACGAACAGC TGAAGTCCGGAACCGCGTCCGTGG TCTGTCTCCTGAACAACTTCTATCC GCGCGAGGCGAAAGTGCAGTGGAA GGTCGACAACGCACTGCAGTCGGG AAACTCCCAGGAATCGGTGACCGA GCAGGACTCGAAGGACTCAACCTA CTCATTGTCCTCCACCCTCACCCTG AGCAAGGCCGATTACGAGAAGCAT AAGGTCTACGCCTGCGAAGTGACC CACCAGGGCCTGAGCAGCCCAGTG ACGAAGTCCTTCAACCGGGGAGAA TGC

	TCCGTCCGTGTTCCTCTTCCCGCCCA AGCCGAAGGACACTCTGATGATTTCA CGCACCCCGGAAGTCACTTGCGTGGT CGTGGACGTGTCGCACGAAGATCCC GAAGTGAAATTCAATTGGTACGTGG ATGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTAC AACTCTACGTACCGGGTGGTGTCCGT GCTGACCGTGCTGCACCAGGACTGG CTGAACGGAAAGGAGTACAAGTGCA AAGTGTCAAACAAGGCTCTCCCTGCC CCTATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTATACTTTGCCGCCTAGCCGGG AAGAAATGACTAAGAACCAAGTGTC CCTGACTTGCCTTGTCAAGGGCTTTT ATCCGTCCGACATCGCCGTGGAGTGG GAGTCCAACGGACAACCGGAGAACA ACTACAAGACCACCCCACCGGTGCTC GATTCCGATGGCTCCTTCTTCCTGTA CTCCAAGCTGACTGTGGACAAGTCA AGATGGCAGCAGGGAAACGTGTTCT CCTGCTCCGTGATGCACGAAGCGCTG CACAACCATTACACCCAGAAATCACT GTCACTTTCGCCGGGAAAA		
SEQ ID 1770	CAGGTGCAGCTGCAGGAGTCGGGGG GAGGCTTGGTACGGCCTGGAGGGTC CCTGAGACTCTCCTGTGGAGACTCTG GATTCAACTTCAGTGGATATGAAATG AACTGGGTCCGCCAGGCTCCAGGGA AGGGGCTGGAGTGGGTTTCATACGTC AGTACTAGTGGTAGTACCAGATACTA CGCAGACTCTGTGAAGGGCCGATTTA CCATCTCCAGAGACAACGCCAAGAA CACCCTGTATTTGCAAATGAACAGTC TGAGAGTCGAGGACACGGCTGTGTA TTACTGTGCAAGAGGACGGACTCACT GGGGCCCCCAGGACTTTGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTC CTCAGCATCCACCAAGGGGCCTTCCG TGTTCCCCCTGGCCCCTTCATCCAAG TCGACCTCTGGTGGAACCGCCGCACT CGGTTGCCTGGTCAAAGACTACTTCC CCGAGCCCGTGACTGTCTCGTGGAAC TCGGGCGCCCTCACATCCGGAGTGCA TACCTTTCCCGCCGTGTTGCAGTCCA GCGGCCTGTACAGCCTGAGCTCCGTC GTGACAGTGCCGTCCTCCTCCCTTGG AACCCAGACCTATATCTGCAACGTCA ATCACAAGCCCTCCAACACCAAAGT GGACAAGAAGGTCGAACCCAAGTCC TGCGACAAGACTCACACCTGTCCGCC TTGTCCAGCCCCTGAGCTGCTGGGTG GTCCGTCCGTGTTCCTCTTCCCGCCC	SEQ ID 1878	GAAATTGTGATGACGCAGTCTCCA CTCTCCCTGTCCGTCACCCCTGGAG AGCCGGCCTCCATCTCCTGCAGGTC TAGTCAGAGCCTCCTACATAGTAG TGGATACAACTATTTGGATTGGTAC CTGCAGAAGCCAGGCCAGTCTCCA CAGCTCCTGATCTATTTGGGTTCTA CTCGGGCCTCCGGGGTCCCTGACA GGTTCAGTGGCAGTGGATCAGGCA CAGATTTTACACTGAAAATCAGCA GAGTGGAGGCTGAGGATGTTGGGG TTTATTATTGCATGCAAGGTCTACA AATTCCGCTCACTTTCGGCGGAGG GACCAAAGTGGATATCAAACGTAC TGTGGCTGCTCCCTCCGTGTTCATT TTTCCTCCGTCGGACGAACAGCTG AAGTCCGGAACCGCGTCCGTGGTC TGTCTCCTGAACAACTTCTATCCGC GCGAGGCGAAAGTGCAGTGGAAG GTCGACAACGCACTGCAGTCGGGA AACTCCCAGGAATCGGTGACCGAG CAGGACTCGAAGGACTCAACCTAC TCATTGTCCTCCACCCTCACCCTGA GCAAGGCCGATTACGAGAAGCATA AGGTCTACGCCTGCGAAGTGACCC ACCAGGGCCTGAGCAGCCCAGTGA CGAAGTCCTTCAACCGGGGAGAAT GC

	AAGCCGAAGGACACTCTGATGATTTC ACGCACCCCGGAAGTCACTTGCGTG GTCGTGGACGTGTCGCACGAAGATC CCGAAGTGAAATTCAATTGGTACGTG GATGGGGTCGAAGTGCACAACGCCA AGACCAAGCCTAGGGAAGAACAGTA CAACTCTACGTACCGGGTGGTGTCCG TGCTGACCGTGCTGCACCAGGACTGG CTGAACGGAAAGGAGTACAAGTGCA AAGTGTCAAACAAGGCTCTCCCTGCC CCTATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTATACTTTGCCGCCTAGCCGGG AAGAAATGACTAAGAACCAAGTGTC CCTGACTTGCCTTGTCAAGGGCTTTT ATCCGTCCGACATCGCCGTGGAGTGG GAGTCCAACGGACAACCGGAGAACA ACTACAAGACCACCCCACCGGTGCTC GATTCCGATGGCTCCTTCTTCCTGTA CTCCAAGCTGACTGTGGACAAGTCA AGATGGCAGCAGGGAAACGTGTTCT CCTGCTCCGTGATGCACGAAGCGCTG CACAACCATTACACCCAGAAATCACT GTCACTTTCGCCGGGAAAA		
SEQ ID 1771	CAGGTGCAGCTGCAGGAGTCGGGGG GAGGCTTGGTACAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTAGCAGCTATGCCATG AGCTGGGTCCGCCAGGCTCCAGGGA AGGGGCTGGAGTGGGTCTCAGCTATT AGTGGTAGTGGTGGTAGCACATACT ACGCAGACTCCGTGAAGGGCCGGTT CACCATCTCCAGAGACAATTCCAAG AACACGCTGTATCTGCAAATGAACA GCCTGAGAGCCGAGGACACGGCCGT ATATTACTGTGCGAAAGGAGGAATG TATTACTATGGTTCGGGGAGCTCGTA CTTTGACTACTGGGGCCAGGGAACCC TGGTGACCGTCTCCTCAGCATCCACC AAGGGGCCTTCCGTGTTCCCCCTGGC CCCTTCATCCAAGTCGACCTCTGGTG GAACCGCCGCACTCGGTTGCCTGGTC AAAGACTACTTCCCCGAGCCCGTGAC TGTCTCGTGGAACTCGGGCGCCCTCA CATCCGGAGTGCATACCTTTCCCGCC GTGTTGCAGTCCAGCGGCCTGTACAG CCTGAGCTCCGTCGTGACAGTGCCGT CCTCCTCCCTTGGAACCCAGACCTAT ATCTGCAACGTCAATCACAAGCCCTC CAACACCAAAGTGGACAAGAAGGTC GAACCCAAGTCCTGCGACAAGACTC ACACCTGTCCGCCTTGTCCAGCCCCT GAGCTGCTGGGTGGTCCGTCCGTGTT	SEQ ID 1879	GATATTGTGATGACCCACACTCCA CTCTCTCTGTCCGTCACCCCTGGAC AGCCGGCCTCCATCTCCTGCAAGTC TAGTCAGAGCCTCCTGCATAGTGA TGGAAAGACCTATTTGTATTGGTAC CTGCAGAAGCCAGGCCAGCCTCCA CAGCTCCTGATCTATGAAGTTTCCA ACCGGTTCTCTGGAGTGCCAGATA GGTTCAGTGGCAGCGGGTCAGGGA CAGATTTCACACTGAAAATCAGCC GGGTGGAGGCTGAGGATGTTGGGG TTTATTACTGCATGCAAAGTATACA GCTTCCGTGGACGTTCGGCCAAGG GACCAAGGTGGAGATCAAACGTAC TGTGGCTGCTCCCTCCGTGTTCATT TTTCCTCCGTCGGACGAACAGCTG AAGTCCGGAACCGCGTCCGTGGTC TGTCTCCTGAACAACTTCTATCCGC GCGAGGCGAAAGTGCAGTGGAAG GTCGACAACGCACTGCAGTCGGGA AACTCCCAGGAATCGGTGACCGAG CAGGACTCGAAGGACTCAACCTAC TCATTGTCCTCCACCCTCACCCTGA GCAAGGCCGATTACGAGAAGCATA AGGTCTACGCCTGCGAAGTGACCC ACCAGGGCCTGAGCAGCCCAGTGA CGAAGTCCTTCAACCGGGGAGAAT GC

	CCTCTTCCCGCCCAAGCCGAAGGACA CTCTGATGATTTCACGCACCCCGGAA GTCACTTGCGTGGTCGTGGACGTGTC GCACGAAGATCCCGAAGTGAAATTC AATTGGTACGTGGATGGGGTCGAAG TGCACAACGCCAAGACCAAGCCTAG GGAAGAACAGTACAACTCTACGTAC CGGGTGGTGTCCGTGCTGACCGTGCT GCACCAGGACTGGCTGAACGGAAAG GAGTACAAGTGCAAAGTGTCAAACA AGGCTCTCCCTGCCCCTATCGAAAAG ACCATCAGCAAGGCCAAGGGTCAAC CTAGGGAGCCCCAGGTCTATACTTTG CCGCCTAGCCGGGAAGAAATGACTA AGAACCAAGTGTCCCTGACTTGCCTT GTCAAGGGCTTTTATCCGTCCGACAT CGCCGTGGAGTGGGAGTCCAACGGA CAACCGGAGAACAACTACAAGACCA CCCCACCGGTGCTCGATTCCGATGGC TCCTTCTTCCTGTACTCCAAGCTGAC TGTGGACAAGTCAAGATGGCAGCAG GGAAACGTGTTCTCCTGCTCCGTGAT GCACGAAGCGCTGCACAACCATTAC ACCCAGAAATCACTGTCACTTTCGCC GGGAAAA		
SEQ ID 1772	CAGGTGCAGCTGGTGCAATCTGGGG GAGGCTTGGTACAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTAGCAGCTATGCCATG AGCTGGGTCCGCCAGGCTCCAGGGA AGGGGCTGGAATGGGTCTCAGGTAT TAGTGGTAGTGGTGGTAGCACATACT ACGCAGACTCCGTGAAGGGCCGGTT CACCATCTCCAGAGACAATTCCAAG AACATGCTGTTTCTGCAAATGAACAG CCCGAGAGCCGAGGACACGGCCGTA TATTACTGTGCGAAGAAAATAGCAG CAGCTGGTAAGCAACCTGTTGACTAC TGGGGCCAGGGAACCCTGGTCACCG TCTCCTCAGCATCCACCAAGGGGCCT TCCGTGTTCCCCCTGGCCCCTTCATC CAAGTCGACCTCTGGTGGAACCGCC GCACTCGGTTGCCTGGTCAAAGACTA CTTCCCCGAGCCCGTGACTGTCTCGT GGAACTCGGGCGCCCTCACATCCGG AGTGCATACCTTTCCCGCCGTGTTGC AGTCCAGCGGCCTGTACAGCCTGAG CTCCGTCGTGACAGTGCCGTCCTCCT CCCTTGGAACCCAGACCTATATCTGC AACGTCAATCACAAGCCCTCCAACA CCAAAGTGGACAAGAAGGTCGAACC CAAGTCCTGCGACAAGACTCACACCT GTCCGCCTTGTCCAGCCCCTGAGCTG CTGGGTGGTCCGTCCGTGTTCCTCTT	SEQ ID 1880	GAAACGACACTCACGCAGTCTCCA GCCACCCTGTCTGTGTCTCCAGGGG AAAGAGCCACCCTCTCCTGCAGGG CCAGTCAGAGTGTTAGCAGCAACT TAGCCTGGTACCAGCAGAAACCTG GCCAGGCTCCCAGGCTCCTCATCTA TGGTGCATCCACCAGGGCCACTGG CATCCCAGCCAGGTTCAGTGGCAG TGGGTCTGGGACAGAGTTCACTCT CACCATCAGCAGCCTGCAGTCTGA AGATTTTGCAGTTTATTACTGTCAG CAGTATAATAACTGGCCTCGGTTC GGCCAAGGGACACGACTGGAGATT AAACGTACTGTGGCTGCTCCCTCCG TGTTCATTTTTCCTCCGTCGGACGA ACAGCTGAAGTCCGGAACCGCGTC CGTGGTCTGTCTCCTGAACAACTTC TATCCGCGCGAGGCGAAAGTGCAG TGGAAGGTCGACAACGCACTGCAG TCGGGAAACTCCCAGGAATCGGTG ACCGAGCAGGACTCGAAGGACTCA ACCTACTCATTGTCCTCCACCCTCA CCCTGAGCAAGGCCGATTACGAGA AGCATAAGGTCTACGCCTGCGAAG TGACCCACCAGGGCCTGAGCAGCC CAGTGACGAAGTCCTTCAACCGGG GAGAATGC

	CCCGCCCAAGCCGAAGGACACTCTG ATGATTTCACGCACCCCGGAAGTCAC TTGCGTGGTCGTGGACGTGTCGCACG AAGATCCCGAAGTGAAATTCAATTG GTACGTGGATGGGGTCGAAGTGCAC AACGCCAAGACCAAGCCTAGGGAAG AACAGTACAACTCTACGTACCGGGT GGTGTCCGTGCTGACCGTGCTGCACC AGGACTGGCTGAACGGAAAGGAGTA CAAGTGCAAAGTGTCAAACAAGGCT CTCCCTGCCCCTATCGAAAAGACCAT CAGCAAGGCCAAGGGTCAACCTAGG GAGCCCCAGGTCTATACTTTGCCGCC TAGCCGGGAAGAAATGACTAAGAAC CAAGTGTCCCTGACTTGCCTTGTCAA GGGCTTTTATCCGTCCGACATCGCCG TGGAGTGGGAGTCCAACGGACAACC GGAGAACAACTACAAGACCACCCCA CCGGTGCTCGATTCCGATGGCTCCTT CTTCCTGTACTCCAAGCTGACTGTGG ACAAGTCAAGATGGCAGCAGGGAAA CGTGTTCTCCTGCTCCGTGATGCACG AAGCGCTGCACAACCATTACACCCA GAAATCACTGTCACTTTCGCCGGGAA AA		
SEQ ID 1773	CAGGTGCAGCTACAGCAGTGGGGCG CAGGACTGTTGAAGCCTTCGGAGAC CCTGTCCCTCACCTGCGCTGTCTATG GTGGGTCCTTCAGTGGTTACTACTGG AGCTGGATCCGCCAGCCCCCAGGGA AGGGGCTGGAGTGGATTGGGGAAAT CAATCATAGTGGAAGCACCAACTAC AACCCGTCCCTCAAGAGTCGAGTCAC CATATCAGTAGACACGTCCAAGAAC CAGTTCTCCCTGAAGCTGAGCTCTGT GACCGCCGCGGACACGGCTGTGTATT ACTGTGCGAGAAGGAAGGTGTATGA TTACGTTTGGGGGAGTTATCGCCTCC CCGGGTCGGTATCGTACTACTTTGAC TACTGGGGCCAGGGAACCCTGGTCA CCGTCTCCTCAGCATCCACCAAGGGG CCTTCCGTGTTCCCCCTGGCCCCTTC ATCCAAGTCGACCTCTGGTGGAACCG CCGCACTCGGTTGCCTGGTCAAAGAC TACTTCCCCGAGCCCGTGACTGTCTC GTGGAACTCGGGCGCCCTCACATCCG GAGTGCATACCTTTCCCGCCGTGTTG CAGTCCAGCGGCCTGTACAGCCTGA GCTCCGTCGTGACAGTGCCGTCCTCC TCCCTTGGAACCCAGACCTATATCTG CAACGTCAATCACAAGCCCTCCAAC ACCAAAGTGGACAAGAAGGTCGAAC CCAAGTCCTGCGACAAGACTCACAC CTGTCCGCCTTGTCCAGCCCCTGAGC	SEQ ID 1881	GATGTTGTGATGACTCAGTCTCCTT CCACCCTGTCTGCATCTGTAGGGG ACAGAGTCACCATCACTTGCCGGG CCAGTCAGACTATTAATAGTTGGTT GGCCTGGTATCAGCAGAAACCAGG GAAGGCCCCTAAGCTCCTCATCTCT AGGGCGTCTCGTTTAGAAAGTGGG GTCCCATCAAGGTTCAGCGGCAGT GCATCTGGCACAGAATACATTCTC ACCATCAACAGCCTGCAGCCTGAT GATTTTGCAATGTACTTCTGCCATC AATATAATAGTTATTCTCCCACTTT TGGCCAGGGGACCAAGCTGGAGAT CAAACGTACTGTGGCTGCTCCCTCC GTGTTCATTTTTCCTCCGTCGGACG AACAGCTGAAGTCCGGAACCGCGT CCGTGGTCTGTCTCCTGAACAACTT CTATCCGCGCGAGGCGAAAGTGCA GTGGAAGGTCGACAACGCACTGCA GTCGGGAAACTCCCAGGAATCGGT GACCGAGCAGGACTCGAAGGACTC AACCTACTCATTGTCCTCCACCCTC ACCCTGAGCAAGGCCGATTACGAG AAGCATAAGGTCTACGCCTGCGAA GTGACCCACCAGGGCCTGAGCAGC CCAGTGACGAAGTCCTTCAACCGG GGAGAATGC

	TGCTGGGTGGTCCGTCCGTGTTCCTC TTCCCGCCCAAGCCGAAGGACACTCT GATGATTTCACGCACCCCGGAAGTCA CTTGCGTGGTCGTGGACGTGTCGCAC GAAGATCCCGAAGTGAAATTCAATT GGTACGTGGATGGGGTCGAAGTGCA CAACGCCAAGACCAAGCCTAGGGAA GAACAGTACAACTCTACGTACCGGG TGGTGTCCGTGCTGACCGTGCTGCAC CAGGACTGGCTGAACGGAAAGGAGT ACAAGTGCAAAGTGTCAAACAAGGC TCTCCCTGCCCCTATCGAAAAGACCA TCAGCAAGGCCAAGGGTCAACCTAG GGAGCCCCAGGTCTATACTTTGCCGC CTAGCCGGGAAGAAATGACTAAGAA CCAAGTGTCCCTGACTTGCCTTGTCA AGGGCTTTTATCCGTCCGACATCGCC GTGGAGTGGGAGTCCAACGGACAAC CGGAGAACAACTACAAGACCACCCC ACCGGTGCTCGATTCCGATGGCTCCT TCTTCCTGTACTCCAAGCTGACTGTG GACAAGTCAAGATGGCAGCAGGGAA ACGTGTTCTCCTGCTCCGTGATGCAC GAAGCGCTGCACAACCATTACACCC AGAAATCACTGTCACTTTCGCCGGGA AAA		
SEQ ID 1774	CAGGTCCAGCTGGTACAGTCTGGAG CAGAGGTGAAAAAGCCCGGGGAGTC TCTGAAGATCTCCTGTAAGGGTTCTG GATACAGCTTTACCAGCTACTGGATC GGCTGGGTGCGCCAGATGCCCGGGA AAGGCCTGGAGTGGATGGGGATCAT CTATCCTGGTGACTCTGATACCAGAT ACAGCCCGTCCTTCCAAGGCCAGGTC ACCATCTCAGCCGACAAGTCCATCAG CACCGCCTACCTGCAGTGGAGCAGC CTGAAGGCCTCGGACACCGCCATGT ATTACTGTGCGAGACTCCCGGGGAG AGCAGCTCGTCCAGACTACTGGGGC CAGGGCACCCTGGTCACCGTCTCCTC AGCATCCACCAAGGGGCCTTCCGTGT TCCCCCTGGCCCCTTCATCCAAGTCG ACCTCTGGTGGAACCGCCGCACTCGG TTGCCTGGTCAAAGACTACTTCCCCG AGCCCGTGACTGTCTCGTGGAACTCG GGCGCCCTCACATCCGGAGTGCATAC CTTTCCCGCCGTGTTGCAGTCCAGCG GCCTGTACAGCCTGAGCTCCGTCGTG ACAGTGCCGTCCTCCTCCCTTGGAAC CCAGACCTATATCTGCAACGTCAATC ACAAGCCCTCCAACACCAAAGTGGA CAAGAAGGTCGAACCCAAGTCCTGC GACAAGACTCACACCTGTCCGCCTTG TCCAGCCCCTGAGCTGCTGGGTGGTC CGTCCGTGTTCCTCTTCCCGCCCAAG	SEQ ID 1882	GAAACGACACTCACGCAGTCTCCA GGCACCCTGTCTTTGTCTCCAGGGG AAAGAGCCACCCTCTCCTGCAGGG CCAGTCAGAGTGTTAGCAGCAGCT ACTTAGCCTGGTACCAGCAGAAAC CTGGCCAGGCTCCCAGGCTCCTCAT CTATGGTGCATCCAGCAGGGCCAC TGGCATCCCAGCCAGGTTCAGTGG CAGTGGGTCTGGGACAGACTTCAC TCTCACCATCAGCAGCCTAGAGCC TGAAGATTTTGCAGTTTATTACTGT CAGCAGCGTTACAACTGGCCTATC ACCTTCGGCCAAGGGACACGACTG GAGATTAAACGTACTGTGGCTGCT CCCTCCGTGTTCATTTTTCCTCCGT CGGACGAACAGCTGAAGTCCGGAA CCGCGTCCGTGGTCTGTCTCCTGAA CAACTTCTATCCGCGCGAGGCGAA AGTGCAGTGGAAGGTCGACAACGC ACTGCAGTCGGGAAACTCCCAGGA ATCGGTGACCGAGCAGGACTCGAA GGACTCAACCTACTCATTGTCCTCC ACCCTCACCCTGAGCAAGGCCGAT TACGAGAAGCATAAGGTCTACGCC TGCGAAGTGACCCACCAGGGCCTG AGCAGCCCAGTGACGAAGTCCTTC AACCGGGGAGAATGC

	CCGAAGGACACTCTGATGATTTCACG CACCCCGGAAGTCACTTGCGTGGTCG TGGACGTGTCGCACGAAGATCCCGA AGTGAAATTCAATTGGTACGTGGATG GGGTCGAAGTGCACAACGCCAAGAC CAAGCCTAGGGAAGAACAGTACAAC TCTACGTACCGGGTGGTGTCCGTGCT GACCGTGCTGCACCAGGACTGGCTG AACGGAAAGGAGTACAAGTGCAAAG TGTCAAACAAGGCTCTCCCTGCCCCT ATCGAAAAGACCATCAGCAAGGCCA AGGGTCAACCTAGGGAGCCCCAGGT CTATACTTTGCCGCCTAGCCGGGAAG AAATGACTAAGAACCAAGTGTCCCT GACTTGCCTTGTCAAGGGCTTTTATC CGTCCGACATCGCCGTGGAGTGGGA GTCCAACGGACAACCGGAGAACAAC TACAAGACCACCCCACCGGTGCTCG ATTCCGATGGCTCCTTCTTCCTGTACT CCAAGCTGACTGTGGACAAGTCAAG ATGGCAGCAGGGAAACGTGTTCTCCT GCTCCGTGATGCACGAAGCGCTGCA CAACCATTACACCCAGAAATCACTGT CACTTTCGCCGGGAAAA		
SEQ ID 1775	CAGGTCACCTTGAAGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTCAGTAGCTATGCTATG CACTGGGTCCGCCAGGCTCCAGGCA AGGGGCTGGAGTGGGTGGCAGTTAT ATCATATGATGGAAGTAATAAATACT ACGCAGACTCCGTGAAGGGCCGATT CACCATCTCCAGAGACAATTCCAAG AACACGCTGTATCTGCAAATGAACA GCCTGAGAGCTGAGGACACGGCTGT GTATTACTGTGCGAGAGGCCCCGGG GCAGTGGCTGGTACTAAGCCAAAGT ACTACTTTGACTACTGGGGCCAGGGA ACCCTGGTCACCGTCTCCTCAGCATC CACCAAGGGGCCTTCCGTGTTCCCCC TGGCCCCTTCATCCAAGTCGACCTCT GGTGGAACCGCCGCACTCGGTTGCCT GGTCAAAGACTACTTCCCCGAGCCCG TGACTGTCTCGTGGAACTCGGGCGCC CTCACATCCGGAGTGCATACCTTTCC CGCCGTGTTGCAGTCCAGCGGCCTGT ACAGCCTGAGCTCCGTCGTGACAGTG CCGTCCTCCTCCCTTGGAACCCAGAC CTATATCTGCAACGTCAATCACAAGC CCTCCAACACCAAAGTGGACAAGAA GGTCGAACCCAAGTCCTGCGACAAG ACTCACACCTGTCCGCCTTGTCCAGC CCCTGAGCTGCTGGGTGGTCCGTCCG	SEQ ID 1883	GAAATTGTGTTGACGCAGTCTCCA GCCACCCTGTCTTTGTCTCCGGGGG AAACAGCCACCCTCTCCTGCAGGG CCAGTCAGACTATTGGTCCCAAGT CCTTCGGCTGGTACCAACAGAGAC CTGGCCAGGCTCCCAGGCTCCTCAT CTATGACTCCAACAGGGCCACTGG CATCCCAGCCAGGTTCAGTGGCAG TGGGTCTGGGACAGACTTCACTCTC ACCATCAGCAGCCTAGAGCCTGAA GATTTTGCAGTTTATTACTGTCAGC AGCGTAGCAGGTGGCCTCTCACTTT CGGCCCTGGGACCAAAGTGGATAT CAAACGTACTGTGGCTGCTCCCTCC GTGTTCATTTTTCCTCCGTCGGACG AACAGCTGAAGTCCGGAACCGCGT CCGTGGTCTGTCTCCTGAACAACTT CTATCCGCGCGAGGCGAAAGTGCA GTGGAAGGTCGACAACGCACTGCA GTCGGGAAACTCCCAGGAATCGGT GACCGAGCAGGACTCGAAGGACTC AACCTACTCATTGTCCTCCACCCTC ACCCTGAGCAAGGCCGATTACGAG AAGCATAAGGTCTACGCCTGCGAA GTGACCCACCAGGGCCTGAGCAGC CCAGTGACGAAGTCCTTCAACCGG GGAGAATGC

	TGTTCCTCTTCCCGCCCAAGCCGAAG GACACTCTGATGATTTCACGCACCCC GGAAGTCACTTGCGTGGTCGTGGAC GTGTCGCACGAAGATCCCGAAGTGA AATTCAATTGGTACGTGGATGGGGTC GAAGTGCACAACGCCAAGACCAAGC CTAGGGAAGAACAGTACAACTCTAC GTACCGGGTGGTGTCCGTGCTGACCG TGCTGCACCAGGACTGGCTGAACGG AAAGGAGTACAAGTGCAAAGTGTCA AACAAGGCTCTCCCTGCCCCTATCGA AAAGACCATCAGCAAGGCCAAGGGT CAACCTAGGGAGCCCCAGGTCTATA CTTTGCCGCCTAGCCGGGAAGAAAT GACTAAGAACCAAGTGTCCCTGACTT GCCTTGTCAAGGGCTTTTATCCGTCC GACATCGCCGTGGAGTGGGAGTCCA ACGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCCG ATGGCTCCTTCTTCCTGTACTCCAAG CTGACTGTGGACAAGTCAAGATGGC AGCAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACTT TCGCCGGGAAAA		
SEQ ID 1776	GAGGTCCAGCTGGTGCAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTCAGTAGCTATGCTATG CACTGGGTCCGCCAGGCTCCAGGCA AGGGGCTGGAGTGGGTGGCAGTTAT ATCATATGATGGAAGTAATAAATACT ACGCAGACTCCGTGAAGGGCCGATT CACCATCTCCAGAGACAATTCCAAG AACACGCTGTATCTGCAAATGAACA GCCTGAGAGCTGAGGACACGGCTGT GTATTACTGTGCGAGGGCCACGTATT ACTATGATAGTAGTGGTTATAGGTTT GACTACTGGGGCCAGGGAACCCTGG TCACCGTCTCCTCAGCATCCACCAAG GGGCCTTCCGTGTTCCCCCTGGCCCC TTCATCCAAGTCGACCTCTGGTGGAA CCGCCGCACTCGGTTGCCTGGTCAAA GACTACTTCCCCGAGCCCGTGACTGT CTCGTGGAACTCGGGCGCCCTCACAT CCGGAGTGCATACCTTTCCCGCCGTG TTGCAGTCCAGCGGCCTGTACAGCCT GAGCTCCGTCGTGACAGTGCCGTCCT CCTCCCTTGGAACCCAGACCTATATC TGCAACGTCAATCACAAGCCCTCCAA CACCAAAGTGGACAAGAAGGTCGAA CCCAAGTCCTGCGACAAGACTCACA CCTGTCCGCCTTGTCCAGCCCCTGAG CTGCTGGGTGGTCCGTCCGTGTTCCT	SEQ ID 1884	GATGTTGTGATGACTCAGTCTCCAC TCTCCCTGCCCGTCACCCTTGGACA GCCGGCCTCCATCTCCTGCAGGTCT AGTCAAAGCCTCGTGTACAGTGAT GGAAACACCTACTTGTATTGGTTTC AGCAGAGGGCAGGCCAATCTCCAA GGCGCCTGATTTATAAGGTTTCTAA GCGGGACTCTGGGGTCCCAGACAG GTTCAGCGGCAGTGGGTCAGGCAC TGATTTCACACTGAAAATCAGCAG GGTGGAGGCTGAGGATGTTGGAAT TTATTACTGCGTGCAAGGTAGACA CTGGCCGTACACTCTTGGCCAGGG GACCAAGCTGGAGATCAAACGTAC TGTGGCTGCTCCCTCCGTGTTCATT TTTCCTCCGTCGGACGAACAGCTG AAGTCCGGAACCGCGTCCGTGGTC TGTCTCCTGAACAACTTCTATCCGC GCGAGGCGAAAGTGCAGTGGAAG GTCGACAACGCACTGCAGTCGGGA AACTCCCAGGAATCGGTGACCGAG CAGGACTCGAAGGACTCAACCTAC TCATTGTCCTCCACCCTCACCCTGA GCAAGGCCGATTACGAGAAGCATA AGGTCTACGCCTGCGAAGTGACCC ACCAGGGCCTGAGCAGCCCAGTGA CGAAGTCCTTCAACCGGGGAGAAT GC

	CTTCCCGCCCAAGCCGAAGGACACTC TGATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGCA CGAAGATCCCGAAGTGAAATTCAAT TGGTACGTGGATGGGGTCGAAGTGC ACAACGCCAAGACCAAGCCTAGGGA AGAACAGTACAACTCTACGTACCGG GTGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGAG TACAAGTGCAAAGTGTCAAACAAGG CTCTCCCTGCCCCTATCGAAAAGACC ATCAGCAAGGCCAAGGGTCAACCTA GGGAGCCCCAGGTCTATACTTTGCCG CCTAGCCGGGAAGAAATGACTAAGA ACCAAGTGTCCCTGACTTGCCTTGTC AAGGGCTTTTATCCGTCCGACATCGC CGTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTCC TTCTTCCTGTACTCCAAGCTGACTGT GGACAAGTCAAGATGGCAGCAGGGA AACGTGTTCTCCTGCTCCGTGATGCA CGAAGCGCTGCACAACCATTACACC CAGAAATCACTGTCACTTTCGCCGGG AAAA		
SEQ ID 1777	GAGGTCCAGCTGGTACAGTCTGGGG GAGGCTTGGTAGAACCGGGGGGGTC CCTTAGACTCTCCTGTGCAGCCTCTC GATTCACTTTCAGTGACGCCTGGATG AGCTGGGTCCGCCAGGCTCCAGGTA AGGGGCTGGAGTGGGTTGGCCGTAT TAAAAGCAAAATAAGTGGTGGGACA ACAGACTACGCTGCACCCGTGCAAG GCAGATTCACCATCTCAAGAGATGAT TCAAAAAACACGCTGTATCTGCAAAT GGACAGCCTGAAAACCGAGGACACA GCCGTGTATTACTGTGCGAACCGAAA CTTAGGCTACTGGGGCCAGGGCACC CTGGTGACCGTCTCCTCAGCATCCAC CAAGGGGCCTTCCGTGTTCCCCCTGG CCCCTTCATCCAAGTCGACCTCTGGT GGAACCGCCGCACTCGGTTGCCTGGT CAAAGACTACTTCCCCGAGCCCGTGA CTGTCTCGTGGAACTCGGGCGCCCTC ACATCCGGAGTGCATACCTTTCCCGC CGTGTTGCAGTCCAGCGGCCTGTACA GCCTGAGCTCCGTCGTGACAGTGCCG TCCTCCTCCCTTGGAACCCAGACCTA TATCTGCAACGTCAATCACAAGCCCT CCAACACCAAAGTGGACAAGAAGGT CGAACCCAAGTCCTGCGACAAGACT CACACCTGTCCGCCTTGTCCAGCCCC TGAGCTGCTGGGTGGTCCGTCCGTGT TCCTCTTCCCGCCCAAGCCGAAGGAC	SEQ ID 1885	GAAATTGTGTTGACGCAGTCTCCA GGCACCCTGTCTTTGTCTCCAGGGG AAAGAGCCACCCTCTCCTGCAGGG CCAGTCAGAGTGTTAGCAGCAGCT ACTTAGCCTGGTACCAGCAGAAAC CTGGCCAGGCTCCCAGGCTCCTCAT CTATGATGCATCCAACAGGGCCAC TGGCATCCCAGCCAGGTTCAGTGG CAGTGGATCTGGGACAGAATTCAC TCTCACCATCAGCAGCCTGCAGCCT GATGATTTTGCAACTTATTACTGCC AACAGTATAATAGTTATTCAAGGA CGTTCGGCCAGGGGACCAAAGTGG ATATCAAACGTACTGTGGCTGCTCC CTCCGTGTTCATTTTTCCTCCGTCG GACGAACAGCTGAAGTCCGGAACC GCGTCCGTGGTCTGTCTCCTGAACA ACTTCTATCCGCGCGAGGCGAAAG TGCAGTGGAAGGTCGACAACGCAC TGCAGTCGGGAAACTCCCAGGAAT CGGTGACCGAGCAGGACTCGAAGG ACTCAACCTACTCATTGTCCTCCAC CCTCACCCTGAGCAAGGCCGATTA CGAGAAGCATAAGGTCTACGCCTG CGAAGTGACCCACCAGGGCCTGAG CAGCCCAGTGACGAAGTCCTTCAA CCGGGGAGAATGC

	ACTCTGATGATTTCACGCACCCCGGA AGTCACTTGCGTGGTCGTGGACGTGT CGCACGAAGATCCCGAAGTGAAATT CAATTGGTACGTGGATGGGGTCGAA GTGCACAACGCCAAGACCAAGCCTA GGGAAGAACAGTACAACTCTACGTA CCGGGTGGTGTCCGTGCTGACCGTGC TGCACCAGGACTGGCTGAACGGAAA GGAGTACAAGTGCAAAGTGTCAAAC AAGGCTCTCCCTGCCCCTATCGAAAA GACCATCAGCAAGGCCAAGGGTCAA CCTAGGGAGCCCCAGGTCTATACTTT GCCGCCTAGCCGGGAAGAAATGACT AAGAACCAAGTGTCCCTGACTTGCCT TGTCAAGGGCTTTTATCCGTCCGACA TCGCCGTGGAGTGGGAGTCCAACGG ACAACCGGAGAACAACTACAAGACC ACCCCACCGGTGCTCGATTCCGATGG CTCCTTCTTCCTGTACTCCAAGCTGA CTGTGGACAAGTCAAGATGGCAGCA GGGAAACGTGTTCTCCTGCTCCGTGA TGCACGAAGCGCTGCACAACCATTA CACCCAGAAATCACTGTCACTTTCGC CGGGAAAA		
SEQ ID 1778	GAGGTCCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTTTCCTGCAAGGCTTCTG GATACACCTTCACTAGCTATGCTATG CATTGGGTGCGCCAGGCCCCCGGAC AAAGGCTTGAGTGGATGGGATGGAT CAACGCTGGCAATGGTAACACAAAA TATTCACAGAAGTTCCAGGGCAGAG TCACCATGACCACAGACACATCCAC GAGCACAGCCTACATGGAGCTGAGG AGCCTGAGATCTGACGACACGGCCG TGTATTACTGTGCGAGAGCTCGTTAC TATGATAGTAGTGGTTATATTGCCCC ATCGGGTTACTTTGACTACTGGGGCC AGGGAACCCTGGTCACCGTCTCCTCA GCATCCACCAAGGGGCCTTCCGTGTT CCCCCTGGCCCCTTCATCCAAGTCGA CCTCTGGTGGAACCGCCGCACTCGGT TGCCTGGTCAAAGACTACTTCCCCGA GCCCGTGACTGTCTCGTGGAACTCGG GCGCCCTCACATCCGGAGTGCATACC TTTCCCGCCGTGTTGCAGTCCAGCGG CCTGTACAGCCTGAGCTCCGTCGTGA CAGTGCCGTCCTCCTCCCTTGGAACC CAGACCTATATCTGCAACGTCAATCA CAAGCCCTCCAACACCAAAGTGGAC AAGAAGGTCGAACCCAAGTCCTGCG ACAAGACTCACACCTGTCCGCCTTGT CCAGCCCCTGAGCTGCTGGGTGGTCC GTCCGTGTTCCTCTTCCCGCCCAAGC	SEQ ID 1886	GATGTTGTGATGACTCAGTCTCCTT CCACCCTGTCTGCATCTGTGGGAG ACAGAGTCACCATCACTTGCCGGG CCAGTCAGAGTATTACTACCTGGTT GGCCTGGTCTCAGCAGCAACCAGG GAAAGCCCCTAAGCTCCTCATCTAT AAGGCCTCTAGTTTAACAAGTGGG GTCCCATCAAGGTTCAGCGGCAGT GGATCTGGGACAGAGTTCACTCTC ACCATCAGCAGCCTGCAGCCTGAT GATTTTGCAAGTTATTACTGCCATC ATTATAATGGTGCTTCTCGTATGTT CGGCCAAGGGACCAAGCTGGAGAT CAAACGTACTGTGGCTGCTCCCTCC GTGTTCATTTTTCCTCCGTCGGACG AACAGCTGAAGTCCGGAACCGCGT CCGTGGTCTGTCTCCTGAACAACTT CTATCCGCGCGAGGCGAAAGTGCA GTGGAAGGTCGACAACGCACTGCA GTCGGGAAACTCCCAGGAATCGGT GACCGAGCAGGACTCGAAGGACTC AACCTACTCATTGTCCTCCACCCTC ACCCTGAGCAAGGCCGATTACGAG AAGCATAAGGTCTACGCCTGCGAA GTGACCCACCAGGGCCTGAGCAGC CCAGTGACGAAGTCCTTCAACCGG GGAGAATGC

	CGAAGGACACTCTGATGATTTCACGC ACCCCGGAAGTCACTTGCGTGGTCGT GGACGTGTCGCACGAAGATCCCGAA GTGAAATTCAATTGGTACGTGGATGG GGTCGAAGTGCACAACGCCAAGACC AAGCCTAGGGAAGAACAGTACAACT CTACGTACCGGGTGGTGTCCGTGCTG ACCGTGCTGCACCAGGACTGGCTGA ACGGAAAGGAGTACAAGTGCAAAGT GTCAAACAAGGCTCTCCCTGCCCCTA TCGAAAAGACCATCAGCAAGGCCAA GGGTCAACCTAGGGAGCCCCAGGTC TATACTTTGCCGCCTAGCCGGGAAGA AATGACTAAGAACCAAGTGTCCCTG ACTTGCCTTGTCAAGGGCTTTTATCC GTCCGACATCGCCGTGGAGTGGGAG TCCAACGGACAACCGGAGAACAACT ACAAGACCACCCCACCGGTGCTCGA TTCCGATGGCTCCTTCTTCCTGTACTC CAAGCTGACTGTGGACAAGTCAAGA TGGCAGCAGGGAAACGTGTTCTCCTG CTCCGTGATGCACGAAGCGCTGCAC AACCATTACACCCAGAAATCACTGTC ACTTTCGCCGGGAAAA		
SEQ ID 1779	CAGGTGCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTTTCCTGCAAGGCTTCTG GATACACCTTCACTAGCTATGCTATG CATTGGGTGCGCCAGGCCCCCGGAC AAAGGCTTGAGTGGATGGGATGGAT CAACGCTGGCAATGGTAACACAAAA TATTCACAGAAGTTCCAGGGCAGAG TCACCATTACCAGGGACACATCCGCG AGCACAGCCTACATGGAGCTGAGCA GCCTGAGATCTGAAGACACGGCTGT GTATTACTGTGCGAGAGATGGCCCCG CCGTTGATGGTGCTGAATACTTCCAG CACTGGGGCCAGGGCACCCTGGTCA CCGTCTCCTCAGCATCCACCAAGGGG CCTTCCGTGTTCCCCCTGGCCCCTTC ATCCAAGTCGACCTCTGGTGGAACCG CCGCACTCGGTTGCCTGGTCAAAGAC TACTTCCCCGAGCCCGTGACTGTCTC GTGGAACTCGGGCGCCCTCACATCCG GAGTGCATACCTTTCCCGCCGTGTTG CAGTCCAGCGGCCTGTACAGCCTGA GCTCCGTCGTGACAGTGCCGTCCTCC TCCCTTGGAACCCAGACCTATATCTG CAACGTCAATCACAAGCCCTCCAAC ACCAAAGTGGACAAGAAGGTCGAAC CCAAGTCCTGCGACAAGACTCACAC CTGTCCGCCTTGTCCAGCCCCTGAGC TGCTGGGTGGTCCGTCCGTGTTCCTC	SEQ ID 1887	GAAACGACACTCACGCAGTCTCCA GCCACCCTGTCTTTGTCTCCAGGGG AAAGAGCCACCCTCTCCTGCAGGG CCAGTCAGAGTGTTAGCAGCTACT TAGCCTGGTACCAACAGAAACCTG GCCAGGCTCCCAGGCTCCTCATCTA TGATGCATCCAACAGGGCCACTGG CATCCCAGCCAGGTTCAGTGGCAG TGGGTCTGGGACAGACTTCACTCTC ACCATCAGCAGCCTAGAGCCTGAA GATTTTGCAGTTTATTACTGTCAGC AGCGTAGCAACTGGCCTTTCTTCGG CCAAGGGACACGACTGGAGATTAA ACGTACTGTGGCTGCTCCCTCCGTG TTCATTTTTCCTCCGTCGGACGAAC AGCTGAAGTCCGGAACCGCGTCCG TGGTCTGTCTCCTGAACAACTTCTA TCCGCGCGAGGCGAAAGTGCAGTG GAAGGTCGACAACGCACTGCAGTC GGGAAACTCCCAGGAATCGGTGAC CGAGCAGGACTCGAAGGACTCAAC CTACTCATTGTCCTCCACCCTCACC CTGAGCAAGGCCGATTACGAGAAG CATAAGGTCTACGCCTGCGAAGTG ACCCACCAGGGCCTGAGCAGCCCA GTGACGAAGTCCTTCAACCGGGGA GAATGC

	TTCCCGCCCAAGCCGAAGGACACTCT GATGATTTCACGCACCCCGGAAGTCA CTTGCGTGGTCGTGGACGTGTCGCAC GAAGATCCCGAAGTGAAATTCAATT GGTACGTGGATGGGGTCGAAGTGCA CAACGCCAAGACCAAGCCTAGGGAA GAACAGTACAACTCTACGTACCGGG TGGTGTCCGTGCTGACCGTGCTGCAC CAGGACTGGCTGAACGGAAAGGAGT ACAAGTGCAAAGTGTCAAACAAGGC TCTCCCTGCCCCTATCGAAAAGACCA TCAGCAAGGCCAAGGGTCAACCTAG GGAGCCCCAGGTCTATACTTTGCCGC CTAGCCGGGAAGAAATGACTAAGAA CCAAGTGTCCCTGACTTGCCTTGTCA AGGGCTTTTATCCGTCCGACATCGCC GTGGAGTGGGAGTCCAACGGACAAC CGGAGAACAACTACAAGACCACCCC ACCGGTGCTCGATTCCGATGGCTCCT TCTTCCTGTACTCCAAGCTGACTGTG GACAAGTCAAGATGGCAGCAGGGAA ACGTGTTCTCCTGCTCCGTGATGCAC GAAGCGCTGCACAACCATTACACCC AGAAATCACTGTCACTTTCGCCGGGA AAA		
SEQ ID 1780	CAGCTGCAGCTGCAGGAGTCGGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCAACAGTGCT GCTTGGAACTGGATCAGGCAGTCCCC ATCGCGAGGCCTTGAGTGGCTGGGA AGGACTTACTACAGGTCCAAGTGGT ATAATGATTATGCAGTATCTCTGAAA AGTCGAATAACCATCAACCCGGACA CATCCAAGAACCAGTTCTCCCTGCAG CTGAACTCTGTGACTCCCGAGGACAC GGCTGTATATTACTGTGCAAGTTTGG CGAGTGGTTCCCCCCCTCCGGGGGAC TACTGGGGCCAGGGAACCCTGGTGA CCGTCTCCTCAGCATCCACCAAGGGG CCTTCCGTGTTCCCCCTGGCCCCTTC ATCCAAGTCGACCTCTGGTGGAACCG CCGCACTCGGTTGCCTGGTCAAAGAC TACTTCCCCGAGCCCGTGACTGTCTC GTGGAACTCGGGCGCCCTCACATCCG GAGTGCATACCTTTCCCGCCGTGTTG CAGTCCAGCGGCCTGTACAGCCTGA GCTCCGTCGTGACAGTGCCGTCCTCC TCCCTTGGAACCCAGACCTATATCTG CAACGTCAATCACAAGCCCTCCAAC ACCAAAGTGGACAAGAAGGTCGAAC CCAAGTCCTGCGACAAGACTCACAC CTGTCCGCCTTGTCCAGCCCCTGAGC TGCTGGGTGGTCCGTCCGTGTTCCTC	SEQ ID 1888	GAAACGACACTCACGCAGTCTCCA GCCACCCTGACTTTGTCTCCAGGGG AAAGAGTCACCCTCTCCTGCAGGG CCAGTCAGAGTATTGGCACTTACG TCGCCTGGTATCAGCAGAAACCTG GCCAGGCTCCCAGATTCCTCATCTA TGATTCATCGAATAGGGCCACTGG CATCCCAGCCAGGTTCAGTGGTAG TGGGTCTGGGACAGACTTCACTCTC ACGATCAGCAGCCTGGAGCCTGAA GATTTTGCATTTTATTACTGTCAAC AGCGTGCCGAGTGGCCTCTCACCTT CGGCCAAGGGACACGACTGGAGAT TAAACGTACTGTGGCTGCTCCCTCC GTGTTCATTTTTCCTCCGTCGGACG AACAGCTGAAGTCCGGAACCGCGT CCGTGGTCTGTCTCCTGAACAACTT CTATCCGCGCGAGGCGAAAGTGCA GTGGAAGGTCGACAACGCACTGCA GTCGGGAAACTCCCAGGAATCGGT GACCGAGCAGGACTCGAAGGACTC AACCTACTCATTGTCCTCCACCCTC ACCCTGAGCAAGGCCGATTACGAG AAGCATAAGGTCTACGCCTGCGAA GTGACCCACCAGGGCCTGAGCAGC CCAGTGACGAAGTCCTTCAACCGG GGAGAATGC

	TTCCCGCCCAAGCCGAAGGACACTCT GATGATTTCACGCACCCCGGAAGTCA CTTGCGTGGTCGTGGACGTGTCGCAC GAAGATCCCGAAGTGAAATTCAATT GGTACGTGGATGGGGTCGAAGTGCA CAACGCCAAGACCAAGCCTAGGGAA GAACAGTACAACTCTACGTACCGGG TGGTGTCCGTGCTGACCGTGCTGCAC CAGGACTGGCTGAACGGAAAGGAGT ACAAGTGCAAAGTGTCAAACAAGGC TCTCCCTGCCCCTATCGAAAAGACCA TCAGCAAGGCCAAGGGTCAACCTAG GGAGCCCCAGGTCTATACTTTGCCGC CTAGCCGGGAAGAAATGACTAAGAA CCAAGTGTCCCTGACTTGCCTTGTCA AGGGCTTTTATCCGTCCGACATCGCC GTGGAGTGGGAGTCCAACGGACAAC CGGAGAACAACTACAAGACCACCCC ACCGGTGCTCGATTCCGATGGCTCCT TCTTCCTGTACTCCAAGCTGACTGTG GACAAGTCAAGATGGCAGCAGGGAA ACGTGTTCTCCTGCTCCGTGATGCAC GAAGCGCTGCACAACCATTACACCC AGAAATCACTGTCACTTTCGCCGGGA AAA		
SEQ ID 1781	CAGGTCACCTTGAAGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTCAGTACCTATGGCATG CACTGGGTCCGCCAGGCTCCAGGCA AGGGGCTGGAGTGGGTGGCACTTAT ATCATATGATGGAAGTAAAAAATAC TATGCAAACTCCGTGAAGGGCCGATT CACCATCTCCAGAGACAATTCCAAG AACACGTTGTATCTGCAAATGAAAA GTCTGAGAGCTGAGGACACGGCTAT GTATTACTGTGCGAAAGGCCCTATAG TGGGAGCGACTATGGACTACTGGGG CCAGGGAGCCCTGGTCACCGTCTCCT CAGCATCCACCAAGGGGCCTTCCGTG TTCCCCCTGGCCCCTTCATCCAAGTC GACCTCTGGTGGAACCGCCGCACTCG GTTGCCTGGTCAAAGACTACTTCCCC GAGCCCGTGACTGTCTCGTGGAACTC GGGCGCCCTCACATCCGGAGTGCAT ACCTTTCCCGCCGTGTTGCAGTCCAG CGGCCTGTACAGCCTGAGCTCCGTCG TGACAGTGCCGTCCTCCTCCCTTGGA ACCCAGACCTATATCTGCAACGTCAA TCACAAGCCCTCCAACACCAAAGTG GACAAGAAGGTCGAACCCAAGTCCT GCGACAAGACTCACACCTGTCCGCCT TGTCCAGCCCCTGAGCTGCTGGGTGG TCCGTCCGTGTTCCTCTTCCCGCCCA	SEQ ID 1889	GATGTTGTGATGACTCAGTCTCCAG GCACCCTGTCTTTGTCTCCAGGGGA AAGAGCCACTCTCTCCTGCAGGGC CAGTCAGAGTGTTAATAGCGGCTA CTTAGCCTGGTACCAGCAGAAACC TGGCCAACCTCCCAGACTCCTCATC TCTGGTGTTTCCACCAGGGCCACTG GCATCCCAGACAGGTTCAGTGGCA GTGGGTCTGGGACAGACTTCACTC TCACCATCAGCAGACTGGAGCCTG AAGATTTTGCAGTGTATTACTGTCA GGAGTATGGTAACTCAGCTATGTA CAATTTTGGCCAGGGGACCAAGCT GGAGATCAAACGTACTGTGGCTGC TCCCTCCGTGTTCATTTTTCCTCCGT CGGACGAACAGCTGAAGTCCGGAA CCGCGTCCGTGGTCTGTCTCCTGAA CAACTTCTATCCGCGCGAGGCGAA AGTGCAGTGGAAGGTCGACAACGC ACTGCAGTCGGGAAACTCCCAGGA ATCGGTGACCGAGCAGGACTCGAA GGACTCAACCTACTCATTGTCCTCC ACCCTCACCCTGAGCAAGGCCGAT TACGAGAAGCATAAGGTCTACGCC TGCGAAGTGACCCACCAGGGCCTG AGCAGCCCAGTGACGAAGTCCTTC AACCGGGGAGAATGC

	AGCCGAAGGACACTCTGATGATTTCA CGCACCCCGGAAGTCACTTGCGTGGT CGTGGACGTGTCGCACGAAGATCCC GAAGTGAAATTCAATTGGTACGTGG ATGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTAC AACTCTACGTACCGGGTGGTGTCCGT GCTGACCGTGCTGCACCAGGACTGG CTGAACGGAAAGGAGTACAAGTGCA AAGTGTCAAACAAGGCTCTCCCTGCC CCTATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTATACTTTGCCGCCTAGCCGGG AAGAAATGACTAAGAACCAAGTGTC CCTGACTTGCCTTGTCAAGGGCTTTT ATCCGTCCGACATCGCCGTGGAGTGG GAGTCCAACGGACAACCGGAGAACA ACTACAAGACCACCCCACCGGTGCTC GATTCCGATGGCTCCTTCTTCCTGTA CTCCAAGCTGACTGTGGACAAGTCA AGATGGCAGCAGGGAAACGTGTTCT CCTGCTCCGTGATGCACGAAGCGCTG CACAACCATTACACCCAGAAATCACT GTCACTTTCGCCGGGAAAA		
SEQ ID 1782	GAGGTGCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGTCCTC GGTGAAGGTCTCCTGCAAGGCTTCTG GAGGCACCTTCAGCAGCTATGCTATC AGCTGGGTGCGACAGGCCCCTGGAC AAGGGCTTGAGTGGATGGGATGGAT CAGCGCTTACAATGGTAACACAAAC TATGCACAGAAGCTCCAGGGCAGAG TCACCATGACCACAGACACATCCAC GAGCACAGCCTACATGGAGCTGAGG AGCCTGAGATCTGACGACACGGCCG TGTATTACTGTGCGAGATGGTACGGT GACTACGGCCTTGACTACTGGGGCCA GGGAACCCTGGTCACCGTCTCCTCAG CATCCACCAAGGGGCCTTCCGTGTTC CCCCTGGCCCCTTCATCCAAGTCGAC CTCTGGTGGAACCGCCGCACTCGGTT GCCTGGTCAAAGACTACTTCCCCGAG CCCGTGACTGTCTCGTGGAACTCGGG CGCCCTCACATCCGGAGTGCATACCT TTCCCGCCGTGTTGCAGTCCAGCGGC CTGTACAGCCTGAGCTCCGTCGTGAC AGTGCCGTCCTCCTCCCTTGGAACCC AGACCTATATCTGCAACGTCAATCAC AAGCCCTCCAACACCAAAGTGGACA AGAAGGTCGAACCCAAGTCCTGCGA CAAGACTCACACCTGTCCGCCTTGTC CAGCCCCTGAGCTGCTGGGTGGTCCG TCCGTGTTCCTCTTCCCGCCCAAGCC	SEQ ID 1890	GAAACGACACTCACGCAGTCTCCA GCCACCCTGTCTGTGTCTCCAGGGG AAAGAGCCACCCTCTCCTGCAGGG CCAGTCAGAGTGTTAGCAGCAACT TAGCCTGGTACCAGCAGAAACCTG GCCAGGCTCCCAGGCTCCTCATCTA TGGTGCATCCACCAGGGCCACTGG TATCCCAGCCAGGTTCAGTGGCAG TGGGTCTGGGACAGAGTTCACTCT CACCATCAGCAGCCTGCAGTCTGA AGATTTTGCAGTTTATTACTGTCAG CAGTATAATAACTGGCCTCCCTTCA CCTTCGGCCAAGGGACACGACTGG AGATTAAACGTACTGTGGCTGCTC CCTCCGTGTTCATTTTTCCTCCGTC GGACGAACAGCTGAAGTCCGGAAC CGCGTCCGTGGTCTGTCTCCTGAAC AACTTCTATCCGCGCGAGGCGAAA GTGCAGTGGAAGGTCGACAACGCA CTGCAGTCGGGAAACTCCCAGGAA TCGGTGACCGAGCAGGACTCGAAG GACTCAACCTACTCATTGTCCTCCA CCCTCACCCTGAGCAAGGCCGATT ACGAGAAGCATAAGGTCTACGCCT GCGAAGTGACCCACCAGGGCCTGA GCAGCCCAGTGACGAAGTCCTTCA ACCGGGGAGAATGC

	GAAGGACACTCTGATGATTTCACGCA CCCCGGAAGTCACTTGCGTGGTCGTG GACGTGTCGCACGAAGATCCCGAAG TGAAATTCAATTGGTACGTGGATGGG GTCGAAGTGCACAACGCCAAGACCA AGCCTAGGGAAGAACAGTACAACTC TACGTACCGGGTGGTGTCCGTGCTGA CCGTGCTGCACCAGGACTGGCTGAA CGGAAAGGAGTACAAGTGCAAAGTG TCAAACAAGGCTCTCCCTGCCCCTAT CGAAAAGACCATCAGCAAGGCCAAG GGTCAACCTAGGGAGCCCCAGGTCT ATACTTTGCCGCCTAGCCGGGAAGA AATGACTAAGAACCAAGTGTCCCTG ACTTGCCTTGTCAAGGGCTTTTATCC GTCCGACATCGCCGTGGAGTGGGAG TCCAACGGACAACCGGAGAACAACT ACAAGACCACCCCACCGGTGCTCGA TTCCGATGGCTCCTTCTTCCTGTACTC CAAGCTGACTGTGGACAAGTCAAGA TGGCAGCAGGGAAACGTGTTCTCCTG CTCCGTGATGCACGAAGCGCTGCAC AACCATTACACCCAGAAATCACTGTC ACTTTCGCCGGGAAAA		
SEQ ID 1783	GAGGTCCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTTTCCTGCAAGGCTTCTG GATACACCTTCACTAGCTATGCTATG CATTGGGTGCGCCAGGCCCCCGGAC AAAGGCTTGCGTGGATGGGATGGAT CAACGCTGGCAATGGTAACACAAAA TATTCAGAGAAGTTCGAAGGCAGAG TCACCATCACCAGGGACACATCCGC GAGCACAGCCTACATGGAGCTGAGC AGCCTGAGATCTGAAGACACGGCTG TGTATTACTGTGCGAGGGTCGCCAAA TATTATTACGAGAGTGGTGGTTATCG GGCCTCCAACTGGTTCGACCCCTGGG GCCAGGGCACCCTGGTCACCGTCTCC TCAGCATCCACCAAGGGGCCTTCCGT GTTCCCCCTGGCCCCTTCATCCAAGT CGACCTCTGGTGGAACCGCCGCACTC GGTTGCCTGGTCAAAGACTACTTCCC CGAGCCCGTGACTGTCTCGTGGAACT CGGGCGCCCTCACATCCGGAGTGCAT ACCTTTCCCGCCGTGTTGCAGTCCAG CGGCCTGTACAGCCTGAGCTCCGTCG TGACAGTGCCGTCCTCCTCCCTTGGA ACCCAGACCTATATCTGCAACGTCAA TCACAAGCCCTCCAACACCAAAGTG GACAAGAAGGTCGAACCCAAGTCCT GCGACAAGACTCACACCTGTCCGCCT TGTCCAGCCCCTGAGCTGCTGGGTGG	SEQ ID 1891	GATGTTGTGATGACTCAGTCTCCAG GCACCCTGTCTTTGTCTCCAGGGGA AAGAGCCACCCTCTCCTGCAGGGC CAGTCAGAGTGTTAGCAGCAGCTA CTTAGGCTGGTATCAGCAGAAATC CGGCCAGGCTCCCAGGCTCCTCAT CTATGGTGCATCCAGCAGGGCCAC TGACATCCCAGACAGGTTCAGTGG CAGTGGGTCTGGGACAGACTTCAC TCTCACCATCAGCAAACTGGAGGC AGAAGATTCTGCAGTGTATTACTGT CAGCAGTATGGTATCTCACCTCTCG CGTTCGGCCAAGGGACCAAGCTGG AGATCAAACGTACTGTGGCTGCTC CCTCCGTGTTCATTTTTCCTCCGTC GGACGAACAGCTGAAGTCCGGAAC CGCGTCCGTGGTCTGTCTCCTGAAC AACTTCTATCCGCGCGAGGCGAAA GTGCAGTGGAAGGTCGACAACGCA CTGCAGTCGGGAAACTCCCAGGAA TCGGTGACCGAGCAGGACTCGAAG GACTCAACCTACTCATTGTCCTCCA CCCTCACCCTGAGCAAGGCCGATT ACGAGAAGCATAAGGTCTACGCCT GCGAAGTGACCCACCAGGGCCTGA GCAGCCCAGTGACGAAGTCCTTCA ACCGGGGAGAATGC

	TCCGTCCGTGTTCCTCTTCCCGCCCA AGCCGAAGGACACTCTGATGATTTCA CGCACCCCGGAAGTCACTTGCGTGGT CGTGGACGTGTCGCACGAAGATCCC GAAGTGAAATTCAATTGGTACGTGG ATGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTAC AACTCTACGTACCGGGTGGTGTCCGT GCTGACCGTGCTGCACCAGGACTGG CTGAACGGAAAGGAGTACAAGTGCA AAGTGTCAAACAAGGCTCTCCCTGCC CCTATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTATACTTTGCCGCCTAGCCGGG AAGAAATGACTAAGAACCAAGTGTC CCTGACTTGCCTTGTCAAGGGCTTTT ATCCGTCCGACATCGCCGTGGAGTGG GAGTCCAACGGACAACCGGAGAACA ACTACAAGACCACCCCACCGGTGCTC GATTCCGATGGCTCCTTCTTCCTGTA CTCCAAGCTGACTGTGGACAAGTCA AGATGGCAGCAGGGAAACGTGTTCT CCTGCTCCGTGATGCACGAAGCGCTG CACAACCATTACACCCAGAAATCACT GTCACTTTCGCCGGGAAAA		
SEQ ID 1784	CAGGTGCAGCTGCAGGAGTCAGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCAACAGTGCT GCTTGGAACTGGATCAGGCAGTCCCC ATCGAGAGGCCTTGAGTGGCTGGGA AGGACATACTACAGGTCCAAGTGGT ATAATGATTATGCAGTATCTGTGAAA AGTCGAATAACCATCAACCCAGACA CATCCAAGAACCAGTTCTCCCTGCAG CTGAACTCTGTGACTCCCGAGGACAC GGCTGTGTATTACTGTGCAAGAGCGC CCCCTCCGACTGTTGGCTGGTACGCC CCCGTCTTTGACTACTGGGGCCAGGG AACCCTGGTCACCGTCTCCTCAGCAT CCACCAAGGGGCCTTCCGTGTTCCCC CTGGCCCCTTCATCCAAGTCGACCTC TGGTGGAACCGCCGCACTCGGTTGCC TGGTCAAAGACTACTTCCCCGAGCCC GTGACTGTCTCGTGGAACTCGGGCGC CCTCACATCCGGAGTGCATACCTTTC CCGCCGTGTTGCAGTCCAGCGGCCTG TACAGCCTGAGCTCCGTCGTGACAGT GCCGTCCTCCTCCCTTGGAACCCAGA CCTATATCTGCAACGTCAATCACAAG CCCTCCAACACCAAAGTGGACAAGA AGGTCGAACCCAAGTCCTGCGACAA GACTCACACCTGTCCGCCTTGTCCAG CCCCTGAGCTGCTGGGTGGTCCGTCC	SEQ ID 1892	GAAACGACACTCACGCAGTCTCCA GCCACCCTGTCTGTGTCTCCAGGGG AGAGAGCCACCCTCTCCTGCAGGG CCAGTCAGAGTATTAGCAACAACT TAGCCTGGTACCAGCAGAAACCTG GCCAGGCTCCCAGGCTCCTCATCTA TGGTACATCCACCAGGGCCACTGG TATCCCAGCCAGGTTCAGTGGCAG TGGGTCTGGGACAGAGTTCACTCT CACCATCAGCAGCCTGCAGTCTGA AGATTTTGCAGTTTATTACTGTCAG CAGTATAATTTCTGGCCTTCGATCA CCTTCGGCCAAGGGACACGACTGG AGATTAAACGTACTGTGGCTGCTC CCTCCGTGTTCATTTTTCCTCCGTC GGACGAACAGCTGAAGTCCGGAAC CGCGTCCGTGGTCTGTCTCCTGAAC AACTTCTATCCGCGCGAGGCGAAA GTGCAGTGGAAGGTCGACAACGCA CTGCAGTCGGGAAACTCCCAGGAA TCGGTGACCGAGCAGGACTCGAAG GACTCAACCTACTCATTGTCCTCCA CCCTCACCCTGAGCAAGGCCGATT ACGAGAAGCATAAGGTCTACGCCT GCGAAGTGACCCACCAGGGCCTGA GCAGCCCAGTGACGAAGTCCTTCA ACCGGGGAGAATGC

	GTGTTCCTCTTCCCGCCCAAGCCGAA GGACACTCTGATGATTTCACGCACCC CGGAAGTCACTTGCGTGGTCGTGGAC GTGTCGCACGAAGATCCCGAAGTGA AATTCAATTGGTACGTGGATGGGGTC GAAGTGCACAACGCCAAGACCAAGC CTAGGGAAGAACAGTACAACTCTAC GTACCGGGTGGTGTCCGTGCTGACCG TGCTGCACCAGGACTGGCTGAACGG AAAGGAGTACAAGTGCAAAGTGTCA AACAAGGCTCTCCCTGCCCCTATCGA AAAGACCATCAGCAAGGCCAAGGGT CAACCTAGGGAGCCCCAGGTCTATA CTTTGCCGCCTAGCCGGGAAGAAAT GACTAAGAACCAAGTGTCCCTGACTT GCCTTGTCAAGGGCTTTTATCCGTCC GACATCGCCGTGGAGTGGGAGTCCA ACGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCCG ATGGCTCCTTCTTCCTGTACTCCAAG CTGACTGTGGACAAGTCAAGATGGC AGCAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACTT TCGCCGGGAAAA		
SEQ ID 1785	CAGCTGCAGCTGCAGGAGTCCGGGG GAGGCTTAGTTCAGCCGGGGGGGTC CCTGAGACTCTCCTGCTCAGCCTCTG GAATCAGCTTCAGAGATTACTGGATG CACTGGATCCGCCAAACTCCAGGGA AGGGGCTGGTGTGGGTCTCACGTATT AATCCTGATGGGAGTAGCACAAGCT ACGCGGACTCCGTGAAGGGCCGATT CACCATCTCCAGAGACAATTCCAAG AACACGCTGTATCTGCAAATGAACA GCCTGAGAGCTGAGGACACGGCTGT GTATTACTGTGCGAAAGTTACGGGAC GGAGAGTGGGAGCCCATGACTACTG GGGCCAGGGAACCCTGGTCACCGTC TCCTCAGCATCCACCAAGGGGCCTTC CGTGTTCCCCCTGGCCCCTTCATCCA AGTCGACCTCTGGTGGAACCGCCGC ACTCGGTTGCCTGGTCAAAGACTACT TCCCCGAGCCCGTGACTGTCTCGTGG AACTCGGGCGCCCTCACATCCGGAGT GCATACCTTTCCCGCCGTGTTGCAGT CCAGCGGCCTGTACAGCCTGAGCTCC GTCGTGACAGTGCCGTCCTCCTCCCT TGGAACCCAGACCTATATCTGCAACG TCAATCACAAGCCCTCCAACACCAA AGTGGACAAGAAGGTCGAACCCAAG TCCTGCGACAAGACTCACACCTGTCC GCCTTGTCCAGCCCCTGAGCTGCTGG GTGGTCCGTCCGTGTTCCTCTTCCCG	SEQ ID 1893	GAAACGACACTCACGCAGTCTCCA GGCACCCTGTCTTTGTCTCCAGGGG AAAGAGCCACCCTCTCCTGCAGGG CCAGTCAGAGTGTTAGCAGCAGCT CCTTAGCCTGGTACCAGCAGAAAC CTGGCCAGGCTCCCAGGCTCCTCAT CTATGGTGCATCCAGCAGGGCCAC TGGCATCCCAGACAGGTTCAGTGG CAGTGGGTCTGGGACAGACTTCAC TCTCACCATCAGCAGACTGGAGCC TGAAGATTTTGCAGTGTATTACTGT CAGCAGTATGGTAGCTCACAGACC TTCGGCCAAGGGACACGACTGGAG ATTAAACGTACTGTGGCTGCTCCCT CCGTGTTCATTTTTCCTCCGTCGGA CGAACAGCTGAAGTCCGGAACCGC GTCCGTGGTCTGTCTCCTGAACAAC TTCTATCCGCGCGAGGCGAAAGTG CAGTGGAAGGTCGACAACGCACTG CAGTCGGGAAACTCCCAGGAATCG GTGACCGAGCAGGACTCGAAGGAC TCAACCTACTCATTGTCCTCCACCC TCACCCTGAGCAAGGCCGATTACG AGAAGCATAAGGTCTACGCCTGCG AAGTGACCCACCAGGGCCTGAGCA GCCCAGTGACGAAGTCCTTCAACC GGGGAGAATGC

	CCCAAGCCGAAGGACACTCTGATGA TTTCACGCACCCCGGAAGTCACTTGC GTGGTCGTGGACGTGTCGCACGAAG ATCCCGAAGTGAAATTCAATTGGTAC GTGGATGGGGTCGAAGTGCACAACG CCAAGACCAAGCCTAGGGAAGAACA GTACAACTCTACGTACCGGGTGGTGT CCGTGCTGACCGTGCTGCACCAGGAC TGGCTGAACGGAAAGGAGTACAAGT GCAAAGTGTCAAACAAGGCTCTCCCT GCCCCTATCGAAAAGACCATCAGCA AGGCCAAGGGTCAACCTAGGGAGCC CCAGGTCTATACTTTGCCGCCTAGCC GGGAAGAAATGACTAAGAACCAAGT GTCCCTGACTTGCCTTGTCAAGGGCT TTTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAGA ACAACTACAAGACCACCCCACCGGT GCTCGATTCCGATGGCTCCTTCTTCC TGTACTCCAAGCTGACTGTGGACAAG TCAAGATGGCAGCAGGGAAACGTGT TCTCCTGCTCCGTGATGCACGAAGCG CTGCACAACCATTACACCCAGAAATC ACTGTCACTTTCGCCGGGAAAA		
SEQ ID 1786	CAGGTGCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTCTCCTGCAAGGCTTCTG GATACACCTTCACCGGCTACTATATG CACTGGGTGCGACAGGCCCCTGGAC AAGGGCTTGAGTGGATGGGATGGAT CAACCCTAACAGTGGTGGCACAAAC TATGCACAGAAGTTTCAGGGCAGGG TCACCATGACCAGGGACACGTCCATC AGCACAGCCTACATGGAGCTGAGCA GGCTGAGATCTGACGACACGGCCGT GTATTACTGTGCCTTTGCCCAGCCGG GCGCTGAGACGTTGAACTTCGATCTC TGGGGCCGTGGCACCCTGGTCACCGT CTCCTCAGCATCCACCAAGGGGCCTT CCGTGTTCCCCCTGGCCCCTTCATCC AAGTCGACCTCTGGTGGAACCGCCG CACTCGGTTGCCTGGTCAAAGACTAC TTCCCCGAGCCCGTGACTGTCTCGTG GAACTCGGGCGCCCTCACATCCGGA GTGCATACCTTTCCCGCCGTGTTGCA GTCCAGCGGCCTGTACAGCCTGAGCT CCGTCGTGACAGTGCCGTCCTCCTCC CTTGGAACCCAGACCTATATCTGCAA CGTCAATCACAAGCCCTCCAACACCA AAGTGGACAAGAAGGTCGAACCCAA GTCCTGCGACAAGACTCACACCTGTC CGCCTTGTCCAGCCCCTGAGCTGCTG GGTGGTCCGTCCGTGTTCCTCTTCCC	SEQ ID 1894	GATGTTGTGATGACTCAGTCTCCAC TCTCCCTGCCCGTCTCCCTTGGACA GCCGGCCTCCATCTCCTGCAGGTCT AATCAAAGCCTCGTATACAGTGAT GGAGGCACCTACTTGAATTGGTTTC AGCAGAGGGCAGGCCAGTCTCCAA GGCGCCTAGTTTATAAGGTTTCTAA CCGGGACTCTGGGGTCCCAGACAG ATTCAGCGGCAGTGGGTCAGGCAC TGATTTCACACTGAGAATCAGCAG GGTGGAGGCTGAGGATGTTGGGGT TTATTACTGCATGCAAGGGACACA CTGGCCGTACACTTTTGGCCAGGG GACCAAGCTGGAGATCAAACGTAC TGTGGCTGCTCCCTCCGTGTTCATT TTTCCTCCGTCGGACGAACAGCTG AAGTCCGGAACCGCGTCCGTGGTC TGTCTCCTGAACAACTTCTATCCGC GCGAGGCGAAAGTGCAGTGGAAG GTCGACAACGCACTGCAGTCGGGA AACTCCCAGGAATCGGTGACCGAG CAGGACTCGAAGGACTCAACCTAC TCATTGTCCTCCACCCTCACCCTGA GCAAGGCCGATTACGAGAAGCATA AGGTCTACGCCTGCGAAGTGACCC ACCAGGGCCTGAGCAGCCCAGTGA CGAAGTCCTTCAACCGGGGAGAAT GC

	GCCCAAGCCGAAGGACACTCTGATG ATTTCACGCACCCCGGAAGTCACTTG CGTGGTCGTGGACGTGTCGCACGAA GATCCCGAAGTGAAATTCAATTGGTA CGTGGATGGGGTCGAAGTGCACAAC GCCAAGACCAAGCCTAGGGAAGAAC AGTACAACTCTACGTACCGGGTGGTG TCCGTGCTGACCGTGCTGCACCAGGA CTGGCTGAACGGAAAGGAGTACAAG TGCAAAGTGTCAAACAAGGCTCTCCC TGCCCCTATCGAAAAGACCATCAGC AAGGCCAAGGGTCAACCTAGGGAGC CCCAGGTCTATACTTTGCCGCCTAGC CGGGAAGAAATGACTAAGAACCAAG TGTCCCTGACTTGCCTTGTCAAGGGC TTTTATCCGTCCGACATCGCCGTGGA GTGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCAAGCTGACTGTGGACAA GTCAAGATGGCAGCAGGGAAACGTG TTCTCCTGCTCCGTGATGCACGAAGC GCTGCACAACCATTACACCCAGAAA TCACTGTCACTTTCGCCGGGAAAA		
SEQ ID 1787	CAGGTACAGCTGCAGCAGTCAGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCAAAAGTGC TGCTTGGAACTGGATCAGGCAGTCCC CATCGAGAGGCCTTGAGTGGCTGGG AAGGACATACTACAGGTCCAAATGG AATAATGATTATGCATTATCTGTGAA AAGTCGAATAACCATCAACCCAGAC ACATCCAAGAACCAGTTCTCCCTGCA GCTGAAGTCTGTGACTCCCGAGGAC ACGGCTCTGTATTACTGTGTAAGACA AGTCGCGGGCGGTATGGACGTCTGG GGCCAAGGGACCACGGTCACCGTCT CCTCAGCATCCACCAAGGGGCCTTCC GTGTTCCCCCTGGCCCCTTCATCCAA GTCGACCTCTGGTGGAACCGCCGCAC TCGGTTGCCTGGTCAAAGACTACTTC CCCGAGCCCGTGACTGTCTCGTGGAA CTCGGGCGCCCTCACATCCGGAGTGC ATACCTTTCCCGCCGTGTTGCAGTCC AGCGGCCTGTACAGCCTGAGCTCCGT CGTGACAGTGCCGTCCTCCTCCCTTG GAACCCAGACCTATATCTGCAACGTC AATCACAAGCCCTCCAACACCAAAG TGGACAAGAAGGTCGAACCCAAGTC CTGCGACAAGACTCACACCTGTCCGC CTTGTCCAGCCCCTGAGCTGCTGGGT GGTCCGTCCGTGTTCCTCTTCCCGCC	SEQ ID 1895	GACATCCAGTTGACCCAGTCTCCAT CCTCCCTGTCTGCATCTGTAGGAGA CAGAGTCACCGTCACTTGCCGGGC AAGTCAGAGCATTAGCAGCTATTT AAATTGGTATCAGCAGAAACCAGG GAAAGCCCCTCAACTCCTGATCTA CGATGCATCCAATTTGGAAACAGG GGTCCCCTCAAGGTTCAGTGGAAG TGGATCTGGGACAGATTTTACTTTC ACCATCAGCAGCCTGCAGCCTGAA GATTTTGCAACATATTACTGTCAGC AGTTTGATAATGTCCCAGTCACTTT CGGCGGAGGGACCAAGGTGGAAAT CAAACGTACTGTGGCTGCTCCCTCC GTGTTCATTTTTCCTCCGTCGGACG AACAGCTGAAGTCCGGAACCGCGT CCGTGGTCTGTCTCCTGAACAACTT CTATCCGCGCGAGGCGAAAGTGCA GTGGAAGGTCGACAACGCACTGCA GTCGGGAAACTCCCAGGAATCGGT GACCGAGCAGGACTCGAAGGACTC AACCTACTCATTGTCCTCCACCCTC ACCCTGAGCAAGGCCGATTACGAG AAGCATAAGGTCTACGCCTGCGAA GTGACCCACCAGGGCCTGAGCAGC CCAGTGACGAAGTCCTTCAACCGG GGAGAATGC

	CAAGCCGAAGGACACTCTGATGATTT CACGCACCCCGGAAGTCACTTGCGTG GTCGTGGACGTGTCGCACGAAGATC CCGAAGTGAAATTCAATTGGTACGTG GATGGGGTCGAAGTGCACAACGCCA AGACCAAGCCTAGGGAAGAACAGTA CAACTCTACGTACCGGGTGGTGTCCG TGCTGACCGTGCTGCACCAGGACTGG CTGAACGGAAAGGAGTACAAGTGCA AAGTGTCAAACAAGGCTCTCCCTGCC CCTATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTATACTTTGCCGCCTAGCCGGG AAGAAATGACTAAGAACCAAGTGTC CCTGACTTGCCTTGTCAAGGGCTTTT ATCCGTCCGACATCGCCGTGGAGTGG GAGTCCAACGGACAACCGGAGAACA ACTACAAGACCACCCCACCGGTGCTC GATTCCGATGGCTCCTTCTTCCTGTA CTCCAAGCTGACTGTGGACAAGTCA AGATGGCAGCAGGGAAACGTGTTCT CCTGCTCCGTGATGCACGAAGCGCTG CACAACCATTACACCCAGAAATCACT GTCACTTTCGCCGGGAAAA		
SEQ ID 1788	CAGGTGCAGCTGGTGCAATCTGGGG GAGGCTTGGTACAGCCAGGGCGGTC CCTGAGACTCTCCTGTACAGCTTCTG GATTCACCTTTGGTGATTATGCTATG AGCTGGTTCCGCCAGGCTCCAGGGA AGGGGCTGGAGTGGGTCTCAGCTATT AGTGGTAGTGGTGGTAGCACATACT ATGCAGACTCCGTGAAGGGCCGATT CACCATCTCCAGAGACAATTCCAAG AACACGCTGTATCTGCAAATGAACA GCCTGAGAGCTGAGGACACGGCTGT GTATTACTGTGCGAAAGGATCGGTAT ATAGTGGGAGCTACTATATGCTCATT GACTACTGGGGCCAGGGCACCCTGG TCACCGTCTCCTCAGCATCCACCAAG GGGCCTTCCGTGTTCCCCCTGGCCCC TTCATCCAAGTCGACCTCTGGTGGAA CCGCCGCACTCGGTTGCCTGGTCAAA GACTACTTCCCCGAGCCCGTGACTGT CTCGTGGAACTCGGGCGCCCTCACAT CCGGAGTGCATACCTTTCCCGCCGTG TTGCAGTCCAGCGGCCTGTACAGCCT GAGCTCCGTCGTGACAGTGCCGTCCT CCTCCCTTGGAACCCAGACCTATATC TGCAACGTCAATCACAAGCCCTCCAA CACCAAAGTGGACAAGAAGGTCGAA CCCAAGTCCTGCGACAAGACTCACA CCTGTCCGCCTTGTCCAGCCCCTGAG CTGCTGGGTGGTCCGTCCGTGTTCCT	SEQ ID 1896	GAAATTGTGCTGACTCAGTCTCCAC TCTCCCTGCCCGTCACCCTTGGACA GCCGGCCTCCATCTCCTGCAGGTCT AGTCAAAGCCTCGTATACAGTGAT GGAAACACCTACTTGAATTGGTTTC AGCAGAGGCCAGGCCAATCTCCAA GGCGCCTAATTTATAAGGTTTCTAA CCGGGACTCTGGGGTCCCAGACAG ATTCAGCGGCAGTGGGTCAGGCAC TGATTTCACACTGAAAATCAGCAG GGTGGAGGCTGAGGATGTTGGGGT TTATTACTGCATGCAAGGTACACA CTGGCCTCGAACGTTCGGCCAAGG GACCAAGCTGGAGATCAAACGTAC TGTGGCTGCTCCCTCCGTGTTCATT TTTCCTCCGTCGGACGAACAGCTG AAGTCCGGAACCGCGTCCGTGGTC TGTCTCCTGAACAACTTCTATCCGC GCGAGGCGAAAGTGCAGTGGAAG GTCGACAACGCACTGCAGTCGGGA AACTCCCAGGAATCGGTGACCGAG CAGGACTCGAAGGACTCAACCTAC TCATTGTCCTCCACCCTCACCCTGA GCAAGGCCGATTACGAGAAGCATA AGGTCTACGCCTGCGAAGTGACCC ACCAGGGCCTGAGCAGCCCAGTGA CGAAGTCCTTCAACCGGGGAGAAT GC

	CTTCCCGCCCAAGCCGAAGGACACTC TGATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGCA CGAAGATCCCGAAGTGAAATTCAAT TGGTACGTGGATGGGGTCGAAGTGC ACAACGCCAAGACCAAGCCTAGGGA AGAACAGTACAACTCTACGTACCGG GTGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGAG TACAAGTGCAAAGTGTCAAACAAGG CTCTCCCTGCCCCTATCGAAAAGACC ATCAGCAAGGCCAAGGGTCAACCTA GGGAGCCCCAGGTCTATACTTTGCCG CCTAGCCGGGAAGAAATGACTAAGA ACCAAGTGTCCCTGACTTGCCTTGTC AAGGGCTTTTATCCGTCCGACATCGC CGTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTCC TTCTTCCTGTACTCCAAGCTGACTGT GGACAAGTCAAGATGGCAGCAGGGA AACGTGTTCTCCTGCTCCGTGATGCA CGAAGCGCTGCACAACCATTACACC CAGAAATCACTGTCACTTTCGCCGGG AAAA		
SEQ ID 1789	CAGGTACAGCTGCAGCAGTCAGGTC CAGGACTGGTGAGGCCCTCGCAGAC CCTCTCACTCACCTGTGTCATCTCCG GGGACAGTGTCTCTAGCGGCAGTGCT GCTTGGAACTGGATCAGGCAGTCCCC ATCGAGAGGCCTTGAGTGGCTGGGA AGGACATATTATAGGGCCAAGTGGT ATAATGAATATGCAGGGTCTGTGAA AAGCCGAATAACCATCAGTCCGGAC ACATCCAAGAACCAGTTCTCCCTGCA ACTGAACTCTGTGACTCCCGAGGACA CGGCTGTGTATTTCTGTACAAGACAA GACAAAGACAACACGAGATATTCCG GTTTGGGCGTCTGGGGCCAAGGGAC CACGGTGACCGTCTCCTCAGCATCCA CCAAGGGGCCTTCCGTGTTCCCCCTG GCCCCTTCATCCAAGTCGACCTCTGG TGGAACCGCCGCACTCGGTTGCCTGG TCAAAGACTACTTCCCCGAGCCCGTG ACTGTCTCGTGGAACTCGGGCGCCCT CACATCCGGAGTGCATACCTTTCCCG CCGTGTTGCAGTCCAGCGGCCTGTAC AGCCTGAGCTCCGTCGTGACAGTGCC GTCCTCCTCCCTTGGAACCCAGACCT ATATCTGCAACGTCAATCACAAGCCC TCCAACACCAAAGTGGACAAGAAGG TCGAACCCAAGTCCTGCGACAAGAC TCACACCTGTCCGCCTTGTCCAGCCC CTGAGCTGCTGGGTGGTCCGTCCGTG	SEQ ID 1897	GATGTTGTGATGACTCAGTCTCCAG CCACCCTGTCTGTGTCTCCAGGGGA AAGAGCCACCCTCTCCTGCAGGGC CAGTCAGAGTGTTAGCAGCAACTT AGCCTGGTACCAGCAGAAACCTGG CCAGGCTCCCAGGCTCCTCATCTAT GGTGCATCCAGCAGGGCCACTGGC ATCCCAGACAGGTTCAGTGGCAGT GGGTCTGGGACAGACTTCACTCTC ACCATCAACAGACTGGAGCCTGAA GATTTTGCAGTGTATTACTGTCAGC AGTATGGTAGCTCATCCATGTACA CTTTTGGCCAGGGGACCAAGCTGG AGATCAAACGTACTGTGGCTGCTC CCTCCGTGTTCATTTTTCCTCCGTC GGACGAACAGCTGAAGTCCGGAAC CGCGTCCGTGGTCTGTCTCCTGAAC AACTTCTATCCGCGCGAGGCGAAA GTGCAGTGGAAGGTCGACAACGCA CTGCAGTCGGGAAACTCCCAGGAA TCGGTGACCGAGCAGGACTCGAAG GACTCAACCTACTCATTGTCCTCCA CCCTCACCCTGAGCAAGGCCGATT ACGAGAAGCATAAGGTCTACGCCT GCGAAGTGACCCACCAGGGCCTGA GCAGCCCAGTGACGAAGTCCTTCA ACCGGGGAGAATGC

	TTCCTCTTCCCGCCCAAGCCGAAGGA CACTCTGATGATTTCACGCACCCCGG AAGTCACTTGCGTGGTCGTGGACGTG TCGCACGAAGATCCCGAAGTGAAAT TCAATTGGTACGTGGATGGGGTCGA AGTGCACAACGCCAAGACCAAGCCT AGGGAAGAACAGTACAACTCTACGT ACCGGGTGGTGTCCGTGCTGACCGTG CTGCACCAGGACTGGCTGAACGGAA AGGAGTACAAGTGCAAAGTGTCAAA CAAGGCTCTCCCTGCCCCTATCGAAA AGACCATCAGCAAGGCCAAGGGTCA ACCTAGGGAGCCCCAGGTCTATACTT TGCCGCCTAGCCGGGAAGAAATGAC TAAGAACCAAGTGTCCCTGACTTGCC TTGTCAAGGGCTTTTATCCGTCCGAC ATCGCCGTGGAGTGGGAGTCCAACG GACAACCGGAGAACAACTACAAGAC CACCCCACCGGTGCTCGATTCCGATG GCTCCTTCTTCCTGTACTCCAAGCTG ACTGTGGACAAGTCAAGATGGCAGC AGGGAAACGTGTTCTCCTGCTCCGTG ATGCACGAAGCGCTGCACAACCATT ACACCCAGAAATCACTGTCACTTTCG CCGGGAAAA		
SEQ ID 1790	GAGGTGCAGCTGGTGGAGACCGGGG GAGGCTTAGTTCAGCCTGGGGGGTCC CTGAGACTCTCCTGTGCAGCCTCTGA ATTCACCCTTAGGAACTATGGCGTGA GCTGGGTCCGCCAGGCTCCAGGGAA GGGGCTGGAGTGGGTCTCAGGTATG AGTGGTAGTGGTTATAGTACATACTA CGCAGACTCCGTGAAGGGCCGGTTC ACCATCTCCAGAGACAGTTCCAAGA ACACGCTGTTTCTGCAAATGGACAGC CTGAGAGCCGAGGACACGGCCATAT ATTACTGTGCGAGAGGGCCCCGAAT GTGGAGCAGTGGCATTGATGCTTTTG ATATCTGGGGCCACGGGACAATGGT GACCGTCTCTTCAGCATCCACCAAGG GGCCTTCCGTGTTCCCCCTGGCCCCT TCATCCAAGTCGACCTCTGGTGGAAC CGCCGCACTCGGTTGCCTGGTCAAAG ACTACTTCCCCGAGCCCGTGACTGTC TCGTGGAACTCGGGCGCCCTCACATC CGGAGTGCATACCTTTCCCGCCGTGT TGCAGTCCAGCGGCCTGTACAGCCTG AGCTCCGTCGTGACAGTGCCGTCCTC CTCCCTTGGAACCCAGACCTATATCT GCAACGTCAATCACAAGCCCTCCAA CACCAAAGTGGACAAGAAGGTCGAA CCCAAGTCCTGCGACAAGACTCACA CCTGTCCGCCTTGTCCAGCCCCTGAG CTGCTGGGTGGTCCGTCCGTGTTCCT	SEQ ID 1898	GATGTTGTGATGACTCAGTCTCCAT CCTCCCTGTCTGCATCTGTGGGGGA CAGCGTCGCCATCACTTGCCGGGC AAGTCAGAGCATTAGCAACTATTT AAATTGGTATCAGCAGAGACCAGG GAAAGCCCCTAAGCTCCTGATCTTT GCTGCATCCAGTTTGCAAAGTGGG GTCCCATCAAGGTTCAGTGGCAGT GGATCTGGGACAGATTTCACTCTC ACCATCAGCAGTCTGCAACCTGAA GATTTTGCAACTTACTCCTGTCAAC AGAGTTACATTACCCCGTGGACGT TCGGCCAAGGGACCAAGCTGGAGA TCAAACGTACTGTGGCTGCTCCCTC CGTGTTCATTTTTCCTCCGTCGGAC GAACAGCTGAAGTCCGGAACCGCG TCCGTGGTCTGTCTCCTGAACAACT TCTATCCGCGCGAGGCGAAAGTGC AGTGGAAGGTCGACAACGCACTGC AGTCGGGAAACTCCCAGGAATCGG TGACCGAGCAGGACTCGAAGGACT CAACCTACTCATTGTCCTCCACCCT CACCCTGAGCAAGGCCGATTACGA GAAGCATAAGGTCTACGCCTGCGA AGTGACCCACCAGGGCCTGAGCAG CCCAGTGACGAAGTCCTTCAACCG GGGAGAATGC

	CTTCCCGCCCAAGCCGAAGGACACTC TGATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGCA CGAAGATCCCGAAGTGAAATTCAAT TGGTACGTGGATGGGGTCGAAGTGC ACAACGCCAAGACCAAGCCTAGGGA AGAACAGTACAACTCTACGTACCGG GTGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGAG TACAAGTGCAAAGTGTCAAACAAGG CTCTCCCTGCCCCTATCGAAAAGACC ATCAGCAAGGCCAAGGGTCAACCTA GGGAGCCCCAGGTCTATACTTTGCCG CCTAGCCGGGAAGAAATGACTAAGA ACCAAGTGTCCCTGACTTGCCTTGTC AAGGGCTTTTATCCGTCCGACATCGC CGTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTCC TTCTTCCTGTACTCCAAGCTGACTGT GGACAAGTCAAGATGGCAGCAGGGA AACGTGTTCTCCTGCTCCGTGATGCA CGAAGCGCTGCACAACCATTACACC CAGAAATCACTGTCACTTTCGCCGGG AAAA		
SEQ ID 1791	CAGGTGCAGCTACAGCAGTGGGGCG CAGGACTGTTGAAGCCTTCGGAGAC CCTGTCCCTCACCTGCGCTGTCTATG GTGGGTCCGTCAGTGGTTACTACTGG AGCTGGATCCGCCAGCCCCCAGGGA AGGGGCTGGAGTGGATGGGGGAAAT CCATCATAGTGGAAGCACCAACTAC AACCCGTCCCTCAAGAGTCGAGTCAC CATATCACTAGACACGCCCAAGAAC CAGTTCTCCCTGAAGCTAAGCTCTGT GACCGCCGCGGACACGGCTGTATATT ACTGTGCGAGACGGGATTGGGCAGG AAAAAGGGTCTGGGGCCAGGGAACC CTGGTCACCGTCTCCTCAGCATCCAC CAAGGGGCCTTCCGTGTTCCCCCTGG CCCCTTCATCCAAGTCGACCTCTGGT GGAACCGCCGCACTCGGTTGCCTGGT CAAAGACTACTTCCCCGAGCCCGTGA CTGTCTCGTGGAACTCGGGCGCCCTC ACATCCGGAGTGCATACCTTTCCCGC CGTGTTGCAGTCCAGCGGCCTGTACA GCCTGAGCTCCGTCGTGACAGTGCCG TCCTCCTCCCTTGGAACCCAGACCTA TATCTGCAACGTCAATCACAAGCCCT CCAACACCAAAGTGGACAAGAAGGT CGAACCCAAGTCCTGCGACAAGACT CACACCTGTCCGCCTTGTCCAGCCCC TGAGCTGCTGGGTGGTCCGTCCGTGT TCCTCTTCCCGCCCAAGCCGAAGGAC	SEQ ID 1899	GATGTTGTGATGACTCAGTCTCCAG GCACCCTGTCTTTGTCTCCAGGGGA AAGAGCCACCCTCTCCTGCAGGGC CAGTCAGAGTGTTAGCACCCTCTTA GCCTGGTACCAACAGAAACCTGGC CAGGCTCCCAGGCTCCTCATCTATG ATGCATCCAACAGGGCCACTGGCA TCCCAGGCAGGTTCAGTGCCAGTG GGTCTGGGACAGACTTCAGTCTCA CCATCAGCAGCCTAGAGACTGAAG ATTCTGCAGTTTATTACTGTCAGCA CCGTTACGTGTGGCCGTTCACTTTC GGCGGAGGGACCAAGCTGGAGATC AAACGTACTGTGGCTGCTCCCTCCG TGTTCATTTTTCCTCCGTCGGACGA ACAGCTGAAGTCCGGAACCGCGTC CGTGGTCTGTCTCCTGAACAACTTC TATCCGCGCGAGGCGAAAGTGCAG TGGAAGGTCGACAACGCACTGCAG TCGGGAAACTCCCAGGAATCGGTG ACCGAGCAGGACTCGAAGGACTCA ACCTACTCATTGTCCTCCACCCTCA CCCTGAGCAAGGCCGATTACGAGA AGCATAAGGTCTACGCCTGCGAAG TGACCCACCAGGGCCTGAGCAGCC CAGTGACGAAGTCCTTCAACCGGG GAGAATGC

	ACTCTGATGATTTCACGCACCCCGGA AGTCACTTGCGTGGTCGTGGACGTGT CGCACGAAGATCCCGAAGTGAAATT CAATTGGTACGTGGATGGGGTCGAA GTGCACAACGCCAAGACCAAGCCTA GGGAAGAACAGTACAACTCTACGTA CCGGGTGGTGTCCGTGCTGACCGTGC TGCACCAGGACTGGCTGAACGGAAA GGAGTACAAGTGCAAAGTGTCAAAC AAGGCTCTCCCTGCCCCTATCGAAAA GACCATCAGCAAGGCCAAGGGTCAA CCTAGGGAGCCCCAGGTCTATACTTT GCCGCCTAGCCGGGAAGAAATGACT AAGAACCAAGTGTCCCTGACTTGCCT TGTCAAGGGCTTTTATCCGTCCGACA TCGCCGTGGAGTGGGAGTCCAACGG ACAACCGGAGAACAACTACAAGACC ACCCCACCGGTGCTCGATTCCGATGG CTCCTTCTTCCTGTACTCCAAGCTGA CTGTGGACAAGTCAAGATGGCAGCA GGGAAACGTGTTCTCCTGCTCCGTGA TGCACGAAGCGCTGCACAACCATTA CACCCAGAAATCACTGTCACTTTCGC CGGGAAAA		
SEQ ID 1792	CAGGTACAGCTGCAGCAGTCAGGTC CAGGACTATTAAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCAACACTGCT ACTTGGAACTGGATCAGGCAGTCCCC ATCGAGAGGCCTTGAGTGGCTGGGA AGGACATACTACAGGTCCAAGTGGT ATAAGGATAATGCACTGTCTGTGAA AAGTCGAATAACCATCAACCCAGAC ACATCCAAGAACCAGTTCTCCCTGCA GCTGAACTCTGTGACTCCCGAGGACA CGGCTGTGTATTACTGTGCAGGAGGT CGGGCTGGTATTGCCGCTTTTGATAT CTGGGGCCAAGGGACCACGGTCACC GTCTCCTCAGCATCCACCAAGGGGCC TTCCGTGTTCCCCCTGGCCCCTTCATC CAAGTCGACCTCTGGTGGAACCGCC GCACTCGGTTGCCTGGTCAAAGACTA CTTCCCCGAGCCCGTGACTGTCTCGT GGAACTCGGGCGCCCTCACATCCGG AGTGCATACCTTTCCCGCCGTGTTGC AGTCCAGCGGCCTGTACAGCCTGAG CTCCGTCGTGACAGTGCCGTCCTCCT CCCTTGGAACCCAGACCTATATCTGC AACGTCAATCACAAGCCCTCCAACA CCAAAGTGGACAAGAAGGTCGAACC CAAGTCCTGCGACAAGACTCACACCT GTCCGCCTTGTCCAGCCCCTGAGCTG CTGGGTGGTCCGTCCGTGTTCCTCTT	SEQ ID 1900	GACATCCAGATGACCCAGTCTCCA TCCTCCCTGTCTGCATCTGTAGGAG ACAGAGTCACCATCACTTGCCGGG CAAGTCAGGGCATTAGAAATGATT TAGGCTGGTATCAGCAGAAACCAG GGAAAGCCCCTAAGCGTCTGATCT ATGGTGCATCCAGTTTGCAAAGTG GAGTCCCATCAAGGTTCAGCGGCA GTGGATCTGGGACAGAATTCACTC TCACAATCAGGAGCCTGCAGCCTG AAGATTTTGCAACTTATTATTGTCT ACAGCATAATTCCTACCCTCGAAC ATTCGGCCAAGGGACCAAGGTGGA AATCAAACGTACTGTGGCTGCTCC CTCCGTGTTCATTTTTCCTCCGTCG GACGAACAGCTGAAGTCCGGAACC GCGTCCGTGGTCTGTCTCCTGAACA ACTTCTATCCGCGCGAGGCGAAAG TGCAGTGGAAGGTCGACAACGCAC TGCAGTCGGGAAACTCCCAGGAAT CGGTGACCGAGCAGGACTCGAAGG ACTCAACCTACTCATTGTCCTCCAC CCTCACCCTGAGCAAGGCCGATTA CGAGAAGCATAAGGTCTACGCCTG CGAAGTGACCCACCAGGGCCTGAG CAGCCCAGTGACGAAGTCCTTCAA CCGGGGAGAATGC

	CCCGCCCAAGCCGAAGGACACTCTG ATGATTTCACGCACCCCGGAAGTCAC TTGCGTGGTCGTGGACGTGTCGCACG AAGATCCCGAAGTGAAATTCAATTG GTACGTGGATGGGGTCGAAGTGCAC AACGCCAAGACCAAGCCTAGGGAAG AACAGTACAACTCTACGTACCGGGT GGTGTCCGTGCTGACCGTGCTGCACC AGGACTGGCTGAACGGAAAGGAGTA CAAGTGCAAAGTGTCAAACAAGGCT CTCCCTGCCCCTATCGAAAAGACCAT CAGCAAGGCCAAGGGTCAACCTAGG GAGCCCCAGGTCTATACTTTGCCGCC TAGCCGGGAAGAAATGACTAAGAAC CAAGTGTCCCTGACTTGCCTTGTCAA GGGCTTTTATCCGTCCGACATCGCCG TGGAGTGGGAGTCCAACGGACAACC GGAGAACAACTACAAGACCACCCCA CCGGTGCTCGATTCCGATGGCTCCTT CTTCCTGTACTCCAAGCTGACTGTGG ACAAGTCAAGATGGCAGCAGGGAAA CGTGTTCTCCTGCTCCGTGATGCACG AAGCGCTGCACAACCATTACACCCA GAAATCACTGTCACTTTCGCCGGGAA AA		
SEQ ID 1793	CAGGTGCAGCTGGTGCAATCTGGAG GAGGCTTGATCCAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCTG GGTTCACCGTCAGTAGCAACTACATG AGCTGGGTCCGCCAGGCTCCAGGGA AGGGGCTGGAATGGGTCTCACTTATT TATAGTGATGGTCGCACAAACTATGC AGACTCCGTGAAGGGCCGATTCACC ATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTG AGAGCCGAGGACACGGCCGTATATT ACTGTGCGAAGGGGGCCCTACAGGG CGAATGGCGGAGATTTGACTACTGG GGCCAGGGCACCCTGGTCACCGTCTC CTCAGCATCCACCAAGGGGCCTTCCG TGTTCCCCCTGGCCCCTTCATCCAAG TCGACCTCTGGTGGAACCGCCGCACT CGGTTGCCTGGTCAAAGACTACTTCC CCGAGCCCGTGACTGTCTCGTGGAAC TCGGGCGCCCTCACATCCGGAGTGCA TACCTTTCCCGCCGTGTTGCAGTCCA GCGGCCTGTACAGCCTGAGCTCCGTC GTGACAGTGCCGTCCTCCTCCCTTGG AACCCAGACCTATATCTGCAACGTCA ATCACAAGCCCTCCAACACCAAAGT GGACAAGAAGGTCGAACCCAAGTCC TGCGACAAGACTCACACCTGTCCGCC TTGTCCAGCCCCTGAGCTGCTGGGTG GTCCGTCCGTGTTCCTCTTCCCGCCC	SEQ ID 1901	GATGTTGTGATGACTCAGTCTCCAG CCACCCTGTCTTTGTCTCCAGGGGA AAGAGCCACCCTCTCCTGCAGGGC CAGTCAGAGTGTTAGCAGCTACTT AGCCTGGTACCAACAGAAACCTGG CCAGGCTCCCAGGCTCCTCATCTAT GATGCATCCAACAGGGCCACTGGC ATCCCAGCCAGGTTCAGTGGCAGT GGGTCTGGGACAGACTTCACTCTC ACCATCAGCAGCCTAGAGCCTGAA GATTTTGCAGTTTATTACTGTCAGC AGCGTAGCAACTGGCCGTGGACGT TCGGCCAAGGGACCAAGCTGGAGA TCAAACGTACTGTGGCTGCTCCCTC CGTGTTCATTTTTCCTCCGTCGGAC GAACAGCTGAAGTCCGGAACCGCG TCCGTGGTCTGTCTCCTGAACAACT TCTATCCGCGCGAGGCGAAAGTGC AGTGGAAGGTCGACAACGCACTGC AGTCGGGAAACTCCCAGGAATCGG TGACCGAGCAGGACTCGAAGGACT CAACCTACTCATTGTCCTCCACCCT CACCCTGAGCAAGGCCGATTACGA GAAGCATAAGGTCTACGCCTGCGA AGTGACCCACCAGGGCCTGAGCAG CCCAGTGACGAAGTCCTTCAACCG GGGAGAATGC

	AAGCCGAAGGACACTCTGATGATTTC ACGCACCCCGGAAGTCACTTGCGTG GTCGTGGACGTGTCGCACGAAGATC CCGAAGTGAAATTCAATTGGTACGTG GATGGGGTCGAAGTGCACAACGCCA AGACCAAGCCTAGGGAAGAACAGTA CAACTCTACGTACCGGGTGGTGTCCG TGCTGACCGTGCTGCACCAGGACTGG CTGAACGGAAAGGAGTACAAGTGCA AAGTGTCAAACAAGGCTCTCCCTGCC CCTATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTATACTTTGCCGCCTAGCCGGG AAGAAATGACTAAGAACCAAGTGTC CCTGACTTGCCTTGTCAAGGGCTTTT ATCCGTCCGACATCGCCGTGGAGTGG GAGTCCAACGGACAACCGGAGAACA ACTACAAGACCACCCCACCGGTGCTC GATTCCGATGGCTCCTTCTTCCTGTA CTCCAAGCTGACTGTGGACAAGTCA AGATGGCAGCAGGGAAACGTGTTCT CCTGCTCCGTGATGCACGAAGCGCTG CACAACCATTACACCCAGAAATCACT GTCACTTTCGCCGGGAAAA		
SEQ ID 1794	CAGGTGCAGCTACAGCAGTCAGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCAACAGTGCT GCTTGGAACTGGATCAGGCAGTCCCC ATCGAGAGGCCTTGAGTGGCTGGGA AGGACATATTACAGGTCCAAGTGGT ATAATGATTATGCAGTATCTGTGAAA AGTCGAATAACCATCAACCCAGACA CATCCAAGAACCAGTTCTCCCTGCAG CTGAACTCTGTGACTCCCGAGGACAC GGCTGTGTATTACTGTACAAGAACCA ACCAGGGATACGGTGGTAACTCCGG GGTATTTGACTACTGGGGCCAGGGA ACCCTGGTCACCGTCTCCTCAGCATC CACCAAGGGGCCTTCCGTGTTCCCCC TGGCCCCTTCATCCAAGTCGACCTCT GGTGGAACCGCCGCACTCGGTTGCCT GGTCAAAGACTACTTCCCCGAGCCCG TGACTGTCTCGTGGAACTCGGGCGCC CTCACATCCGGAGTGCATACCTTTCC CGCCGTGTTGCAGTCCAGCGGCCTGT ACAGCCTGAGCTCCGTCGTGACAGTG CCGTCCTCCTCCCTTGGAACCCAGAC CTATATCTGCAACGTCAATCACAAGC CCTCCAACACCAAAGTGGACAAGAA GGTCGAACCCAAGTCCTGCGACAAG ACTCACACCTGTCCGCCTTGTCCAGC CCCTGAGCTGCTGGGTGGTCCGTCCG	SEQ ID 1902	GATGTTGTGATGACTCAGTCTCCGC TCTCCCTGCCCGTCACCCTTGGACA GGCGGCCTCCATCTCCTGCAGGTCT AGTCATAGCCTCACAACTACTGAT GGACGTACTTACGTGGCTTGGTTTC AGCAGAGGCCAGGCCAATCTCCAA GGCGCCTTCTTTATGAGGTTTCTAA GCGGGACTCTGGGGCCCCAGACAG ATTCAGCGGCAGTGGGTCAGGCAC TGATTTCACTCTGAAAATCAGCAG GGTGGAGGCTGACGATGTTGGAAT TTATCATTGCATGCAAGGAACACA TGGGCCTCACACGTTCGGCCAAGG GACCAAGCTGGAGATCAAACGTAC TGTGGCTGCTCCCTCCGTGTTCATT TTTCCTCCGTCGGACGAACAGCTG AAGTCCGGAACCGCGTCCGTGGTC TGTCTCCTGAACAACTTCTATCCGC GCGAGGCGAAAGTGCAGTGGAAG GTCGACAACGCACTGCAGTCGGGA AACTCCCAGGAATCGGTGACCGAG CAGGACTCGAAGGACTCAACCTAC TCATTGTCCTCCACCCTCACCCTGA GCAAGGCCGATTACGAGAAGCATA AGGTCTACGCCTGCGAAGTGACCC ACCAGGGCCTGAGCAGCCCAGTGA CGAAGTCCTTCAACCGGGGAGAAT GC

	TGTTCCTCTTCCCGCCCAAGCCGAAG GACACTCTGATGATTTCACGCACCCC GGAAGTCACTTGCGTGGTCGTGGAC GTGTCGCACGAAGATCCCGAAGTGA AATTCAATTGGTACGTGGATGGGGTC GAAGTGCACAACGCCAAGACCAAGC CTAGGGAAGAACAGTACAACTCTAC GTACCGGGTGGTGTCCGTGCTGACCG TGCTGCACCAGGACTGGCTGAACGG AAAGGAGTACAAGTGCAAAGTGTCA AACAAGGCTCTCCCTGCCCCTATCGA AAAGACCATCAGCAAGGCCAAGGGT CAACCTAGGGAGCCCCAGGTCTATA CTTTGCCGCCTAGCCGGGAAGAAAT GACTAAGAACCAAGTGTCCCTGACTT GCCTTGTCAAGGGCTTTTATCCGTCC GACATCGCCGTGGAGTGGGAGTCCA ACGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCCG ATGGCTCCTTCTTCCTGTACTCCAAG CTGACTGTGGACAAGTCAAGATGGC AGCAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACTT TCGCCGGGAAAA		
SEQ ID 1795	CAGGTGCAGCTACAGCAGTCAGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTGGCAACAGTGCT GCTTGGAACTGGATCAGGCAGTCCCC ATCGAGAGGCCTTGAGTGGCTGGGA AGGACATACTACAGGTCCAAGTGGT ATAATGATTATGCAGTATCTGTGAAA AGTCGAATAACCATCAACCCAGACA CATCCAAGAACCAGTTCTCCCTGCAG TTGAATTCTGTGACTCCCGAGGACAC GGCTGTGTATTACTGTGCGAGGATAG TGGGAGGTGCCGTTGACTGCTGGGG CCAGGGAACCCTGGTGACCGTCTCCT CAGCATCCACCAAGGGGCCTTCCGTG TTCCCCCTGGCCCCTTCATCCAAGTC GACCTCTGGTGGAACCGCCGCACTCG GTTGCCTGGTCAAAGACTACTTCCCC GAGCCCGTGACTGTCTCGTGGAACTC GGGCGCCCTCACATCCGGAGTGCAT ACCTTTCCCGCCGTGTTGCAGTCCAG CGGCCTGTACAGCCTGAGCTCCGTCG TGACAGTGCCGTCCTCCTCCCTTGGA ACCCAGACCTATATCTGCAACGTCAA TCACAAGCCCTCCAACACCAAAGTG GACAAGAAGGTCGAACCCAAGTCCT GCGACAAGACTCACACCTGTCCGCCT TGTCCAGCCCCTGAGCTGCTGGGTGG TCCGTCCGTGTTCCTCTTCCCGCCCA	SEQ ID 1903	GAAACGACACTCACGCAGTCTCCA GCCACCCTGTCTGTGTCTCCAGGGG AAAGAGCCACCCTCTCCTGCAGGG CCAGTCAAAGTGTTACCAGCAACT TAGCCTGGTACCAGCAGAAACCTG GCCAGGCTCCCAGGCTCCTCATCTA TGGTGCATCCAACAGGGCCACTGG TATCCCAGCCAGGTTCAGTGTCAGT GGGTCTGGGACAGACTTCACTCTC ACCATCAGCAGACTGGAGCCTGAA GATTTTGCAGTGTATTACTGTCAGC AGTATGGTAGTCCACCTCCGACCA CCTTCGGCCAAGGGACACGACTGG AGATTAAACGTACTGTGGCTGCTC CCTCCGTGTTCATTTTTCCTCCGTC GGACGAACAGCTGAAGTCCGGAAC CGCGTCCGTGGTCTGTCTCCTGAAC AACTTCTATCCGCGCGAGGCGAAA GTGCAGTGGAAGGTCGACAACGCA CTGCAGTCGGGAAACTCCCAGGAA TCGGTGACCGAGCAGGACTCGAAG GACTCAACCTACTCATTGTCCTCCA CCCTCACCCTGAGCAAGGCCGATT ACGAGAAGCATAAGGTCTACGCCT GCGAAGTGACCCACCAGGGCCTGA GCAGCCCAGTGACGAAGTCCTTCA ACCGGGGAGAATGC

	AGCCGAAGGACACTCTGATGATTTCA CGCACCCCGGAAGTCACTTGCGTGGT CGTGGACGTGTCGCACGAAGATCCC GAAGTGAAATTCAATTGGTACGTGG ATGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTAC AACTCTACGTACCGGGTGGTGTCCGT GCTGACCGTGCTGCACCAGGACTGG CTGAACGGAAAGGAGTACAAGTGCA AAGTGTCAAACAAGGCTCTCCCTGCC CCTATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTATACTTTGCCGCCTAGCCGGG AAGAAATGACTAAGAACCAAGTGTC CCTGACTTGCCTTGTCAAGGGCTTTT ATCCGTCCGACATCGCCGTGGAGTGG GAGTCCAACGGACAACCGGAGAACA ACTACAAGACCACCCCACCGGTGCTC GATTCCGATGGCTCCTTCTTCCTGTA CTCCAAGCTGACTGTGGACAAGTCA AGATGGCAGCAGGGAAACGTGTTCT CCTGCTCCGTGATGCACGAAGCGCTG CACAACCATTACACCCAGAAATCACT GTCACTTTCGCCGGGAAAA		
SEQ ID 1796	GAGGTGCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTTTCCTGCAAGGCTTCTG GATACACCTTCACTAGCTATGCTATG CATTGGGTGCGCCAGGCCCCCGGAC AAAGGCTTGAGTGGATGGGATGGAT CAACGCTGGCAATGGTAACACAAAA TATTCACAGAAGTTCCAGGGCAGAG TCACCATTACCAGGGACACATCCGCG AGCACAGCCTACATGGAGCTGAGCA GCCTGAGATCTGAAGACACGGCTGT GTATTACTGTGCGAGAGTTAGAGTGG GAGCTACTACTGTTTACGACAGCTGG TTCGACCCCTGGGGCCAGGGAACCCT GGTGACCGTCTCCTCAGCATCCACCA AGGGGCCTTCCGTGTTCCCCCTGGCC CCTTCATCCAAGTCGACCTCTGGTGG AACCGCCGCACTCGGTTGCCTGGTCA AAGACTACTTCCCCGAGCCCGTGACT GTCTCGTGGAACTCGGGCGCCCTCAC ATCCGGAGTGCATACCTTTCCCGCCG TGTTGCAGTCCAGCGGCCTGTACAGC CTGAGCTCCGTCGTGACAGTGCCGTC CTCCTCCCTTGGAACCCAGACCTATA TCTGCAACGTCAATCACAAGCCCTCC AACACCAAAGTGGACAAGAAGGTCG AACCCAAGTCCTGCGACAAGACTCA CACCTGTCCGCCTTGTCCAGCCCCTG AGCTGCTGGGTGGTCCGTCCGTGTTC	SEQ ID 1904	GATGTTGTGATGACTCAGTCTCCAG GCACCCTGTCTTTGTCTCCAGGGGA AAGAGCCACCCTCTCCTGCAGGGC CAGTCAGAGTGTTAGCAGCAGCTA CTTAGCCTGGTACCAGCAGAAACC TGGCCAGGCTCCCAGGCTCCTCATC TATGGTGCATCCAGCAGGGCCACT GGCATCCCAGACAGGTTCAGTGGC AGTGGGTCTGGGACAGACTTCACT CTCACCATCAGCAGACTGGAGCCT GAAGATTTTGCAGTGTATTACTGTC AGCAGTATGGTAGCTCACGTCGGA CGTTCGGCCAAGGGACCAAGCTGG AGATCAAACGTACTGTGGCTGCTC CCTCCGTGTTCATTTTTCCTCCGTC GGACGAACAGCTGAAGTCCGGAAC CGCGTCCGTGGTCTGTCTCCTGAAC AACTTCTATCCGCGCGAGGCGAAA GTGCAGTGGAAGGTCGACAACGCA CTGCAGTCGGGAAACTCCCAGGAA TCGGTGACCGAGCAGGACTCGAAG GACTCAACCTACTCATTGTCCTCCA CCCTCACCCTGAGCAAGGCCGATT ACGAGAAGCATAAGGTCTACGCCT GCGAAGTGACCCACCAGGGCCTGA GCAGCCCAGTGACGAAGTCCTTCA ACCGGGGAGAATGC

	CTCTTCCCGCCCAAGCCGAAGGACAC TCTGATGATTTCACGCACCCCGGAAG TCACTTGCGTGGTCGTGGACGTGTCG CACGAAGATCCCGAAGTGAAATTCA ATTGGTACGTGGATGGGGTCGAAGT GCACAACGCCAAGACCAAGCCTAGG GAAGAACAGTACAACTCTACGTACC GGGTGGTGTCCGTGCTGACCGTGCTG CACCAGGACTGGCTGAACGGAAAGG AGTACAAGTGCAAAGTGTCAAACAA GGCTCTCCCTGCCCCTATCGAAAAGA CCATCAGCAAGGCCAAGGGTCAACC TAGGGAGCCCCAGGTCTATACTTTGC CGCCTAGCCGGGAAGAAATGACTAA GAACCAAGTGTCCCTGACTTGCCTTG TCAAGGGCTTTTATCCGTCCGACATC GCCGTGGAGTGGGAGTCCAACGGAC AACCGGAGAACAACTACAAGACCAC CCCACCGGTGCTCGATTCCGATGGCT CCTTCTTCCTGTACTCCAAGCTGACT GTGGACAAGTCAAGATGGCAGCAGG GAAACGTGTTCTCCTGCTCCGTGATG CACGAAGCGCTGCACAACCATTACA CCCAGAAATCACTGTCACTTTCGCCG GGAAAA		
SEQ ID 1797	CAGGTGCAGCTGGTGCAGTCTGGGG GAGGCTTGGTACAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTAGCAGCTATGCCATG AGCTGGGTCCGCCAGGCTCCAGGGA AGGGGCTGGAGTGGGTCTCAGCTATT AGTGGTAGTGGTGGTAGCACATACT ACGCAGACTCCGTGAAGGGCCGGTT CACCATCTCCAGAGACAATTCCAAG AACACGCTGTATCTGCAAATGAACA GCCTGAGAGCCGAGGACACGGCCGT ATATTACTGTGCGAAAGATGGGGGG TCCAGCCCATACTATGATAGTAGTGG TTTACTACCCTGGTACTTCGATCTCT GGGGCCGTGGCACCCTGGTCACCGTC TCCTCAGCATCCACCAAGGGGCCTTC CGTGTTCCCCCTGGCCCCTTCATCCA AGTCGACCTCTGGTGGAACCGCCGC ACTCGGTTGCCTGGTCAAAGACTACT TCCCCGAGCCCGTGACTGTCTCGTGG AACTCGGGCGCCCTCACATCCGGAGT GCATACCTTTCCCGCCGTGTTGCAGT CCAGCGGCCTGTACAGCCTGAGCTCC GTCGTGACAGTGCCGTCCTCCTCCCT TGGAACCCAGACCTATATCTGCAACG TCAATCACAAGCCCTCCAACACCAA AGTGGACAAGAAGGTCGAACCCAAG TCCTGCGACAAGACTCACACCTGTCC GCCTTGTCCAGCCCCTGAGCTGCTGG	SEQ ID 1905	GAAACGACACTCACGCAGTCTCCA GGCACCCTGTCCTTGTCTCCAGGGG AAAGAGCCACCCTCTCCTGCAGGG CCAGTCAGAGTGTTTTCAACAACT ACTTAGCCTGGTACCAACAGAGAC CTGGCCAGGCTCCCAGGCTCCTCAT CTATGGTGCATCCAGCAGGGCCAC TGGCATCCCAGACAGGTTCAGTGG CGGTGGGTCTGGGACAGACTTCAC TCTCACCATCAGCAGACTGGAGCC TGAAGATTTCGCAGTGTATTGCTGT CAGCAGTATGGTAGTTCACCGATC ACCTTCGGCCAAGGGACACGACTG GAGATTAAACGTACTGTGGCTGCT CCCTCCGTGTTCATTTTTCCTCCGT CGGACGAACAGCTGAAGTCCGGAA CCGCGTCCGTGGTCTGTCTCCTGAA CAACTTCTATCCGCGCGAGGCGAA AGTGCAGTGGAAGGTCGACAACGC ACTGCAGTCGGGAAACTCCCAGGA ATCGGTGACCGAGCAGGACTCGAA GGACTCAACCTACTCATTGTCCTCC ACCCTCACCCTGAGCAAGGCCGAT TACGAGAAGCATAAGGTCTACGCC TGCGAAGTGACCCACCAGGGCCTG AGCAGCCCAGTGACGAAGTCCTTC AACCGGGGAGAATGC

	GTGGTCCGTCCGTGTTCCTCTTCCCG CCCAAGCCGAAGGACACTCTGATGA TTTCACGCACCCCGGAAGTCACTTGC GTGGTCGTGGACGTGTCGCACGAAG ATCCCGAAGTGAAATTCAATTGGTAC GTGGATGGGGTCGAAGTGCACAACG CCAAGACCAAGCCTAGGGAAGAACA GTACAACTCTACGTACCGGGTGGTGT CCGTGCTGACCGTGCTGCACCAGGAC TGGCTGAACGGAAAGGAGTACAAGT GCAAAGTGTCAAACAAGGCTCTCCCT GCCCCTATCGAAAAGACCATCAGCA AGGCCAAGGGTCAACCTAGGGAGCC CCAGGTCTATACTTTGCCGCCTAGCC GGGAAGAAATGACTAAGAACCAAGT GTCCCTGACTTGCCTTGTCAAGGGCT TTTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAGA ACAACTACAAGACCACCCCACCGGT GCTCGATTCCGATGGCTCCTTCTTCC TGTACTCCAAGCTGACTGTGGACAAG TCAAGATGGCAGCAGGGAAACGTGT TCTCCTGCTCCGTGATGCACGAAGCG CTGCACAACCATTACACCCAGAAATC ACTGTCACTTTCGCCGGGAAAA		
SEQ ID 1798	CAGGTGCAGCTGCAGGAGTCGGGGG GAGGCTTGGTCCAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTCAGTAGCTATGCTATG CACTGGGTCCGCCAGGCTCCAGGGA AGGGACTGGAATATGTTTCAGCTATT AGTAGTAATGGGGGTAGCACATATT ATGCAAACTCTGTGAAGGGCAGATT CACCATCTCCAGAGACAATTCCAAG AACACGCTGTATCTTCAAATGGGCAG CCTGAGAGCTGAGGACATGGCTGTG TATTACTGTGCGAGAGCTAAGTTTTG GACATACTACTTTGACTACTGGGGCC AGGGAACCCTGGTGACCGTCTCCTCA GCATCCACCAAGGGGCCTTCCGTGTT CCCCCTGGCCCCTTCATCCAAGTCGA CCTCTGGTGGAACCGCCGCACTCGGT TGCCTGGTCAAAGACTACTTCCCCGA GCCCGTGACTGTCTCGTGGAACTCGG GCGCCCTCACATCCGGAGTGCATACC TTTCCCGCCGTGTTGCAGTCCAGCGG CCTGTACAGCCTGAGCTCCGTCGTGA CAGTGCCGTCCTCCTCCCTTGGAACC CAGACCTATATCTGCAACGTCAATCA CAAGCCCTCCAACACCAAAGTGGAC AAGAAGGTCGAACCCAAGTCCTGCG ACAAGACTCACACCTGTCCGCCTTGT CCAGCCCCTGAGCTGCTGGGTGGTCC GTCCGTGTTCCTCTTCCCGCCCAAGC	SEQ ID 1906	GAAATTGTGCTGACTCAGTCTCCA GCCACCCTGTCTTTGTCTCCAGGGG AAAGAGCCACCCTCTCCTGCAGGG CCAGTCAGAGTGTTAGCAGCTACT TAGCCTGGTACCAACAGAAACCTG GCCAGGCTCCCAGGCTCCTCATCTA TGATGCATCCAACAGGGCCACTGG CATCCCAGCCAGGTTCAGTGGCAG TGGGTCTGGGACAGACTTCACTCTC ACCATCAGCAGACTGGAGCCTGAA GATTTTGCAGTGTATTACTGTCAGC AGTATGGTAGCTCACTCAGGTACA CTTTTGGCCAGGGGACCAAGCTGG AGATCAAACGTACTGTGGCTGCTC CCTCCGTGTTCATTTTTCCTCCGTC GGACGAACAGCTGAAGTCCGGAAC CGCGTCCGTGGTCTGTCTCCTGAAC AACTTCTATCCGCGCGAGGCGAAA GTGCAGTGGAAGGTCGACAACGCA CTGCAGTCGGGAAACTCCCAGGAA TCGGTGACCGAGCAGGACTCGAAG GACTCAACCTACTCATTGTCCTCCA CCCTCACCCTGAGCAAGGCCGATT ACGAGAAGCATAAGGTCTACGCCT GCGAAGTGACCCACCAGGGCCTGA GCAGCCCAGTGACGAAGTCCTTCA ACCGGGGAGAATGC

	CGAAGGACACTCTGATGATTTCACGC ACCCCGGAAGTCACTTGCGTGGTCGT GGACGTGTCGCACGAAGATCCCGAA GTGAAATTCAATTGGTACGTGGATGG GGTCGAAGTGCACAACGCCAAGACC AAGCCTAGGGAAGAACAGTACAACT CTACGTACCGGGTGGTGTCCGTGCTG ACCGTGCTGCACCAGGACTGGCTGA ACGGAAAGGAGTACAAGTGCAAAGT GTCAAACAAGGCTCTCCCTGCCCCTA TCGAAAAGACCATCAGCAAGGCCAA GGGTCAACCTAGGGAGCCCCAGGTC TATACTTTGCCGCCTAGCCGGGAAGA AATGACTAAGAACCAAGTGTCCCTG ACTTGCCTTGTCAAGGGCTTTTATCC GTCCGACATCGCCGTGGAGTGGGAG TCCAACGGACAACCGGAGAACAACT ACAAGACCACCCCACCGGTGCTCGA TTCCGATGGCTCCTTCTTCCTGTACTC CAAGCTGACTGTGGACAAGTCAAGA TGGCAGCAGGGAAACGTGTTCTCCTG CTCCGTGATGCACGAAGCGCTGCAC AACCATTACACCCAGAAATCACTGTC ACTTTCGCCGGGAAAA		
SEQ ID 1799	CAGGTGCAGCTACAGCAGTGGGGCG CAGGACTGTTGAAGCCTTCGGAGAC CCTGTCCCTCACCTGCGCTGTCTATG GTGGGTCCTTCAGTGGTTACTACTGG AGCTGGATCCGCCAGCCCCCAGGGA AGGGGCTGGAGTGGATTGGGGAAAT CAATCATAGTGGAAGCACCAACTAC AACCCGTCCCTCAAGAGTCGAGTCAC CATATCAGTAGACACGTCCAAGAAC CAGTTCTCCCTGAAGCTGAGCTCTGT GACCGCCGCGGACACGGCTGTGTATT ACTGTGCGAGAGGCGGTGGTTCGGG GAGTTATTATAAGAGGTTCTTTGACT ACTGGGGCCAGGGAACCCTGGTCAC CGTCTCCTCAGCATCCACCAAGGGGC CTTCCGTGTTCCCCCTGGCCCCTTCAT CCAAGTCGACCTCTGGTGGAACCGCC GCACTCGGTTGCCTGGTCAAAGACTA CTTCCCCGAGCCCGTGACTGTCTCGT GGAACTCGGGCGCCCTCACATCCGG AGTGCATACCTTTCCCGCCGTGTTGC AGTCCAGCGGCCTGTACAGCCTGAG CTCCGTCGTGACAGTGCCGTCCTCCT CCCTTGGAACCCAGACCTATATCTGC AACGTCAATCACAAGCCCTCCAACA CCAAAGTGGACAAGAAGGTCGAACC CAAGTCCTGCGACAAGACTCACACCT GTCCGCCTTGTCCAGCCCCTGAGCTG CTGGGTGGTCCGTCCGTGTTCCTCTT	SEQ ID 1907	GAAATTGTGCTGACTCAGTCTCCA GACTCCCTGGCTGTGTCTCTGGGCG AGAGGGCCACCATCAACTGCAAGT CCAGCCAGAGTGTTTTATATGATTC CAACAGTAAGAACTACTTAAGTTG GTATCAGCAGAAACCAGGCCAGCC TCCTAAGTTGCTCATTTCCTGGGCG TCTACCCGGGGGTCCGGGGTCCCT GACCGATTCAGTGGCAGCGGGTCT GGGACAGATTTCACTCTCACCATC AGCAGCCTGCAGGCTGAAGATGTG GCAGTTTATTACTGTCAGCAATTTT ATGGTATTCCCCACTTCGGCCAAG GGACACGACTGGAGATTAAACGTA CTGTGGCTGCTCCCTCCGTGTTCAT TTTTCCTCCGTCGGACGAACAGCTG AAGTCCGGAACCGCGTCCGTGGTC TGTCTCCTGAACAACTTCTATCCGC GCGAGGCGAAAGTGCAGTGGAAG GTCGACAACGCACTGCAGTCGGGA AACTCCCAGGAATCGGTGACCGAG CAGGACTCGAAGGACTCAACCTAC TCATTGTCCTCCACCCTCACCCTGA GCAAGGCCGATTACGAGAAGCATA AGGTCTACGCCTGCGAAGTGACCC ACCAGGGCCTGAGCAGCCCAGTGA CGAAGTCCTTCAACCGGGGAGAAT GC

	CCCGCCCAAGCCGAAGGACACTCTG ATGATTTCACGCACCCCGGAAGTCAC TTGCGTGGTCGTGGACGTGTCGCACG AAGATCCCGAAGTGAAATTCAATTG GTACGTGGATGGGGTCGAAGTGCAC AACGCCAAGACCAAGCCTAGGGAAG AACAGTACAACTCTACGTACCGGGT GGTGTCCGTGCTGACCGTGCTGCACC AGGACTGGCTGAACGGAAAGGAGTA CAAGTGCAAAGTGTCAAACAAGGCT CTCCCTGCCCCTATCGAAAAGACCAT CAGCAAGGCCAAGGGTCAACCTAGG GAGCCCCAGGTCTATACTTTGCCGCC TAGCCGGGAAGAAATGACTAAGAAC CAAGTGTCCCTGACTTGCCTTGTCAA GGGCTTTTATCCGTCCGACATCGCCG TGGAGTGGGAGTCCAACGGACAACC GGAGAACAACTACAAGACCACCCCA CCGGTGCTCGATTCCGATGGCTCCTT CTTCCTGTACTCCAAGCTGACTGTGG ACAAGTCAAGATGGCAGCAGGGAAA CGTGTTCTCCTGCTCCGTGATGCACG AAGCGCTGCACAACCATTACACCCA GAAATCACTGTCACTTTCGCCGGGAA AA		
SEQ ID 1800	GAGGTGCAGCTGGTGCAGTCTGGAG CTGAGGTGAGGAAGCCTGGGGCCTC AGTGAAGGTCTCCTGCAAGGCTTCTG GTTACACATTTACCAGTTATGCCATC AGCTGGGTGCGACAGGCCCCTGGAC AAGGGCTTGAGTGGATGGGGTGGAT CAGCGCTTACGACGGTAACACAAAC TATGCACAGAAGCTCCAGGGCAGAG TCACCATGACCACAGACACATCCAC GAGCACAGCCTACATGGAGGTGAGG AGCCTGAGATCTGACGACACGGCCG TGTATTACTGTGCGAGAGATGGTACG GTCCGAAGGGTAGTGGGAGCTACTA CCCCTGGAAACTTTGACTACAGGGGC CAGGGAACCCTGGTCACCGTCTCCTC AGCATCCACCAAGGGGCCTTCCGTGT TCCCCCTGGCCCCTTCATCCAAGTCG ACCTCTGGTGGAACCGCCGCACTCGG TTGCCTGGTCAAAGACTACTTCCCCG AGCCCGTGACTGTCTCGTGGAACTCG GGCGCCCTCACATCCGGAGTGCATAC CTTTCCCGCCGTGTTGCAGTCCAGCG GCCTGTACAGCCTGAGCTCCGTCGTG ACAGTGCCGTCCTCCTCCCTTGGAAC CCAGACCTATATCTGCAACGTCAATC ACAAGCCCTCCAACACCAAAGTGGA CAAGAAGGTCGAACCCAAGTCCTGC GACAAGACTCACACCTGTCCGCCTTG TCCAGCCCCTGAGCTGCTGGGTGGTC	SEQ ID 1908	GATGTTGTGATGACTCAGTCTCCAG CCACCCTGTCTTTGTCTCCAGGGGA AAGAGCCACCCTCTCCTGCAGGGC CAGTCAGAGTGTTGGTACCAATTT AGCCTGGTACCAGCAGAAACCTGG CCAGGCTCCCAGGCTCCTCATCTAT GATGCATCCAACAGGGCCACTGGC ATCCCAGCCAGGTTCAGTGGCAGT GGGTCTGGGACAGAGTTCACTCTC ACCATCAGCAGCCTGCAGTCTGAA GATTTTGCAGTTTATTACTGTCAGC AGTATAATAACTGGCCTCCGATAA CTTTCGGCGGAGGGACCAAGCTGG AGATCAAACGTACTGTGGCTGCTC CCTCCGTGTTCATTTTTCCTCCGTC GGACGAACAGCTGAAGTCCGGAAC CGCGTCCGTGGTCTGTCTCCTGAAC AACTTCTATCCGCGCGAGGCGAAA GTGCAGTGGAAGGTCGACAACGCA CTGCAGTCGGGAAACTCCCAGGAA TCGGTGACCGAGCAGGACTCGAAG GACTCAACCTACTCATTGTCCTCCA CCCTCACCCTGAGCAAGGCCGATT ACGAGAAGCATAAGGTCTACGCCT GCGAAGTGACCCACCAGGGCCTGA GCAGCCCAGTGACGAAGTCCTTCA ACCGGGGAGAATGC

	CGTCCGTGTTCCTCTTCCCGCCCAAG CCGAAGGACACTCTGATGATTTCACG CACCCCGGAAGTCACTTGCGTGGTCG TGGACGTGTCGCACGAAGATCCCGA AGTGAAATTCAATTGGTACGTGGATG GGGTCGAAGTGCACAACGCCAAGAC CAAGCCTAGGGAAGAACAGTACAAC TCTACGTACCGGGTGGTGTCCGTGCT GACCGTGCTGCACCAGGACTGGCTG AACGGAAAGGAGTACAAGTGCAAAG TGTCAAACAAGGCTCTCCCTGCCCCT ATCGAAAAGACCATCAGCAAGGCCA AGGGTCAACCTAGGGAGCCCCAGGT CTATACTTTGCCGCCTAGCCGGGAAG AAATGACTAAGAACCAAGTGTCCCT GACTTGCCTTGTCAAGGGCTTTTATC CGTCCGACATCGCCGTGGAGTGGGA GTCCAACGGACAACCGGAGAACAAC TACAAGACCACCCCACCGGTGCTCG ATTCCGATGGCTCCTTCTTCCTGTACT CCAAGCTGACTGTGGACAAGTCAAG ATGGCAGCAGGGAAACGTGTTCTCCT GCTCCGTGATGCACGAAGCGCTGCA CAACCATTACACCCAGAAATCACTGT CACTTTCGCCGGGAAAA		
SEQ ID 1801	GAGGTGCAGCTGGTGCAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCGTCTG GATTCACCTTCAGTAGCTATGGCATG CACTGGGTCCGCCAGGCTCCAGGCA AGGGGCTGGAGTGGGTGGCAGTTAT ATGGTATGATGGAAGTAATAAATAC TATGCAGACTCCGTGAAGGGCCGATT CACCATCTCCAGAGACAATTCCAAG AACACGCTGTATCTGCAAATGAACA GCCTGAGAGCCGAGGACACGGCTGT GTATTACTGTGCGAGAGATCTGAATC GAGGATATTGTAGTGGTGGTAGCTGC TTTGGCTACTGGGGCCAGGGAACCCT GGTCACCGTCTCCTCAGCATCCACCA AGGGGCCTTCCGTGTTCCCCCTGGCC CCTTCATCCAAGTCGACCTCTGGTGG AACCGCCGCACTCGGTTGCCTGGTCA AAGACTACTTCCCCGAGCCCGTGACT GTCTCGTGGAACTCGGGCGCCCTCAC ATCCGGAGTGCATACCTTTCCCGCCG TGTTGCAGTCCAGCGGCCTGTACAGC CTGAGCTCCGTCGTGACAGTGCCGTC CTCCTCCCTTGGAACCCAGACCTATA TCTGCAACGTCAATCACAAGCCCTCC AACACCAAAGTGGACAAGAAGGTCG AACCCAAGTCCTGCGACAAGACTCA CACCTGTCCGCCTTGTCCAGCCCCTG AGCTGCTGGGTGGTCCGTCCGTGTTC	SEQ ID 1909	GATGTTGTGATGACTCAGTCTCCAC TCTCCCTGCCCGTCACCCTTGGACA GCCGGCCTCCATCTCCTGCAGGTCT AGTCAAAGCCTCGTATACAGTGAT GGAAACACCTACTTGAGTTGGCTT CAGCAGAGGCCAGGCCAGCCTCCA AGACTCCTAATTTATAAGATTTCTA ACCGGTTCTCTGGGGTCCCAGACA GATTCAGTGGCAGTGGGGCAGGGA CAGATTTCACACTGAAAATCAGCA GGGTGGAAGCTGAGGATGTCGGGG TTTATTACTGCATGCAAGGTACACA ATTTCCTCAAACGTTCGGCCAAGG GACCAAGCTGGAGATCAAACGTAC TGTGGCTGCTCCCTCCGTGTTCATT TTTCCTCCGTCGGACGAACAGCTG AAGTCCGGAACCGCGTCCGTGGTC TGTCTCCTGAACAACTTCTATCCGC GCGAGGCGAAAGTGCAGTGGAAG GTCGACAACGCACTGCAGTCGGGA AACTCCCAGGAATCGGTGACCGAG CAGGACTCGAAGGACTCAACCTAC TCATTGTCCTCCACCCTCACCCTGA GCAAGGCCGATTACGAGAAGCATA AGGTCTACGCCTGCGAAGTGACCC ACCAGGGCCTGAGCAGCCCAGTGA CGAAGTCCTTCAACCGGGGAGAAT GC

	CTCTTCCCGCCCAAGCCGAAGGACAC TCTGATGATTTCACGCACCCCGGAAG TCACTTGCGTGGTCGTGGACGTGTCG CACGAAGATCCCGAAGTGAAATTCA ATTGGTACGTGGATGGGGTCGAAGT GCACAACGCCAAGACCAAGCCTAGG GAAGAACAGTACAACTCTACGTACC GGGTGGTGTCCGTGCTGACCGTGCTG CACCAGGACTGGCTGAACGGAAAGG AGTACAAGTGCAAAGTGTCAAACAA GGCTCTCCCTGCCCCTATCGAAAAGA CCATCAGCAAGGCCAAGGGTCAACC TAGGGAGCCCCAGGTCTATACTTTGC CGCCTAGCCGGGAAGAAATGACTAA GAACCAAGTGTCCCTGACTTGCCTTG TCAAGGGCTTTTATCCGTCCGACATC GCCGTGGAGTGGGAGTCCAACGGAC AACCGGAGAACAACTACAAGACCAC CCCACCGGTGCTCGATTCCGATGGCT CCTTCTTCCTGTACTCCAAGCTGACT GTGGACAAGTCAAGATGGCAGCAGG GAAACGTGTTCTCCTGCTCCGTGATG CACGAAGCGCTGCACAACCATTACA CCCAGAAATCACTGTCACTTTCGCCG GGAAAA		
SEQ ID 1802	CAGGTGCAGCTGCAGGAGTCTGGGG GAGGCTTGGTACAGCCGGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTAGCAGCTATGCCATG AGCTGGGTCCGCCAGGCTCCAGGGA AGGGGCTGGAGTGGGTTTCATACATT AGTAGTAGTGGTACTACCATATACTA CGCAGACTCTGTGAAGGGCCGATTC ACCGTCTCCAGAGACAATGCCAAGA ACTCACTGTATCTGCAAATGAACAGC CTGAGAGCCGAGGACACGGCCGTGT ATTACTGTGCGAGGGATTATAGCAGC TCGGGGGAGTGCTTTGACTACTGGGG CCAGGGAACCCTGGTCACCGTCTCCT CAGCATCCACCAAGGGGCCTTCCGTG TTCCCCCTGGCCCCTTCATCCAAGTC GACCTCTGGTGGAACCGCCGCACTCG GTTGCCTGGTCAAAGACTACTTCCCC GAGCCCGTGACTGTCTCGTGGAACTC GGGCGCCCTCACATCCGGAGTGCAT ACCTTTCCCGCCGTGTTGCAGTCCAG CGGCCTGTACAGCCTGAGCTCCGTCG TGACAGTGCCGTCCTCCTCCCTTGGA ACCCAGACCTATATCTGCAACGTCAA TCACAAGCCCTCCAACACCAAAGTG GACAAGAAGGTCGAACCCAAGTCCT GCGACAAGACTCACACCTGTCCGCCT TGTCCAGCCCCTGAGCTGCTGGGTGG TCCGTCCGTGTTCCTCTTCCCGCCCA	SEQ ID 1910	GAAATTGTGCTGACTCAGTCTCCA GGCACCCTGTCTTTGTCTCCAGGGG AAAGAGCCACCCTCTCCTGCAGGG CCAGTCAGAGTGTAATAAGCAGGT ACTTAGCCTGGTATCAGCAGAAAC CTGGCCAGGCTCCCAGGCTCCTCAT CCATGGTGCATCCACCAGGGCCAC TGGCATCCCAGACAGGTTCAGTGG CAGTGGGTCTGGGACAGACTTCAC TCTCACCATCAGCAGACTGGAGCC TGAAGACTTTGCAGTGTATTACTGT CAGCAGTATGGTAGCTCACCTCCG TACACTTTTGGCCAGGGGACCAAG GTGGAAATCAAACGTACTGTGGCT GCTCCCTCCGTGTTCATTTTTCCTC CGTCGGACGAACAGCTGAAGTCCG GAACCGCGTCCGTGGTCTGTCTCCT GAACAACTTCTATCCGCGCGAGGC GAAAGTGCAGTGGAAGGTCGACAA CGCACTGCAGTCGGGAAACTCCCA GGAATCGGTGACCGAGCAGGACTC GAAGGACTCAACCTACTCATTGTC CTCCACCCTCACCCTGAGCAAGGC CGATTACGAGAAGCATAAGGTCTA CGCCTGCGAAGTGACCCACCAGGG CCTGAGCAGCCCAGTGACGAAGTC CTTCAACCGGGGAGAATGC

	AGCCGAAGGACACTCTGATGATTTCA CGCACCCCGGAAGTCACTTGCGTGGT CGTGGACGTGTCGCACGAAGATCCC GAAGTGAAATTCAATTGGTACGTGG ATGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTAC AACTCTACGTACCGGGTGGTGTCCGT GCTGACCGTGCTGCACCAGGACTGG CTGAACGGAAAGGAGTACAAGTGCA AAGTGTCAAACAAGGCTCTCCCTGCC CCTATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTATACTTTGCCGCCTAGCCGGG AAGAAATGACTAAGAACCAAGTGTC CCTGACTTGCCTTGTCAAGGGCTTTT ATCCGTCCGACATCGCCGTGGAGTGG GAGTCCAACGGACAACCGGAGAACA ACTACAAGACCACCCCACCGGTGCTC GATTCCGATGGCTCCTTCTTCCTGTA CTCCAAGCTGACTGTGGACAAGTCA AGATGGCAGCAGGGAAACGTGTTCT CCTGCTCCGTGATGCACGAAGCGCTG CACAACCATTACACCCAGAAATCACT GTCACTTTCGCCGGGAAAA		
SEQ ID 1803	GAGGTGCAGCTGGTGCAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCGTCTG GATTCACCTTCAGTAGCTATGGCATG CACTGGGTCCGCCAGGCTCCAGGCA AGGGGCTGGAGTGGGTGGCAGTTAT ATGGTATGATGGAAGTAATAAATAC TATGCAGACTCCGTGAAGGGCCGATT CACCATCTCCAGAGACAATTCCAAG AACACGCTGTATCTGCAAATGAACA GCCTGAGAGCCGAGGACACGGCTGT GTATTACTGTGCGAGAGATCAGGCA GCTATGGTAGGCTACTTTGACTACTG GGGCCAGGGAACCCTGGTCACCGTC TCCTCAGCATCCACCAAGGGGCCTTC CGTGTTCCCCCTGGCCCCTTCATCCA AGTCGACCTCTGGTGGAACCGCCGC ACTCGGTTGCCTGGTCAAAGACTACT TCCCCGAGCCCGTGACTGTCTCGTGG AACTCGGGCGCCCTCACATCCGGAGT GCATACCTTTCCCGCCGTGTTGCAGT CCAGCGGCCTGTACAGCCTGAGCTCC GTCGTGACAGTGCCGTCCTCCTCCCT TGGAACCCAGACCTATATCTGCAACG TCAATCACAAGCCCTCCAACACCAA AGTGGACAAGAAGGTCGAACCCAAG TCCTGCGACAAGACTCACACCTGTCC GCCTTGTCCAGCCCCTGAGCTGCTGG GTGGTCCGTCCGTGTTCCTCTTCCCG	SEQ ID 1911	GACATCCAGTTGACCCAGTCTCCTT CCACCCTGGCTGCATCTGTAGGAG ACAGAGTCACCATCACTTGCCGGG CCAGTCAGAGTATTAGTAGCTGGT TGGCCTGGTATCAGCAGAAACCAG GGAAAGCCCCTAAGGTCCTGATCT ATAAGGCGTCTAGTTTAGAAAGTG GGGTCCCATCAAGGTTCAGCGGCA GTGGATCTGGGACAGAATTCACTC TCACCATCAGCAGCCTGCAGCCTG ATGATTTTGCAACTTATTACTGCCA ACAGTATAATAGTTATTCGGGGAC GTTCGGCCAAGGGACCAAGGTGGA AATCAAACGTACTGTGGCTGCTCC CTCCGTGTTCATTTTTCCTCCGTCG GACGAACAGCTGAAGTCCGGAACC GCGTCCGTGGTCTGTCTCCTGAACA ACTTCTATCCGCGCGAGGCGAAAG TGCAGTGGAAGGTCGACAACGCAC TGCAGTCGGGAAACTCCCAGGAAT CGGTGACCGAGCAGGACTCGAAGG ACTCAACCTACTCATTGTCCTCCAC CCTCACCCTGAGCAAGGCCGATTA CGAGAAGCATAAGGTCTACGCCTG CGAAGTGACCCACCAGGGCCTGAG CAGCCCAGTGACGAAGTCCTTCAA CCGGGGAGAATGC

	CCCAAGCCGAAGGACACTCTGATGA TTTCACGCACCCCGGAAGTCACTTGC GTGGTCGTGGACGTGTCGCACGAAG ATCCCGAAGTGAAATTCAATTGGTAC GTGGATGGGGTCGAAGTGCACAACG CCAAGACCAAGCCTAGGGAAGAACA GTACAACTCTACGTACCGGGTGGTGT CCGTGCTGACCGTGCTGCACCAGGAC TGGCTGAACGGAAAGGAGTACAAGT GCAAAGTGTCAAACAAGGCTCTCCCT GCCCCTATCGAAAAGACCATCAGCA AGGCCAAGGGTCAACCTAGGGAGCC CCAGGTCTATACTTTGCCGCCTAGCC GGGAAGAAATGACTAAGAACCAAGT GTCCCTGACTTGCCTTGTCAAGGGCT TTTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAGA ACAACTACAAGACCACCCCACCGGT GCTCGATTCCGATGGCTCCTTCTTCC TGTACTCCAAGCTGACTGTGGACAAG TCAAGATGGCAGCAGGGAAACGTGT TCTCCTGCTCCGTGATGCACGAAGCG CTGCACAACCATTACACCCAGAAATC ACTGTCACTTTCGCCGGGAAAA		
SEQ ID 1804	CAGGTCACCTTGAAGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCCTCTG GATTCATCTTCAGTAACTATGCTATA CACTGGGTCCGCCAGGCTCCAGGCA AGGGGCTGGAGTGGGTGGCAGTTAT ATCATATGATGGAAGTAATAAATACT ACGCAGACTCCGTGAAGGGCCGATT CACCATCTCCAGAGACAATTCCAAG AACACGCTGTATCTGCAAATGAACA GCCTGAGAGCTGAGGACACGGCTGT GTATTACTGTGCGAGGACTTTTGCGG GGTATAGCAGCAAACTGGGGTACTT CGATCTCTGGGGCCGTGGCACCCTGG TCACCGTCTCCTCAGCATCCACCAAG GGGCCTTCCGTGTTCCCCCTGGCCCC TTCATCCAAGTCGACCTCTGGTGGAA CCGCCGCACTCGGTTGCCTGGTCAAA GACTACTTCCCCGAGCCCGTGACTGT CTCGTGGAACTCGGGCGCCCTCACAT CCGGAGTGCATACCTTTCCCGCCGTG TTGCAGTCCAGCGGCCTGTACAGCCT GAGCTCCGTCGTGACAGTGCCGTCCT CCTCCCTTGGAACCCAGACCTATATC TGCAACGTCAATCACAAGCCCTCCAA CACCAAAGTGGACAAGAAGGTCGAA CCCAAGTCCTGCGACAAGACTCACA CCTGTCCGCCTTGTCCAGCCCCTGAG CTGCTGGGTGGTCCGTCCGTGTTCCT	SEQ ID 1912	GATGTTGTGATGACTCAGTCTCCAG CCATCCTGTCTGTGTCTCCAGGGGA AAGAGCCACCCTCTCCTGCAGGGC CAGTCAGAGTGTTAGTAGCAGCTT AGCCTGGTACCAGCAGAAACCTGG CCAGCCTCCCAGGCTCCTCATCTAT GGTGCCTCCACCAGGGCCACTGCT ATCCCAGCCAGGTTCAGTGGCAGT GGGTCTGGGACAGAGTTCACTCTC ACCATCAGCAGCCTGCAGTCTGAA GATTTTGCAGTTTATTACTGTCAGC GCTATGATAACTGGCCTCCCCTTTT TGGCCAGGGGACCAAGCTGGAGAT CAAACGTACTGTGGCTGCTCCCTCC GTGTTCATTTTTCCTCCGTCGGACG AACAGCTGAAGTCCGGAACCGCGT CCGTGGTCTGTCTCCTGAACAACTT CTATCCGCGCGAGGCGAAAGTGCA GTGGAAGGTCGACAACGCACTGCA GTCGGGAAACTCCCAGGAATCGGT GACCGAGCAGGACTCGAAGGACTC AACCTACTCATTGTCCTCCACCCTC ACCCTGAGCAAGGCCGATTACGAG AAGCATAAGGTCTACGCCTGCGAA GTGACCCACCAGGGCCTGAGCAGC CCAGTGACGAAGTCCTTCAACCGG GGAGAATGC

	CTTCCCGCCCAAGCCGAAGGACACTC TGATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGCA CGAAGATCCCGAAGTGAAATTCAAT TGGTACGTGGATGGGGTCGAAGTGC ACAACGCCAAGACCAAGCCTAGGGA AGAACAGTACAACTCTACGTACCGG GTGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGAG TACAAGTGCAAAGTGTCAAACAAGG CTCTCCCTGCCCCTATCGAAAAGACC ATCAGCAAGGCCAAGGGTCAACCTA GGGAGCCCCAGGTCTATACTTTGCCG CCTAGCCGGGAAGAAATGACTAAGA ACCAAGTGTCCCTGACTTGCCTTGTC AAGGGCTTTTATCCGTCCGACATCGC CGTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTCC TTCTTCCTGTACTCCAAGCTGACTGT GGACAAGTCAAGATGGCAGCAGGGA AACGTGTTCTCCTGCTCCGTGATGCA CGAAGCGCTGCACAACCATTACACC CAGAAATCACTGTCACTTTCGCCGGG AAAA		

Table 39. Anti-CLEC21D IgG4 antibody Variable Heavy and Light Chain amino acid and DNA sequence

SEQ ID	VH+CH+AA_IgG4	SEQ ID	VH+CH+DNA_IgG4
SEQ ID 1913	EVQLVQSGAEVKKPGASVKVSCKASG YTFTSYAMHWVRQAPGQRLEWMGWI NAGNGNTKYSQKFQGRVTITRDTSAST AYMELSSLRSEDTAVYYCARGSLSRSG WYAGLFDYWGQGTLVTVSSASTKGPS VFPLAPCSRSTSESTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTKTYTCNVDHKP SNTKVDKRVESKYGPPCPPCPAPEFLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKT KPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKGQ PREPQVYTLPPSQEEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSRLTVDKSRWQEGNV FSCSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2021	GAAGTGCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTTTCCTGCAAGGCTTCT GGATACACCTTCACTAGCTATGCTA TGCATTGGGTGCGCCAGGCCCCCGG ACAAAGGCTTGAGTGGATGGGATG GATCAACGCTGGCAATGGTAACACA AAATATTCACAGAAGTTCCAGGGCA GAGTCACCATTACCAGGGACACATC CGCGAGCACAGCCTACATGGAGCTG AGCAGCCTGAGATCTGAAGACACG GCTGTGTATTACTGTGCGAGAGGCT CCTTGTCCCGAAGTGGCTGGTACGC CGGACTCTTTGACTACTGGGGCCAG GGAACCCTGGTCACCGTCTCCTCAG CATCCACCAAGGGGCCTTCCGTGTT CCCCCTGGCCCCTTGCTCCCGCTCG ACCTCTGAATCCACCGCCGCACTCG GTTGCCTGGTCAAAGACTACTTCCC CGAGCCCGTGACTGTCTCGTGGAAC TCGGGCGCCCTCACATCCGGAGTGC ATACCTTTCCCGCCGTGTTGCAGTCC AGCGGCCTGTACAGCCTGAGCTCCG

			TCGTGACAGTGCCGTCCTCCTCCCTT GGAACCAAGACCTATACCTGCAACG TCGACCACAAGCCCTCCAACACCAA AGTGGACAAGCGCGTCGAATCCAA GTACGGCCCCCCTTGTCCGCCTTGTC CAGCCCCTGAGTTCCTGGGTGGTCC GTCCGTGTTCCTCTTCCCGCCCAAGC CGAAGGACACTCTGATGATTTCACG CACCCCGGAAGTCACTTGCGTGGTC GTGGACGTGTCGCAGGAAGATCCCG AAGTGCAGTTCAATTGGTACGTGGA TGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTT CAACTCTACGTACCGGGTGGTGTCC GTGCTGACCGTGCTGCACCAGGACT GGCTGAACGGAAAGGAGTACAAGT GCAAAGTGTCAAACAAGGGCCTCCC TTCATCCATCGAAAAGACCATCAGC AAGGCCAAGGGTCAACCTAGGGAG CCCCAGGTCTACACTTTGCCGCCTA GCCAAGAAGAAATGACTAAGAACC AAGTGTCCCTGACTTGCCTTGTCAA GGGCTTTTATCCGTCCGACATCGCC GTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACC CCACCGGTGCTCGATTCCGATGGCT CCTTCTTCCTGTACTCCCGGCTGACT GTGGACAAGTCAAGATGGCAGGAG GGAAACGTGTTCTCCTGCTCCGTGA TGCACGAAGCGCTGCACAACCATTA CACCCAGAAATCACTGTCACTTTCG CTGGGAAAA
SEQ ID 1914	QITLKESGGGVVQPGRSLRLSCAASGF TFSSYSMNWVRQAPGKGLQWVAIISD DGSKSYYADSVQGRFTISRDNSRNTVF LQMNSLRAEDTAMYYCARDRGTKWN QLNDVFDMWGQGTMVTVSSASTKGP SVFPLAPCSRSTSESTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSG LYSLSSVVTVPSSSLGTKTYTCNVDHK PSNTKVDKRVESKYGPPCPPCPAPEFL GGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSQEDPEVQFNWYVDGVEVHNAK TKPREEQFNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKGLPSSIEKTISKAKG QPREPQVYTLPPSQEEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSRLTVDKSRWQEGN VFSCSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2022	CAGATCACCTTGAAGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTCAGTAGTTATAGCA TGAACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGCAGTGGGTGGCAATT ATATCAGATGATGGAAGTAAGAGTT ACTACGCAGACTCCGTGCAGGGCCG ATTCACCATCTCCAGAGACAATTCG AGGAACACAGTATTTCTGCAAATGA ACAGCCTGAGAGCTGAGGACACGG CTATGTATTACTGTGCGAGAGACAG GGGAACTAAATGGAACCAATTGAAT GATGTTTTTGATATGTGGGGCCAAG GGACAATGGTCACCGTCTCTTCAGC ATCCACCAAGGGGCCTTCCGTGTTC CCCCTGGCCCCTTGCTCCCGCTCGA CCTCTGAATCCACCGCCGCACTCGG TTGCCTGGTCAAAGACTACTTCCCC GAGCCCGTGACTGTCTCGTGGAACT CGGGCGCCCTCACATCCGGAGTGCA TACCTTTCCCGCCGTGTTGCAGTCCA GCGGCCTGTACAGCCTGAGCTCCGT CGTGACAGTGCCGTCCTCCTCCCTT

			GGAACCAAGACCTATACCTGCAACG TCGACCACAAGCCCTCCAACACCAA AGTGGACAAGCGCGTCGAATCCAA GTACGGCCCCCCTTGTCCGCCTTGTC CAGCCCCTGAGTTCCTGGGTGGTCC GTCCGTGTTCCTCTTCCCGCCCAAGC CGAAGGACACTCTGATGATTTCACG CACCCCGGAAGTCACTTGCGTGGTC GTGGACGTGTCGCAGGAAGATCCCG AAGTGCAGTTCAATTGGTACGTGGA TGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTT CAACTCTACGTACCGGGTGGTGTCC GTGCTGACCGTGCTGCACCAGGACT GGCTGAACGGAAAGGAGTACAAGT GCAAAGTGTCAAACAAGGGCCTCCC TTCATCCATCGAAAAGACCATCAGC AAGGCCAAGGGTCAACCTAGGGAG CCCCAGGTCTACACTTTGCCGCCTA GCCAAGAAGAAATGACTAAGAACC AAGTGTCCCTGACTTGCCTTGTCAA GGGCTTTTATCCGTCCGACATCGCC GTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACC CCACCGGTGCTCGATTCCGATGGCT CCTTCTTCCTGTACTCCCGGCTGACT GTGGACAAGTCAAGATGGCAGGAG GGAAACGTGTTCTCCTGCTCCGTGA TGCACGAAGCGCTGCACAACCATTA CACCCAGAAATCACTGTCACTTTCG CTGGGAAAA
SEQ ID 1915	EVQLVQSGAEVKKPGASVKVSCKASG YTFTSYYMHWVRQAPGQGLEWMGIIN PSGGSTSYAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARGRGYSSS RLYYFDYWGQGTLVTVSSASTKGPSV FPLAPCSRSTSESTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTKTYTCNVDHKP SNTKVDKRVESKYGPPCPPCPAPEFLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKT KPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKGQ PREPQVYTLPPSQEEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSRLTVDKSRWQEGNV FSCSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2023	GAAGTGCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTTTCCTGCAAGGCATCT GGATACACCTTCACCAGCTACTATA TGCACTGGGTGCGACAGGCCCCTGG ACAAGGGCTTGAGTGGATGGGAAT AATCAACCCTAGTGGTGGTAGCACA AGCTACGCACAGAAGTTCCAGGGCA GAGTCACCATGACCAGGGACACGTC CACGAGCACAGTCTACATGGAGCTG AGCAGCCTGAGATCTGAGGACACG GCCGTGTATTACTGTGCGAGAGGCC GAGGGTATAGCAGCAGTCGGCTCTA CTACTTTGACTACTGGGGCCAGGGA ACCCTGGTCACCGTCTCCTCAGCAT CCACCAAGGGGCCTTCCGTGTTCCC CCTGGCCCCTTGCTCCCGCTCGACCT CTGAATCCACCGCCGCACTCGGTTG CCTGGTCAAAGACTACTTCCCCGAG CCCGTGACTGTCTCGTGGAACTCGG GCGCCCTCACATCCGGAGTGCATAC CTTTCCCGCCGTGTTGCAGTCCAGC GGCCTGTACAGCCTGAGCTCCGTCG TGACAGTGCCGTCCTCCTCCCTTGG AACCAAGACCTATACCTGCAACGTC

			GACCACAAGCCCTCCAACACCAAAG TGGACAAGCGCGTCGAATCCAAGTA CGGCCCCCCTTGTCCGCCTTGTCCA GCCCCTGAGTTCCTGGGTGGTCCGT CCGTGTTCCTCTTCCCGCCCAAGCC GAAGGACACTCTGATGATTTCACGC ACCCCGGAAGTCACTTGCGTGGTCG TGGACGTGTCGCAGGAAGATCCCGA AGTGCAGTTCAATTGGTACGTGGAT GGGGTCGAAGTGCACAACGCCAAG ACCAAGCCTAGGGAAGAACAGTTC AACTCTACGTACCGGGTGGTGTCCG TGCTGACCGTGCTGCACCAGGACTG GCTGAACGGAAAGGAGTACAAGTG CAAAGTGTCAAACAAGGGCCTCCCT TCATCCATCGAAAAGACCATCAGCA AGGCCAAGGGTCAACCTAGGGAGC CCCAGGTCTACACTTTGCCGCCTAG CCAAGAAGAAATGACTAAGAACCA AGTGTCCCTGACTTGCCTTGTCAAG GGCTTTTATCCGTCCGACATCGCCG TGGAGTGGGAGTCCAACGGACAAC CGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTC CTTCTTCCTGTACTCCCGGCTGACTG TGGACAAGTCAAGATGGCAGGAGG GAAACGTGTTCTCCTGCTCCGTGAT GCACGAAGCGCTGCACAACCATTAC ACCCAGAAATCACTGTCACTTTCGC TGGGAAAA
SEQ ID 1916	QVTLKESGGGLVRPGGSLRLSCEASGF TFSDPYMDWVRQAPGKGLEWVGRITN KRTGYATTYAASVKDRFTISRDDSRKS VYLQMNSLKTEDTAVYYCATDVSGSF AAYGGQGTLVTVSSASTKGPSVFPLAP CSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTKTYTCNVDHKPSNTKV DKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQE DPEVQFNWYVDGVEVHNAKTKPREE QFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSLGK	SEQ ID 2024	CAGGTCACCTTGAAGGAGTCTGGGG GAGGCTTGGTCCGGCCTGGAGGGTC CCTGAGACTCTCCTGTGAAGCCTCT GGATTCACCTTCAGTGACCCCTACA TGGACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTTGGCCG AATTACAAATAAGCGTACCGGTTAC GCCACAACATATGCCGCGTCTGTGA AGGACAGATTCACCATCTCAAGAGA TGATTCAAGGAAGTCAGTATATCTG CAAATGAACAGCCTGAAGACCGAG GACACGGCCGTATATTATTGTGCAA CAGATGTCAGTGGGTCCTTCGCGGC CTACGGGGGCCAGGGCACCCTGGTC ACCGTCTCCTCAGCATCCACCAAGG GGCCTTCCGTGTTCCCCCTGGCCCCT TGCTCCCGCTCGACCTCTGAATCCA CCGCCGCACTCGGTTGCCTGGTCAA AGACTACTTCCCCGAGCCCGTGACT GTCTCGTGGAACTCGGGCGCCCTCA CATCCGGAGTGCATACCTTTCCCGC CGTGTTGCAGTCCAGCGGCCTGTAC AGCCTGAGCTCCGTCGTGACAGTGC CGTCCTCCTCCCTTGGAACCAAGAC CTATACCTGCAACGTCGACCACAAG CCCTCCAACACCAAAGTGGACAAGC

			GCGTCGAATCCAAGTACGGCCCCCC TTGTCCGCCTTGTCCAGCCCCTGAGT TCCTGGGTGGTCCGTCCGTGTTCCTC TTCCCGCCCAAGCCGAAGGACACTC TGATGATTTCACGCACCCCGGAAGT CACTTGCGTGGTCGTGGACGTGTCG CAGGAAGATCCCGAAGTGCAGTTCA ATTGGTACGTGGATGGGGTCGAAGT GCACAACGCCAAGACCAAGCCTAG GGAAGAACAGTTCAACTCTACGTAC CGGGTGGTGTCCGTGCTGACCGTGC TGCACCAGGACTGGCTGAACGGAA AGGAGTACAAGTGCAAAGTGTCAA ACAAGGGCCTCCCTTCATCCATCGA AAAGACCATCAGCAAGGCCAAGGG TCAACCTAGGGAGCCCCAGGTCTAC ACTTTGCCGCCTAGCCAAGAAGAAA TGACTAAGAACCAAGTGTCCCTGAC TTGCCTTGTCAAGGGCTTTTATCCGT CCGACATCGCCGTGGAGTGGGAGTC CAACGGACAACCGGAGAACAACTA CAAGACCACCCCACCGGTGCTCGAT TCCGATGGCTCCTTCTTCCTGTACTC CCGGCTGACTGTGGACAAGTCAAGA TGGCAGGAGGGAAACGTGTTCTCCT GCTCCGTGATGCACGAAGCGCTGCA CAACCATTACACCCAGAAATCACTG TCACTTTCGCTGGGAAAA
SEQ ID 1917	EVQLVQSGGGVVQPGRSLRLSCAASG FTFSSYAMHWVRQAPGQRLEWMGWI NAGNGNTKYSQKFQGRVTITRDTSAST AYMELSSLRSEDTAVYYCAGEGGAVA GTVYWGQGTLVTVSSASTKGPSVFPL APCSRSTSESTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDV SQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKGLPSSIEKTISKAKGQPRE PQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCS VMHEALHNHYTQKSLSLSLGK	SEQ ID 2025	GAGGTCCAGCTGGTACAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCGTCT GGATTCACCTTCAGTAGCTATGCTA TGCATTGGGTGCGCCAGGCCCCCGG ACAAAGGCTTGAGTGGATGGGATG GATCAACGCTGGCAATGGTAACACA AAATATTCACAGAAGTTCCAGGGCA GAGTCACCATTACCAGGGACACATC CGCGAGCACAGCCTACATGGAGCTG AGCAGCCTGAGATCTGAAGACACG GCTGTGTATTACTGTGCGGGAGAGG GCGGAGCAGTGGCTGGTACTGTCTA CTGGGGCCAGGGAACCCTGGTCACC GTCTCCTCAGCATCCACCAAGGGGC CTTCCGTGTTCCCCCTGGCCCCTTGC TCCCGCTCGACCTCTGAATCCACCG CCGCACTCGGTTGCCTGGTCAAAGA CTACTTCCCCGAGCCCGTGACTGTC TCGTGGAACTCGGGCGCCCTCACAT CCGGAGTGCATACCTTTCCCGCCGT GTTGCAGTCCAGCGGCCTGTACAGC CTGAGCTCCGTCGTGACAGTGCCGT CCTCCTCCCTTGGAACCAAGACCTA TACCTGCAACGTCGACCACAAGCCC TCCAACACCAAAGTGGACAAGCGC GTCGAATCCAAGTACGGCCCCCCTT GTCCGCCTTGTCCAGCCCCTGAGTT

			CCTGGGTGGTCCGTCCGTGTTCCTCT TCCCGCCCAAGCCGAAGGACACTCT GATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGC AGGAAGATCCCGAAGTGCAGTTCAA TTGGTACGTGGATGGGGTCGAAGTG CACAACGCCAAGACCAAGCCTAGG GAAGAACAGTTCAACTCTACGTACC GGGTGGTGTCCGTGCTGACCGTGCT GCACCAGGACTGGCTGAACGGAAA GGAGTACAAGTGCAAAGTGTCAAA CAAGGGCCTCCCTTCATCCATCGAA AAGACCATCAGCAAGGCCAAGGGT CAACCTAGGGAGCCCCAGGTCTACA CTTTGCCGCCTAGCCAAGAAGAAAT GACTAAGAACCAAGTGTCCCTGACT TGCCTTGTCAAGGGCTTTTATCCGTC CGACATCGCCGTGGAGTGGGAGTCC AACGGACAACCGGAGAACAACTAC AAGACCACCCCACCGGTGCTCGATT CCGATGGCTCCTTCTTCCTGTACTCC CGGCTGACTGTGGACAAGTCAAGAT GGCAGGAGGGAAACGTGTTCTCCTG CTCCGTGATGCACGAAGCGCTGCAC AACCATTACACCCAGAAATCACTGT CACTTTCGCTGGGAAAA
SEQ ID 1918	QVQLVQSGGGLVKPGGSLRLSCAASG FTFSNAWMSWVRQAPGKGLEWVGRI KSKTDGGTTDYAAPVKGRFTISRDDSK NTLYLQMNSLKTEDTAVYYCTTDEYF YWGQGTLVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTKTYTCNVDHKPSNTKVDK RVESKYGPPCPPCPAPEFLGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSQEDP EVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKC KVSNKGLPSSIEKTISKAKGQPREPQVY TLPPSQEEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGS FFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSLGK	SEQ ID 2026	CAGGTCCAGCTGGTGCAGTCTGGGG GAGGCTTGGTAAAGCCTGGGGGGTC CCTTAGACTCTCCTGTGCAGCCTCTG GATTCACTTTCAGTAACGCCTGGAT GAGCTGGGTCCGCCAGGCTCCAGGG AAGGGGCTGGAGTGGGTTGGCCGTA TTAAAAGCAAAACTGATGGTGGGAC AACAGACTACGCTGCACCCGTGAAA GGCAGATTCACCATCTCAAGAGATG ATTCAAAAAACACGCTGTATCTGCA AATGAACAGCCTGAAAACCGAGGA CACAGCCGTGTATTACTGTACCACA GACGAGTATTTCTACTGGGGCCAGG GAACCCTGGTCACCGTCTCCTCAGC ATCCACCAAGGGGCCTTCCGTGTTC CCCCTGGCCCCTTGCTCCCGCTCGA CCTCTGAATCCACCGCCGCACTCGG TTGCCTGGTCAAAGACTACTTCCCC GAGCCCGTGACTGTCTCGTGGAACT CGGGCGCCCTCACATCCGGAGTGCA TACCTTTCCCGCCGTGTTGCAGTCCA GCGGCCTGTACAGCCTGAGCTCCGT CGTGACAGTGCCGTCCTCCTCCCTT GGAACCAAGACCTATACCTGCAACG TCGACCACAAGCCCTCCAACACCAA AGTGGACAAGCGCGTCGAATCCAA GTACGGCCCCCCTTGTCCGCCTTGTC CAGCCCCTGAGTTCCTGGGTGGTCC GTCCGTGTTCCTCTTCCCGCCCAAGC CGAAGGACACTCTGATGATTTCACG

			CACCCCGGAAGTCACTTGCGTGGTC GTGGACGTGTCGCAGGAAGATCCCG AAGTGCAGTTCAATTGGTACGTGGA TGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTT CAACTCTACGTACCGGGTGGTGTCC GTGCTGACCGTGCTGCACCAGGACT GGCTGAACGGAAAGGAGTACAAGT GCAAAGTGTCAAACAAGGGCCTCCC TTCATCCATCGAAAAGACCATCAGC AAGGCCAAGGGTCAACCTAGGGAG CCCCAGGTCTACACTTTGCCGCCTA GCCAAGAAGAAATGACTAAGAACC AAGTGTCCCTGACTTGCCTTGTCAA GGGCTTTTATCCGTCCGACATCGCC GTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACC CCACCGGTGCTCGATTCCGATGGCT CCTTCTTCCTGTACTCCCGGCTGACT GTGGACAAGTCAAGATGGCAGGAG GGAAACGTGTTCTCCTGCTCCGTGA TGCACGAAGCGCTGCACAACCATTA CACCCAGAAATCACTGTCACTTTCG CTGGGAAAA
SEQ ID 1919	QVQLQQWGAGLLKPSETLSLTCAVYG GSFSGYYWSWIRQPPGKGLEWIGEINH SGSTNYNPSLKSRVTISVDTSKNQFSLK LSSVTAADTAVYYCARVNPGSYTREV SNFDYWGQGTLVTVSSASTKGPSVFPL APCSRSTSESTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDV SQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKGLPSSIEKTISKAKGQPRE PQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCS VMHEALHNHYTQKSLSLSLGK	SEQ ID 2027	CAGGTGCAGCTACAGCAGTGGGGC GCAGGACTGTTGAAGCCTTCGGAGA CCCTGTCCCTCACCTGCGCTGTCTAT GGTGGGTCCTTCAGTGGTTACTACT GGAGCTGGATCCGCCAGCCCCCAGG GAAGGGGCTGGAGTGGATTGGGGA AATCAATCATAGTGGAAGCACCAAC TACAACCCGTCCCTCAAGAGTCGAG TCACCATATCAGTAGACACGTCCAA GAACCAGTTCTCCCTGAAGCTGAGC TCTGTGACCGCCGCGGACACGGCTG TGTATTACTGTGCGAGAGTAAATCC GGGGAGTTATACGAGGGAGGTGAG CAACTTTGACTACTGGGGCCAGGGA ACCCTGGTGACCGTCTCCTCAGCAT CCACCAAGGGGCCTTCCGTGTTCCC CCTGGCCCCTTGCTCCCGCTCGACCT CTGAATCCACCGCCGCACTCGGTTG CCTGGTCAAAGACTACTTCCCCGAG CCCGTGACTGTCTCGTGGAACTCGG GCGCCCTCACATCCGGAGTGCATAC CTTTCCCGCCGTGTTGCAGTCCAGC GGCCTGTACAGCCTGAGCTCCGTCG TGACAGTGCCGTCCTCCTCCCTTGG AACCAAGACCTATACCTGCAACGTC GACCACAAGCCCTCCAACACCAAAG TGGACAAGCGCGTCGAATCCAAGTA CGGCCCCCCTTGTCCGCCTTGTCCA GCCCCTGAGTTCCTGGGTGGTCCGT CCGTGTTCCTCTTCCCGCCCAAGCC GAAGGACACTCTGATGATTTCACGC ACCCCGGAAGTCACTTGCGTGGTCG

			TGGACGTGTCGCAGGAAGATCCCGA AGTGCAGTTCAATTGGTACGTGGAT GGGGTCGAAGTGCACAACGCCAAG ACCAAGCCTAGGGAAGAACAGTTC AACTCTACGTACCGGGTGGTGTCCG TGCTGACCGTGCTGCACCAGGACTG GCTGAACGGAAAGGAGTACAAGTG CAAAGTGTCAAACAAGGGCCTCCCT TCATCCATCGAAAAGACCATCAGCA AGGCCAAGGGTCAACCTAGGGAGC CCCAGGTCTACACTTTGCCGCCTAG CCAAGAAGAAATGACTAAGAACCA AGTGTCCCTGACTTGCCTTGTCAAG GGCTTTTATCCGTCCGACATCGCCG TGGAGTGGGAGTCCAACGGACAAC CGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTC CTTCTTCCTGTACTCCCGGCTGACTG TGGACAAGTCAAGATGGCAGGAGG GAAACGTGTTCTCCTGCTCCGTGAT GCACGAAGCGCTGCACAACCATTAC ACCCAGAAATCACTGTCACTTTCGC TGGGAAAA
SEQ ID 1920	QVQLQQSGPELVKPSQTLTLTCGISGD SVSSNSVTWNWVRQSPSRGLEWLGRT YYRSQWYYNYAVSVKSRITISPDTSKN QFSLQLNSVTPEDTAVYYCATRGHNY GVDYWGPGTTVTVSSASTKGPSVFPL APCSRSTSESTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDV SQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKGLPSSIEKTISKAKGQPRE PQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCS VMHEALHNHYTQKSLSLSLGK	SEQ ID 2028	CAGGTACAGCTGCAGCAGTCAGGTC CAGAATTGGTGAAGCCCTCGCAGAC CCTCACACTCACCTGTGGCATCTCC GGGGACAGTGTCTCTAGCAACAGTG TTACTTGGAACTGGGTCAGGCAGTC CCCATCGAGAGGCCTTGAGTGGCTG GGAAGGACTTACTACCGGTCCCAGT GGTATTATAATTATGCGGTGTCTGT GAAAAGTCGAATAACCATCAGCCCA GACACATCCAAGAACCAGTTCTCCC TGCAGTTGAATTCTGTGACTCCCGA GGACACGGCTGTCTATTACTGTGCA ACCAGGGGACATAACTACGGTGTAG ATTACTGGGGCCCGGGGACCACGGT CACCGTCTCCTCAGCATCCACCAAG GGGCCTTCCGTGTTCCCCCTGGCCC CTTGCTCCCGCTCGACCTCTGAATCC ACCGCCGCACTCGGTTGCCTGGTCA AAGACTACTTCCCCGAGCCCGTGAC TGTCTCGTGGAACTCGGGCGCCCTC ACATCCGGAGTGCATACCTTTCCCG CCGTGTTGCAGTCCAGCGGCCTGTA CAGCCTGAGCTCCGTCGTGACAGTG CCGTCCTCCTCCCTTGGAACCAAGA CCTATACCTGCAACGTCGACCACAA GCCCTCCAACACCAAAGTGGACAAG CGCGTCGAATCCAAGTACGGCCCCC CTTGTCCGCCTTGTCCAGCCCCTGA GTTCCTGGGTGGTCCGTCCGTGTTCC TCTTCCCGCCCAAGCCGAAGGACAC TCTGATGATTTCACGCACCCCGGAA GTCACTTGCGTGGTCGTGGACGTGT CGCAGGAAGATCCCGAAGTGCAGTT

			CAATTGGTACGTGGATGGGGTCGAA GTGCACAACGCCAAGACCAAGCCTA GGGAAGAACAGTTCAACTCTACGTA CCGGGTGGTGTCCGTGCTGACCGTG CTGCACCAGGACTGGCTGAACGGAA AGGAGTACAAGTGCAAAGTGTCAA ACAAGGGCCTCCCTTCATCCATCGA AAAGACCATCAGCAAGGCCAAGGG TCAACCTAGGGAGCCCCAGGTCTAC ACTTTGCCGCCTAGCCAAGAAGAAA TGACTAAGAACCAAGTGTCCCTGAC TTGCCTTGTCAAGGGCTTTTATCCGT CCGACATCGCCGTGGAGTGGGAGTC CAACGGACAACCGGAGAACAACTA CAAGACCACCCCACCGGTGCTCGAT TCCGATGGCTCCTTCTTCCTGTACTC CCGGCTGACTGTGGACAAGTCAAGA TGGCAGGAGGGAAACGTGTTCTCCT GCTCCGTGATGCACGAAGCGCTGCA CAACCATTACACCCAGAAATCACTG TCACTTTCGCTGGGAAAA
SEQ ID 1921	QVQLVQSGGGLVKPGGSLRLSCAASG FTFSNAWMSWVRQAPGKGLEWVCRI KSKTDGETTDYAAPVKGRFTISRDDSK NTLYLQMNSLKTEDTAVYHCTTGVG WSPFQYWGQGTLVTVSSASTKGPSVF PLAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSN TKVDKRVESKYGPPCPPCPAPEFLGGP SVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2029	CAGGTGCAGCTGGTGCAGTCTGGGG GAGGCTTGGTAAAGCCTGGGGGGTC CCTTAGACTCTCCTGTGCAGCCTCTG GATTCACTTTCAGTAACGCCTGGAT GAGCTGGGTCCGCCAGGCTCCAGGG AAGGGGCTGGAGTGGGTTTGCCGTA TTAAAAGCAAAACTGATGGTGAGAC AACAGACTACGCTGCACCCGTGAAA GGCAGATTCACCATCTCAAGAGATG ATTCAAAAAACACGCTGTATCTGCA AATGAACAGCCTGAAAACTGAGGA CACAGCCGTGTATCACTGTACCACA GGGGTGGGATGGTCGCCCTTCCAAT ACTGGGGCCAGGGCACCCTGGTCAC CGTCTCCTCAGCATCCACCAAGGGG CCTTCCGTGTTCCCCCTGGCCCCTTG CTCCCGCTCGACCTCTGAATCCACC GCCGCACTCGGTTGCCTGGTCAAAG ACTACTTCCCCGAGCCCGTGACTGT CTCGTGGAACTCGGGCGCCCTCACA TCCGGAGTGCATACCTTTCCCGCCG TGTTGCAGTCCAGCGGCCTGTACAG CCTGAGCTCCGTCGTGACAGTGCCG TCCTCCTCCCTTGGAACCAAGACCT ATACCTGCAACGTCGACCACAAGCC CTCCAACACCAAAGTGGACAAGCGC GTCGAATCCAAGTACGGCCCCCCTT GTCCGCCTTGTCCAGCCCCTGAGTT CCTGGGTGGTCCGTCCGTGTTCCTCT TCCCGCCCAAGCCGAAGGACACTCT GATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGC AGGAAGATCCCGAAGTGCAGTTCAA TTGGTACGTGGATGGGGTCGAAGTG CACAACGCCAAGACCAAGCCTAGG

			GAAGAACAGTTCAACTCTACGTACC GGGTGGTGTCCGTGCTGACCGTGCT GCACCAGGACTGGCTGAACGGAAA GGAGTACAAGTGCAAAGTGTCAAA CAAGGGCCTCCCTTCATCCATCGAA AAGACCATCAGCAAGGCCAAGGGT CAACCTAGGGAGCCCCAGGTCTACA CTTTGCCGCCTAGCCAAGAAGAAAT GACTAAGAACCAAGTGTCCCTGACT TGCCTTGTCAAGGGCTTTTATCCGTC CGACATCGCCGTGGAGTGGGAGTCC AACGGACAACCGGAGAACAACTAC AAGACCACCCCACCGGTGCTCGATT CCGATGGCTCCTTCTTCCTGTACTCC CGGCTGACTGTGGACAAGTCAAGAT GGCAGGAGGGAAACGTGTTCTCCTG CTCCGTGATGCACGAAGCGCTGCAC AACCATTACACCCAGAAATCACTGT CACTTTCGCTGGGAAAA
SEQ ID 1922	EVQLVQSGGGLVQPGRSLRLSCTASGF TFGDYAMSWFRQAPGKGLEWVGFIRS KAYGGTTEYAASVKGRFTISRDDSKSI AYLQMNSLKTEDTAVYYCTRDDKIAA AGFTYWYFDLWGRGTLVTVSSASTKG PSVFPLAPCSRSTSESTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTKTYTCNVDH KPSNTKVDKRVESKYGPPCPPCPAPEF LGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSQEDPEVQFNWYVDGVEVHNA KTKPREEQFNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKGLPSSIEKTISKAK GQPREPQVYTLPPSQEEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSRLTVDKSRWQEG NVFSCSVMHEALHNHYTQKSLSLSLG K	SEQ ID 2030	GAGGTCCAGCTGGTACAGTCTGGGG GAGGCTTGGTACAGCCAGGGCGGTC CCTGAGACTCTCCTGTACAGCTTCT GGATTCACCTTTGGTGATTATGCTAT GAGCTGGTTCCGCCAGGCTCCAGGG AAGGGGCTGGAGTGGGTAGGTTTCA TTAGAAGCAAAGCTTATGGTGGGAC AACAGAATACGCCGCGTCTGTGAAA GGCAGATTCACCATCTCAAGAGATG ATTCCAAAAGCATCGCCTATCTGCA AATGAACAGCCTGAAAACCGAGGA CACAGCCGTGTATTACTGTACTAGA GACGACAAAATAGCAGCAGCTGGA TTCACATACTGGTACTTCGATCTCTG GGGCCGTGGCACCCTGGTCACCGTC TCCTCAGCATCCACCAAGGGGCCTT CCGTGTTCCCCCTGGCCCCTTGCTCC CGCTCGACCTCTGAATCCACCGCCG CACTCGGTTGCCTGGTCAAAGACTA CTTCCCCGAGCCCGTGACTGTCTCG TGGAACTCGGGCGCCCTCACATCCG GAGTGCATACCTTTCCCGCCGTGTT GCAGTCCAGCGGCCTGTACAGCCTG AGCTCCGTCGTGACAGTGCCGTCCT CCTCCCTTGGAACCAAGACCTATAC CTGCAACGTCGACCACAAGCCCTCC AACACCAAAGTGGACAAGCGCGTC GAATCCAAGTACGGCCCCCCTTGTC CGCCTTGTCCAGCCCCTGAGTTCCT GGGTGGTCCGTCCGTGTTCCTCTTCC CGCCCAAGCCGAAGGACACTCTGAT GATTTCACGCACCCCGGAAGTCACT TGCGTGGTCGTGGACGTGTCGCAGG AAGATCCCGAAGTGCAGTTCAATTG GTACGTGGATGGGGTCGAAGTGCAC AACGCCAAGACCAAGCCTAGGGAA GAACAGTTCAACTCTACGTACCGGG

			TGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGA GTACAAGTGCAAAGTGTCAAACAA GGGCCTCCCTTCATCCATCGAAAAG ACCATCAGCAAGGCCAAGGGTCAA CCTAGGGAGCCCCAGGTCTACACTT TGCCGCCTAGCCAAGAAGAAATGAC TAAGAACCAAGTGTCCCTGACTTGC CTTGTCAAGGGCTTTTATCCGTCCG ACATCGCCGTGGAGTGGGAGTCCAA CGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCC GATGGCTCCTTCTTCCTGTACTCCCG GCTGACTGTGGACAAGTCAAGATGG CAGGAGGGAAACGTGTTCTCCTGCT CCGTGATGCACGAAGCGCTGCACAA CCATTACACCCAGAAATCACTGTCA CTTTCGCTGGGAAAA
SEQ ID 1923	QVQLVQSGAEVKKPGASVKVSCKASG YTFAAYYLHWVRQAPGQGLEWMGRI SPGNGVTSYAQKFQGRVTMTGDTSIN TVYMQLNNLISGDTAVYYCAREAADD PFDHWGQGALVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTKTYTCNVDHKPSNTKV DKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQE DPEVQFNWYVDGVEVHNAKTKPREE QFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSLGK	SEQ ID 2031	CAGGTGCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTCTCCTGCAAGGCTTCT GGATACACCTTCGCCGCCTATTATTT ACACTGGGTGCGACAGGCCCCTGGA CAAGGCCTTGAGTGGATGGGGCGG ATCAGCCCTGGTAACGGTGTCACAA GTTATGCACAGAAATTTCAGGGCAG AGTCACCATGACCGGGGACACGTCC ATTAACACAGTCTACATGCAACTGA ACAATTTGATTTCTGGCGACACGGC CGTATATTACTGTGCGAGAGAGGCT GCCGACGACCCGTTTGACCATTGGG GCCAGGGAGCCCTGGTCACCGTCTC CTCAGCATCCACCAAGGGGCCTTCC GTGTTCCCCCTGGCCCCTTGCTCCCG CTCGACCTCTGAATCCACCGCCGCA CTCGGTTGCCTGGTCAAAGACTACT TCCCCGAGCCCGTGACTGTCTCGTG GAACTCGGGCGCCCTCACATCCGGA GTGCATACCTTTCCCGCCGTGTTGC AGTCCAGCGGCCTGTACAGCCTGAG CTCCGTCGTGACAGTGCCGTCCTCC TCCCTTGGAACCAAGACCTATACCT GCAACGTCGACCACAAGCCCTCCAA CACCAAAGTGGACAAGCGCGTCGA ATCCAAGTACGGCCCCCCTTGTCCG CCTTGTCCAGCCCCTGAGTTCCTGG GTGGTCCGTCCGTGTTCCTCTTCCCG CCCAAGCCGAAGGACACTCTGATGA TTTCACGCACCCCGGAAGTCACTTG CGTGGTCGTGGACGTGTCGCAGGAA GATCCCGAAGTGCAGTTCAATTGGT ACGTGGATGGGGTCGAAGTGCACA ACGCCAAGACCAAGCCTAGGGAAG AACAGTTCAACTCTACGTACCGGGT GGTGTCCGTGCTGACCGTGCTGCAC CAGGACTGGCTGAACGGAAAGGAG

			TACAAGTGCAAAGTGTCAAACAAG GGCCTCCCTTCATCCATCGAAAAGA CCATCAGCAAGGCCAAGGGTCAACC TAGGGAGCCCCAGGTCTACACTTTG CCGCCTAGCCAAGAAGAAATGACTA AGAACCAAGTGTCCCTGACTTGCCT TGTCAAGGGCTTTTATCCGTCCGAC ATCGCCGTGGAGTGGGAGTCCAACG GACAACCGGAGAACAACTACAAGA CCACCCCACCGGTGCTCGATTCCGA TGGCTCCTTCTTCCTGTACTCCCGGC TGACTGTGGACAAGTCAAGATGGCA GGAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACT TTCGCTGGGAAAA
SEQ ID 1924	EVQLVQSGGGVVQPGRSLTLSCAASG FTFSSHLMHWVRQAPGKGLEWVAVIS YDGTSKYYGDSVKGRFTISRDNSKNTL YLQMNSLRAEDTAIYYCAKADYKYD WGQGTLVTVSSASTKGPSVFPLAPCSR STSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTKTYTCNVDHKPSNTKVDK RVESKYGPPCPPCPAPEFLGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSQEDP EVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKC KVSNKGLPSSIEKTISKAKGQPREPQVY TLPPSQEEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGS FFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSLGK	SEQ ID 2032	GAAGTGCAGCTGGTGCAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGACACTCTCCTGTGCAGCCTCT GGATTCACCTTCAGTTCCCATCTTAT GCACTGGGTCCGCCAGGCTCCAGGC AAGGGGCTGGAGTGGGTGGCAGTT ATATCATATGATGGAACTAGTAAAT ATTACGGAGACTCCGTGAAGGGCCG CTTCACCATCTCCAGAGACAATTCC AAGAACACGTTGTATCTGCAAATGA ACAGCCTGCGAGCTGAAGACACGG CTATATATTACTGTGCGAAAGCAGA TTATAAATATGACTGGGGCCAGGGA ACCCTGGTCACCGTCTCCTCAGCAT CCACCAAGGGGCCTTCCGTGTTCCC CCTGGCCCCTTGCTCCCGCTCGACCT CTGAATCCACCGCCGCACTCGGTTG CCTGGTCAAAGACTACTTCCCCGAG CCCGTGACTGTCTCGTGGAACTCGG GCGCCCTCACATCCGGAGTGCATAC CTTTCCCGCCGTGTTGCAGTCCAGC GGCCTGTACAGCCTGAGCTCCGTCG TGACAGTGCCGTCCTCCTCCCTTGG AACCAAGACCTATACCTGCAACGTC GACCACAAGCCCTCCAACACCAAAG TGGACAAGCGCGTCGAATCCAAGTA CGGCCCCCCTTGTCCGCCTTGTCCA GCCCCTGAGTTCCTGGGTGGTCCGT CCGTGTTCCTCTTCCCGCCCAAGCC GAAGGACACTCTGATGATTTCACGC ACCCCGGAAGTCACTTGCGTGGTCG TGGACGTGTCGCAGGAAGATCCCGA AGTGCAGTTCAATTGGTACGTGGAT GGGGTCGAAGTGCACAACGCCAAG ACCAAGCCTAGGGAAGAACAGTTC AACTCTACGTACCGGGTGGTGTCCG TGCTGACCGTGCTGCACCAGGACTG GCTGAACGGAAAGGAGTACAAGTG CAAAGTGTCAAACAAGGGCCTCCCT

			TCATCCATCGAAAAGACCATCAGCA AGGCCAAGGGTCAACCTAGGGAGC CCCAGGTCTACACTTTGCCGCCTAG CCAAGAAGAAATGACTAAGAACCA AGTGTCCCTGACTTGCCTTGTCAAG GGCTTTTATCCGTCCGACATCGCCG TGGAGTGGGAGTCCAACGGACAAC CGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTC CTTCTTCCTGTACTCCCGGCTGACTG TGGACAAGTCAAGATGGCAGGAGG GAAACGTGTTCTCCTGCTCCGTGAT GCACGAAGCGCTGCACAACCATTAC ACCCAGAAATCACTGTCACTTTCGC TGGGAAAA
SEQ ID 1925	EVQLVQSGGGLVKPGGSLRLSCTASGF TFGDYAMSWVRQAPGKGLEWVGFIRS KAYGGTTEYAASVKGRFTISRDDSKSI AYLQMNSLKTEDTAVYYCTTHRRPIY DILTGFDYWGQGTLVTVSSASTKGPSV FPLAPCSRSTSESTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTKTYTCNVDHKP SNTKVDKRVESKYGPPCPPCPAPEFLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKT KPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKGQ PREPQVYTLPPSQEEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSRLTVDKSRWQEGNV FSCSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2033	GAGGTGCAGCTGGTGCAGTCTGGGG GAGGCTTGGTCAAGCCTGGAGGGTC CCTGAGACTCTCCTGTACAGCTTCT GGATTCACCTTTGGTGATTATGCTAT GAGCTGGGTCCGCCAGGCTCCAGGG AAGGGGCTGGAGTGGGTAGGTTTCA TTAGAAGCAAAGCTTATGGTGGGAC AACAGAATACGCCGCGTCTGTGAAA GGCAGATTCACCATCTCAAGAGATG ATTCCAAAAGCATCGCCTATCTGCA AATGAACAGCCTGAAAACCGAGGA CACAGCCGTGTATTACTGTACTACT CATAGACGCCCAATTTACGATATTT TGACTGGTTTTGACTACTGGGGCCA GGGAACCCTGGTCACCGTCTCCTCA GCATCCACCAAGGGGCCTTCCGTGT TCCCCCTGGCCCCTTGCTCCCGCTCG ACCTCTGAATCCACCGCCGCACTCG GTTGCCTGGTCAAAGACTACTTCCC CGAGCCCGTGACTGTCTCGTGGAAC TCGGGCGCCCTCACATCCGGAGTGC ATACCTTTCCCGCCGTGTTGCAGTCC AGCGGCCTGTACAGCCTGAGCTCCG TCGTGACAGTGCCGTCCTCCTCCCTT GGAACCAAGACCTATACCTGCAACG TCGACCACAAGCCCTCCAACACCAA AGTGGACAAGCGCGTCGAATCCAA GTACGGCCCCCCTTGTCCGCCTTGTC CAGCCCCTGAGTTCCTGGGTGGTCC GTCCGTGTTCCTCTTCCCGCCCAAGC CGAAGGACACTCTGATGATTTCACG CACCCCGGAAGTCACTTGCGTGGTC GTGGACGTGTCGCAGGAAGATCCCG AAGTGCAGTTCAATTGGTACGTGGA TGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTT CAACTCTACGTACCGGGTGGTGTCC GTGCTGACCGTGCTGCACCAGGACT GGCTGAACGGAAAGGAGTACAAGT

			GCAAAGTGTCAAACAAGGGCCTCCC TTCATCCATCGAAAAGACCATCAGC AAGGCCAAGGGTCAACCTAGGGAG CCCCAGGTCTACACTTTGCCGCCTA GCCAAGAAGAAATGACTAAGAACC AAGTGTCCCTGACTTGCCTTGTCAA GGGCTTTTATCCGTCCGACATCGCC GTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACC CCACCGGTGCTCGATTCCGATGGCT CCTTCTTCCTGTACTCCCGGCTGACT GTGGACAAGTCAAGATGGCAGGAG GGAAACGTGTTCTCCTGCTCCGTGA TGCACGAAGCGCTGCACAACCATTA CACCCAGAAATCACTGTCACTTTCG CTGGGAAAA
SEQ ID 1926	QLQLQESGGGLVQPGRSLRLSCTASGF TFGDYAMSWVRQAPGKGLEWVGFIRS KAYGGTTEYAASVKGRFTISRDDSKSI AYLQMNSLKTEDTAVYYCTREDTMV RGVIPWGQGTLVTVSSASTKGPSVFPL APCSRSTSESTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDV SQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKGLPSSIEKTISKAKGQPRE PQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCS VMHEALHNHYTQKSLSLSLGK	SEQ ID 2034	CAGCTGCAGCTGCAGGAGTCCGGGG GAGGCTTGGTACAGCCAGGGCGGTC CCTGAGACTCTCCTGTACAGCTTCT GGATTCACCTTTGGTGATTATGCTAT GAGCTGGGTCCGCCAGGCTCCAGGG AAGGGGCTGGAGTGGGTAGGTTTCA TTAGAAGCAAAGCTTATGGTGGGAC AACAGAATACGCCGCGTCTGTGAAA GGCAGATTCACCATCTCAAGAGATG ATTCCAAAAGCATCGCCTATCTGCA AATGAACAGCCTGAAAACCGAGGA CACAGCCGTGTATTACTGTACTAGA GAGGATACTATGGTTCGGGGAGTTA TTCCCTGGGGCCAGGGAACCCTGGT CACCGTCTCCTCAGCATCCACCAAG GGGCCTTCCGTGTTCCCCCTGGCCC CTTGCTCCCGCTCGACCTCTGAATCC ACCGCCGCACTCGGTTGCCTGGTCA AAGACTACTTCCCCGAGCCCGTGAC TGTCTCGTGGAACTCGGGCGCCCTC ACATCCGGAGTGCATACCTTTCCCG CCGTGTTGCAGTCCAGCGGCCTGTA CAGCCTGAGCTCCGTCGTGACAGTG CCGTCCTCCTCCCTTGGAACCAAGA CCTATACCTGCAACGTCGACCACAA GCCCTCCAACACCAAAGTGGACAAG CGCGTCGAATCCAAGTACGGCCCCC CTTGTCCGCCTTGTCCAGCCCCTGA GTTCCTGGGTGGTCCGTCCGTGTTCC TCTTCCCGCCCAAGCCGAAGGACAC TCTGATGATTTCACGCACCCCGGAA GTCACTTGCGTGGTCGTGGACGTGT CGCAGGAAGATCCCGAAGTGCAGTT CAATTGGTACGTGGATGGGGTCGAA GTGCACAACGCCAAGACCAAGCCTA GGGAAGAACAGTTCAACTCTACGTA CCGGGTGGTGTCCGTGCTGACCGTG CTGCACCAGGACTGGCTGAACGGAA

			AGGAGTACAAGTGCAAAGTGTCAA ACAAGGGCCTCCCTTCATCCATCGA AAAGACCATCAGCAAGGCCAAGGG TCAACCTAGGGAGCCCCAGGTCTAC ACTTTGCCGCCTAGCCAAGAAGAAA TGACTAAGAACCAAGTGTCCCTGAC TTGCCTTGTCAAGGGCTTTTATCCGT CCGACATCGCCGTGGAGTGGGAGTC CAACGGACAACCGGAGAACAACTA CAAGACCACCCCACCGGTGCTCGAT TCCGATGGCTCCTTCTTCCTGTACTC CCGGCTGACTGTGGACAAGTCAAGA TGGCAGGAGGGAAACGTGTTCTCCT GCTCCGTGATGCACGAAGCGCTGCA CAACCATTACACCCAGAAATCACTG TCACTTTCGCTGGGAAAA
SEQ ID 1927	QLQLQESGSGLVKPSQTLSLTCAVSGG SISSGGYSWSWIRQPPGKGLEWIGYIY HSGSTYYNPSLKSRVTISVDRSKNQFSL KLSSVTAADTAVYYCARDRRYYDSSG YYPAYYFDYWGQGTLVTVSSASTKGP SVFPLAPCSRSTSESTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSG LYSLSSVVTVPSSSLGTKTYTCNVDHK PSNTKVDKRVESKYGPPCPPCPAPEFL GGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSQEDPEVQFNWYVDGVEVHNAK TKPREEQFNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKGLPSSIEKTISKAKG QPREPQVYTLPPSQEEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSRLTVDKSRWQEGN VFSCSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2035	CAGCTGCAGCTGCAGGAGTCCGGCT CAGGACTGGTGAAGCCTTCACAGAC CCTGTCCCTCACCTGCGCTGTCTCTG GTGGCTCCATCAGCAGTGGTGGTTA CTCCTGGAGCTGGATCCGGCAGCCA CCAGGGAAGGGCCTGGAGTGGATT GGGTACATCTATCATAGTGGGAGCA CCTACTACAACCCGTCCCTCAAGAG TCGAGTCACCATATCAGTAGACAGG TCCAAGAACCAGTTCTCCCTGAAGC TGAGCTCTGTGACCGCCGCGGACAC GGCTGTGTATTACTGTGCGAGAGAT CGGCGTTACTATGATAGTAGTGGTT ATTATCCCGCCTACTACTTTGACTAC TGGGGCCAGGGAACCCTGGTCACCG TCTCCTCAGCATCCACCAAGGGGCC TTCCGTGTTCCCCCTGGCCCCTTGCT CCCGCTCGACCTCTGAATCCACCGC CGCACTCGGTTGCCTGGTCAAAGAC TACTTCCCCGAGCCCGTGACTGTCT CGTGGAACTCGGGCGCCCTCACATC CGGAGTGCATACCTTTCCCGCCGTG TTGCAGTCCAGCGGCCTGTACAGCC TGAGCTCCGTCGTGACAGTGCCGTC CTCCTCCCTTGGAACCAAGACCTAT ACCTGCAACGTCGACCACAAGCCCT CCAACACCAAAGTGGACAAGCGCG TCGAATCCAAGTACGGCCCCCCTTG TCCGCCTTGTCCAGCCCCTGAGTTCC TGGGTGGTCCGTCCGTGTTCCTCTTC CCGCCCAAGCCGAAGGACACTCTGA TGATTTCACGCACCCCGGAAGTCAC TTGCGTGGTCGTGGACGTGTCGCAG GAAGATCCCGAAGTGCAGTTCAATT GGTACGTGGATGGGGTCGAAGTGCA CAACGCCAAGACCAAGCCTAGGGA AGAACAGTTCAACTCTACGTACCGG GTGGTGTCCGTGCTGACCGTGCTGC ACCAGGACTGGCTGAACGGAAAGG

			AGTACAAGTGCAAAGTGTCAAACA AGGGCCTCCCTTCATCCATCGAAAA GACCATCAGCAAGGCCAAGGGTCA ACCTAGGGAGCCCCAGGTCTACACT TTGCCGCCTAGCCAAGAAGAAATGA CTAAGAACCAAGTGTCCCTGACTTG CCTTGTCAAGGGCTTTTATCCGTCCG ACATCGCCGTGGAGTGGGAGTCCAA CGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCC GATGGCTCCTTCTTCCTGTACTCCCG GCTGACTGTGGACAAGTCAAGATGG CAGGAGGGAAACGTGTTCTCCTGCT CCGTGATGCACGAAGCGCTGCACAA CCATTACACCCAGAAATCACTGTCA CTTTCGCTGGGAAAA
SEQ ID 1928	EVQLVQSGGGLVKPGGSLRLSCAASG FTFSSYSMNWVRQAPGKGLEWVSYIS SSGSYTNYADSVKGRFTISRDNAKNSL YLQINSLRAEDTAIYYCARDGGYDSSG FHFDYWGQGTLVTVSSASTKGPSVFPL APCSRSTSESTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDV SQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKGLPSSIEKTISKAKGQPRE PQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCS VMHEALHNHYTQKSLSLSLGK	SEQ ID 2036	GAAGTGCAGCTGGTGCAGTCTGGGG GAGGCCTGGTCAAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTCAGTAGCTATAGCA TGAACTGGGTCCGCCAGGCTCCAGG GAAGGGGCTGGAGTGGGTTTCATAC ATTAGTAGTAGTGGTAGTTACACAA ACTACGCAGACTCTGTGAAGGGCCG ATTCACCATCTCCAGAGACAACGCC AAGAACTCACTGTATCTGCAAATAA ACAGCCTGAGAGCCGAGGACACGG CCATTTATTACTGTGCGAGAGACGG GGGCTATGATAGTAGTGGTTTTCAC TTTGACTACTGGGGCCAGGGAACCC TGGTCACCGTCTCCTCAGCATCCAC CAAGGGGCCTTCCGTGTTCCCCCTG GCCCCTTGCTCCCGCTCGACCTCTG AATCCACCGCCGCACTCGGTTGCCT GGTCAAAGACTACTTCCCCGAGCCC GTGACTGTCTCGTGGAACTCGGGCG CCCTCACATCCGGAGTGCATACCTT TCCCGCCGTGTTGCAGTCCAGCGGC CTGTACAGCCTGAGCTCCGTCGTGA CAGTGCCGTCCTCCTCCCTTGGAAC CAAGACCTATACCTGCAACGTCGAC CACAAGCCCTCCAACACCAAAGTGG ACAAGCGCGTCGAATCCAAGTACGG CCCCCCTTGTCCGCCTTGTCCAGCCC CTGAGTTCCTGGGTGGTCCGTCCGT GTTCCTCTTCCCGCCCAAGCCGAAG GACACTCTGATGATTTCACGCACCC CGGAAGTCACTTGCGTGGTCGTGGA CGTGTCGCAGGAAGATCCCGAAGTG CAGTTCAATTGGTACGTGGATGGGG TCGAAGTGCACAACGCCAAGACCA AGCCTAGGGAAGAACAGTTCAACTC TACGTACCGGGTGGTGTCCGTGCTG ACCGTGCTGCACCAGGACTGGCTGA

			ACGGAAAGGAGTACAAGTGCAAAG TGTCAAACAAGGGCCTCCCTTCATC CATCGAAAAGACCATCAGCAAGGC CAAGGGTCAACCTAGGGAGCCCCA GGTCTACACTTTGCCGCCTAGCCAA GAAGAAATGACTAAGAACCAAGTG TCCCTGACTTGCCTTGTCAAGGGCTT TTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCCGGCTGACTGTGGACA AGTCAAGATGGCAGGAGGGAAACG TGTTCTCCTGCTCCGTGATGCACGA AGCGCTGCACAACCATTACACCCAG AAATCACTGTCACTTTCGCTGGGAA AA
SEQ ID 1929	QVQLQQSGPGLVKPSQTLSLTCAISGD SVSNNRAAWNWIRQSPSRGLEWLGRT YYRSKWYNEYAVSVKSRITINPDTSKN QFSLQLNSMTPEDSAVYYCAILPSSGY LQDHHYYGMDVWGQGTTVTVSSAST KGPSVFPLAPCSRSTSESTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTKTYTCN VDHKPSNTKVDKRVESKYGPPCPPCPA PEFLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSQEDPEVQFNWYVDGVEV HNAKTKPREEQFNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKGLPSSIEKTIS KAKGQPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSRLTVDKSRW QEGNVFSCSVMHEALHNHYTQKSLSL SLGK	SEQ ID 2037	CAGGTACAGCTGCAGCAGTCAGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAACAACAGGGC TGCTTGGAACTGGATCAGGCAGTCG CCATCGAGAGGCCTTGAGTGGCTGG GAAGGACATACTACAGGTCCAAGTG GTATAATGAATATGCAGTCTCTGTG AAAAGTCGAATAACCATCAACCCAG ACACATCCAAGAACCAGTTCTCCCT GCAGCTGAACTCTATGACTCCCGAG GACTCGGCTGTGTATTACTGTGCAA TTTTGCCTAGTAGTGGTTATCTACAG GACCACCACTACTACGGTATGGACG TCTGGGGCCAAGGGACCACGGTCAC CGTCTCCTCAGCATCCACCAAGGGG CCTTCCGTGTTCCCCCTGGCCCCTTG CTCCCGCTCGACCTCTGAATCCACC GCCGCACTCGGTTGCCTGGTCAAAG ACTACTTCCCCGAGCCCGTGACTGT CTCGTGGAACTCGGGCGCCCTCACA TCCGGAGTGCATACCTTTCCCGCCG TGTTGCAGTCCAGCGGCCTGTACAG CCTGAGCTCCGTCGTGACAGTGCCG TCCTCCTCCCTTGGAACCAAGACCT ATACCTGCAACGTCGACCACAAGCC CTCCAACACCAAAGTGGACAAGCGC GTCGAATCCAAGTACGGCCCCCCTT GTCCGCCTTGTCCAGCCCCTGAGTT CCTGGGTGGTCCGTCCGTGTTCCTCT TCCCGCCCAAGCCGAAGGACACTCT GATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGC AGGAAGATCCCGAAGTGCAGTTCAA TTGGTACGTGGATGGGGTCGAAGTG CACAACGCCAAGACCAAGCCTAGG GAAGAACAGTTCAACTCTACGTACC GGGTGGTGTCCGTGCTGACCGTGCT GCACCAGGACTGGCTGAACGGAAA

			GGAGTACAAGTGCAAAGTGTCAAA CAAGGGCCTCCCTTCATCCATCGAA AAGACCATCAGCAAGGCCAAGGGT CAACCTAGGGAGCCCCAGGTCTACA CTTTGCCGCCTAGCCAAGAAGAAAT GACTAAGAACCAAGTGTCCCTGACT TGCCTTGTCAAGGGCTTTTATCCGTC CGACATCGCCGTGGAGTGGGAGTCC AACGGACAACCGGAGAACAACTAC AAGACCACCCCACCGGTGCTCGATT CCGATGGCTCCTTCTTCCTGTACTCC CGGCTGACTGTGGACAAGTCAAGAT GGCAGGAGGGAAACGTGTTCTCCTG CTCCGTGATGCACGAAGCGCTGCAC AACCATTACACCCAGAAATCACTGT CACTTTCGCTGGGAAAA
SEQ ID 1930	EVQLVQSGAEVKKPGASVKVSCKASG YTFTSYGISWVRQAPGQGLEWMGWIS AYNGNTNYAQKLQGRVTMTTDTSTST AYMELSSLRSEDTAVYYCARAAVGDG YSYGRLDWGQGTLVTVSSASTKGPSV FPLAPCSRSTSESTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTKTYTCNVDHKP SNTKVDKRVESKYGPPCPPCPAPEFLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKT KPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKGQ PREPQVYTLPPSQEEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSRLTVDKSRWQEGNV FSCSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2038	GAGGTGCAGCTGGTGCAGTCTGGAG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTCTCCTGCAAGGCTTCT GGTTACACCTTTACCAGCTACGGTA TCAGCTGGGTGCGACAGGCCCCTGG ACAAGGGCTTGAGTGGATGGGATG GATCAGCGCTTACAATGGTAACACA AACTATGCACAGAAGCTCCAGGGCA GAGTCACCATGACCACAGACACATC CACGAGCACAGCCTACATGGAGCTG AGCAGCCTGAGATCTGAGGACACG GCCGTGTATTACTGTGCGAGAGCCG CGGTGGGGGATGGATACAGCTATGG TCGGCTCGATTGGGGCCAGGGAACC CTGGTCACCGTCTCCTCAGCATCCA CCAAGGGGCCTTCCGTGTTCCCCCT GGCCCCTTGCTCCCGCTCGACCTCT GAATCCACCGCCGCACTCGGTTGCC TGGTCAAAGACTACTTCCCCGAGCC CGTGACTGTCTCGTGGAACTCGGGC GCCCTCACATCCGGAGTGCATACCT TTCCCGCCGTGTTGCAGTCCAGCGG CCTGTACAGCCTGAGCTCCGTCGTG ACAGTGCCGTCCTCCTCCCTTGGAA CCAAGACCTATACCTGCAACGTCGA CCACAAGCCCTCCAACACCAAAGTG GACAAGCGCGTCGAATCCAAGTACG GCCCCCCTTGTCCGCCTTGTCCAGCC CCTGAGTTCCTGGGTGGTCCGTCCG TGTTCCTCTTCCCGCCCAAGCCGAA GGACACTCTGATGATTTCACGCACC CCGGAAGTCACTTGCGTGGTCGTGG ACGTGTCGCAGGAAGATCCCGAAGT GCAGTTCAATTGGTACGTGGATGGG GTCGAAGTGCACAACGCCAAGACC AAGCCTAGGGAAGAACAGTTCAACT CTACGTACCGGGTGGTGTCCGTGCT GACCGTGCTGCACCAGGACTGGCTG

			AACGGAAAGGAGTACAAGTGCAAA GTGTCAAACAAGGGCCTCCCTTCAT CCATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTACACTTTGCCGCCTAGCCAA GAAGAAATGACTAAGAACCAAGTG TCCCTGACTTGCCTTGTCAAGGGCTT TTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCCGGCTGACTGTGGACA AGTCAAGATGGCAGGAGGGAAACG TGTTCTCCTGCTCCGTGATGCACGA AGCGCTGCACAACCATTACACCCAG AAATCACTGTCACTTTCGCTGGGAA AA
SEQ ID 1931	EVQLVQSGAEVKKPGESLKISCKGSGY SFTSYWIGWVRQMPGKGLEWMGIIYP GDSDTRYSPSFQGQVTISADKSISTAYL QWSSLKASDTAMYYCARLPSYYYDSS GYFTWYFDLWGRGTLVTVSSASTKGP SVFPLAPCSRSTSESTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSG LYSLSSVVTVPSSSLGTKTYTCNVDHK PSNTKVDKRVESKYGPPCPPCPAPEFL GGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSQEDPEVQFNWYVDGVEVHNAK TKPREEQFNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKGLPSSIEKTISKAKG QPREPQVYTLPPSQEEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSRLTVDKSRWQEGN VFSCSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2039	GAGGTCCAGCTGGTACAGTCTGGAG CAGAGGTGAAAAAGCCCGGGGAGT CTCTGAAGATCTCCTGTAAGGGTTC TGGATACAGCTTTACCAGCTACTGG ATCGGCTGGGTGCGCCAGATGCCCG GGAAAGGCCTGGAGTGGATGGGGA TCATCTATCCTGGTGACTCTGATACC AGATACAGCCCGTCCTTCCAAGGCC AGGTCACCATCTCAGCCGACAAGTC CATCAGCACCGCCTACCTGCAGTGG AGCAGCCTGAAGGCCTCGGACACCG CCATGTATTACTGTGCGAGACTCCC CTCGTATTACTATGATAGTAGTGGT TACTTTACCTGGTACTTCGATCTCTG GGGCCGTGGCACCCTGGTGACCGTC TCTTCAGCATCCACCAAGGGGCCTT CCGTGTTCCCCCTGGCCCCTTGCTCC CGCTCGACCTCTGAATCCACCGCCG CACTCGGTTGCCTGGTCAAAGACTA CTTCCCCGAGCCCGTGACTGTCTCG TGGAACTCGGGCGCCCTCACATCCG GAGTGCATACCTTTCCCGCCGTGTT GCAGTCCAGCGGCCTGTACAGCCTG AGCTCCGTCGTGACAGTGCCGTCCT CCTCCCTTGGAACCAAGACCTATAC CTGCAACGTCGACCACAAGCCCTCC AACACCAAAGTGGACAAGCGCGTC GAATCCAAGTACGGCCCCCCTTGTC CGCCTTGTCCAGCCCCTGAGTTCCT GGGTGGTCCGTCCGTGTTCCTCTTCC CGCCCAAGCCGAAGGACACTCTGAT GATTTCACGCACCCCGGAAGTCACT TGCGTGGTCGTGGACGTGTCGCAGG AAGATCCCGAAGTGCAGTTCAATTG GTACGTGGATGGGGTCGAAGTGCAC AACGCCAAGACCAAGCCTAGGGAA GAACAGTTCAACTCTACGTACCGGG TGGTGTCCGTGCTGACCGTGCTGCA

			CCAGGACTGGCTGAACGGAAAGGA GTACAAGTGCAAAGTGTCAAACAA GGGCCTCCCTTCATCCATCGAAAAG ACCATCAGCAAGGCCAAGGGTCAA CCTAGGGAGCCCCAGGTCTACACTT TGCCGCCTAGCCAAGAAGAAATGAC TAAGAACCAAGTGTCCCTGACTTGC CTTGTCAAGGGCTTTTATCCGTCCG ACATCGCCGTGGAGTGGGAGTCCAA CGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCC GATGGCTCCTTCTTCCTGTACTCCCG GCTGACTGTGGACAAGTCAAGATGG CAGGAGGGAAACGTGTTCTCCTGCT CCGTGATGCACGAAGCGCTGCACAA CCATTACACCCAGAAATCACTGTCA CTTTCGCTGGGAAAA
SEQ ID 1932	EVQLVQSGAEVKKPGASVKVSCKASG YTFTSYGISWVRQAPGQGLEWMGWII PIFGIANYAQKFQGRVTITADKSTSTAY MELSSLRSEDTAVYYCARELYNYGSK DYFDYWGQGTLVTVSSASTKGPSVFP LAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSN TKVDKRVESKYGPPCPPCPAPEFLGGP SVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2040	GAGGTCCAGCTGGTACAGTCTGGAG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTCTCCTGCAAGGCTTCT GGTTACACCTTTACCAGCTATGGTA TCAGCTGGGTGCGACAGGCCCCTGG ACAAGGGCTTGAGTGGATGGGATG GATCATCCCTATCTTTGGTATAGCA AACTACGCACAGAAGTTCCAGGGCA GAGTCACGATTACCGCGGACAAATC CACGAGCACAGCCTACATGGAGCTG AGCAGCCTGAGATCTGAGGACACG GCCGTGTATTACTGTGCGAGAGAAC TATACAACTATGGTTCAAAGGACTA CTTTGACTACTGGGGCCAGGGAACC CTGGTCACCGTCTCCTCAGCATCCA CCAAGGGGCCTTCCGTGTTCCCCCT GGCCCCTTGCTCCCGCTCGACCTCT GAATCCACCGCCGCACTCGGTTGCC TGGTCAAAGACTACTTCCCCGAGCC CGTGACTGTCTCGTGGAACTCGGGC GCCCTCACATCCGGAGTGCATACCT TTCCCGCCGTGTTGCAGTCCAGCGG CCTGTACAGCCTGAGCTCCGTCGTG ACAGTGCCGTCCTCCTCCCTTGGAA CCAAGACCTATACCTGCAACGTCGA CCACAAGCCCTCCAACACCAAAGTG GACAAGCGCGTCGAATCCAAGTACG GCCCCCCTTGTCCGCCTTGTCCAGCC CCTGAGTTCCTGGGTGGTCCGTCCG TGTTCCTCTTCCCGCCCAAGCCGAA GGACACTCTGATGATTTCACGCACC CCGGAAGTCACTTGCGTGGTCGTGG ACGTGTCGCAGGAAGATCCCGAAGT GCAGTTCAATTGGTACGTGGATGGG GTCGAAGTGCACAACGCCAAGACC AAGCCTAGGGAAGAACAGTTCAACT CTACGTACCGGGTGGTGTCCGTGCT GACCGTGCTGCACCAGGACTGGCTG

			AACGGAAAGGAGTACAAGTGCAAA GTGTCAAACAAGGGCCTCCCTTCAT CCATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTACACTTTGCCGCCTAGCCAA GAAGAAATGACTAAGAACCAAGTG TCCCTGACTTGCCTTGTCAAGGGCTT TTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCCGGCTGACTGTGGACA AGTCAAGATGGCAGGAGGGAAACG TGTTCTCCTGCTCCGTGATGCACGA AGCGCTGCACAACCATTACACCCAG AAATCACTGTCACTTTCGCTGGGAA AA
SEQ ID 1933	EVQLVQSGAEVKKPGESLKISCKGSGY SFTSYWIGWVRQMPGKGLEWMGIIYP GDSDTRYSPSFQGQVTISADKSISTAYL QWSSLKASDTAMYYCARGGTWDTAM VTGFDYWGQGTLVTVSSASTKGPSVF PLAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSN TKVDKRVESKYGPPCPPCPAPEFLGGP SVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2041	GAAGTGCAGCTGGTGCAGTCTGGAG CAGAGGTGAAAAAGCCCGGGGAGT CTCTGAAGATCTCCTGTAAGGGTTC TGGATACAGCTTTACCAGCTACTGG ATCGGCTGGGTGCGCCAGATGCCCG GGAAAGGCCTGGAGTGGATGGGGA TCATCTATCCTGGTGACTCTGATACC AGATACAGCCCGTCCTTCCAAGGCC AGGTCACCATCTCAGCCGACAAGTC CATCAGCACCGCCTACCTGCAGTGG AGCAGCCTGAAGGCCTCGGACACCG CCATGTATTACTGTGCGAGGGGCGG TACTTGGGATACAGCTATGGTTACG GGCTTTGACTACTGGGGCCAGGGAA CCCTGGTCACCGTCTCCTCAGCATC CACCAAGGGGCCTTCCGTGTTCCCC CTGGCCCCTTGCTCCCGCTCGACCTC TGAATCCACCGCCGCACTCGGTTGC CTGGTCAAAGACTACTTCCCCGAGC CCGTGACTGTCTCGTGGAACTCGGG CGCCCTCACATCCGGAGTGCATACC TTTCCCGCCGTGTTGCAGTCCAGCG GCCTGTACAGCCTGAGCTCCGTCGT GACAGTGCCGTCCTCCTCCCTTGGA ACCAAGACCTATACCTGCAACGTCG ACCACAAGCCCTCCAACACCAAAGT GGACAAGCGCGTCGAATCCAAGTAC GGCCCCCCTTGTCCGCCTTGTCCAG CCCCTGAGTTCCTGGGTGGTCCGTC CGTGTTCCTCTTCCCGCCCAAGCCG AAGGACACTCTGATGATTTCACGCA CCCCGGAAGTCACTTGCGTGGTCGT GGACGTGTCGCAGGAAGATCCCGA AGTGCAGTTCAATTGGTACGTGGAT GGGGTCGAAGTGCACAACGCCAAG ACCAAGCCTAGGGAAGAACAGTTC AACTCTACGTACCGGGTGGTGTCCG TGCTGACCGTGCTGCACCAGGACTG GCTGAACGGAAAGGAGTACAAGTG

			CAAAGTGTCAAACAAGGGCCTCCCT TCATCCATCGAAAAGACCATCAGCA AGGCCAAGGGTCAACCTAGGGAGC CCCAGGTCTACACTTTGCCGCCTAG CCAAGAAGAAATGACTAAGAACCA AGTGTCCCTGACTTGCCTTGTCAAG GGCTTTTATCCGTCCGACATCGCCG TGGAGTGGGAGTCCAACGGACAAC CGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTC CTTCTTCCTGTACTCCCGGCTGACTG TGGACAAGTCAAGATGGCAGGAGG GAAACGTGTTCTCCTGCTCCGTGAT GCACGAAGCGCTGCACAACCATTAC ACCCAGAAATCACTGTCACTTTCGC TGGGAAAA
SEQ ID 1934	EVQLVQSGAEVKKPGESLKISCKGSGY SFTSYWIAWVRQMPGKGLEWMGVIYP GDSDTRYSPSFQGQVTISADKSINTAYL QWSSLKASDTAMYYCARPHYDILTGS RAPFDYWGQGTLVTVSSASTKGPSVFP LAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSN TKVDKRVESKYGPPCPPCPAPEFLGGP SVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2042	GAAGTGCAGCTGGTGCAGTCTGGAG CAGAGGTGAAAAAGCCCGGGGAGT CTCTGAAGATCTCCTGTAAGGGTTC TGGATACAGCTTTACCAGCTACTGG ATCGCCTGGGTGCGCCAGATGCCCG GGAAAGGCCTGGAGTGGATGGGGG TCATCTATCCTGGTGACTCTGATACC AGATACAGCCCGTCCTTCCAAGGCC AGGTCACCATCTCAGCCGACAAGTC CATCAATACCGCCTACCTGCAGTGG AGCAGCCTGAAGGCCTCGGACACCG CCATGTATTACTGTGCGAGACCCCA TTACGATATTTTGACTGGTTCCCGG GCGCCCTTTGACTACTGGGGCCAGG GAACCCTGGTCACCGTCTCCTCAGC ATCCACCAAGGGGCCTTCCGTGTTC CCCCTGGCCCCTTGCTCCCGCTCGA CCTCTGAATCCACCGCCGCACTCGG TTGCCTGGTCAAAGACTACTTCCCC GAGCCCGTGACTGTCTCGTGGAACT CGGGCGCCCTCACATCCGGAGTGCA TACCTTTCCCGCCGTGTTGCAGTCCA GCGGCCTGTACAGCCTGAGCTCCGT CGTGACAGTGCCGTCCTCCTCCCTT GGAACCAAGACCTATACCTGCAACG TCGACCACAAGCCCTCCAACACCAA AGTGGACAAGCGCGTCGAATCCAA GTACGGCCCCCCTTGTCCGCCTTGTC CAGCCCCTGAGTTCCTGGGTGGTCC GTCCGTGTTCCTCTTCCCGCCCAAGC CGAAGGACACTCTGATGATTTCACG CACCCCGGAAGTCACTTGCGTGGTC GTGGACGTGTCGCAGGAAGATCCCG AAGTGCAGTTCAATTGGTACGTGGA TGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTT CAACTCTACGTACCGGGTGGTGTCC GTGCTGACCGTGCTGCACCAGGACT GGCTGAACGGAAAGGAGTACAAGT

			GCAAAGTGTCAAACAAGGGCCTCCC TTCATCCATCGAAAAGACCATCAGC AAGGCCAAGGGTCAACCTAGGGAG CCCCAGGTCTACACTTTGCCGCCTA GCCAAGAAGAAATGACTAAGAACC AAGTGTCCCTGACTTGCCTTGTCAA GGGCTTTTATCCGTCCGACATCGCC GTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACC CCACCGGTGCTCGATTCCGATGGCT CCTTCTTCCTGTACTCCCGGCTGACT GTGGACAAGTCAAGATGGCAGGAG GGAAACGTGTTCTCCTGCTCCGTGA TGCACGAAGCGCTGCACAACCATTA CACCCAGAAATCACTGTCACTTTCG CTGGGAAAA
SEQ ID 1935	QVQLQQWGAGLLKPSETLSLTCAVYG GSFSGYYWSWIRQPPGKGLEWIGEINH SGSTNYNPSLKSRVTISVDTSKNQFSLK LSSVTAADTAVYYCARARVESKDGYF DYWGQGTLVTVSSASTKGPSVFPLAPC SRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTKTYTCNVDHKPSNTKVD KRVESKYGPPCPPCPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSQED PEVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKC KVSNKGLPSSIEKTISKAKGQPREPQVY TLPPSQEEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGS FFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSLGK	SEQ ID 2043	CAGGTGCAGCTACAGCAGTGGGGC GCAGGACTGTTGAAGCCTTCGGAGA CCCTGTCCCTCACCTGCGCTGTCTAT GGTGGGTCCTTCAGTGGTTACTACT GGAGCTGGATCCGCCAGCCCCCAGG GAAGGGGCTGGAGTGGATTGGGGA AATCAATCATAGTGGAAGCACCAAC TACAACCCGTCCCTCAAGAGTCGAG TCACCATATCAGTAGACACGTCCAA GAACCAGTTCTCCCTGAAGCTGAGC TCTGTGACCGCCGCGGACACGGCTG TGTATTACTGTGCGAGAGCCCGAGT GGAATCCAAGGATGGGTACTTTGAC TACTGGGGCCAGGGAACCCTGGTCA CCGTCTCCTCAGCATCCACCAAGGG GCCTTCCGTGTTCCCCCTGGCCCCTT GCTCCCGCTCGACCTCTGAATCCAC CGCCGCACTCGGTTGCCTGGTCAAA GACTACTTCCCCGAGCCCGTGACTG TCTCGTGGAACTCGGGCGCCCTCAC ATCCGGAGTGCATACCTTTCCCGCC GTGTTGCAGTCCAGCGGCCTGTACA GCCTGAGCTCCGTCGTGACAGTGCC GTCCTCCTCCCTTGGAACCAAGACC TATACCTGCAACGTCGACCACAAGC CCTCCAACACCAAAGTGGACAAGCG CGTCGAATCCAAGTACGGCCCCCCT TGTCCGCCTTGTCCAGCCCCTGAGTT CCTGGGTGGTCCGTCCGTGTTCCTCT TCCCGCCCAAGCCGAAGGACACTCT GATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGC AGGAAGATCCCGAAGTGCAGTTCAA TTGGTACGTGGATGGGGTCGAAGTG CACAACGCCAAGACCAAGCCTAGG GAAGAACAGTTCAACTCTACGTACC GGGTGGTGTCCGTGCTGACCGTGCT GCACCAGGACTGGCTGAACGGAAA

			GGAGTACAAGTGCAAAGTGTCAAA CAAGGGCCTCCCTTCATCCATCGAA AAGACCATCAGCAAGGCCAAGGGT CAACCTAGGGAGCCCCAGGTCTACA CTTTGCCGCCTAGCCAAGAAGAAAT GACTAAGAACCAAGTGTCCCTGACT TGCCTTGTCAAGGGCTTTTATCCGTC CGACATCGCCGTGGAGTGGGAGTCC AACGGACAACCGGAGAACAACTAC AAGACCACCCCACCGGTGCTCGATT CCGATGGCTCCTTCTTCCTGTACTCC CGGCTGACTGTGGACAAGTCAAGAT GGCAGGAGGGAAACGTGTTCTCCTG CTCCGTGATGCACGAAGCGCTGCAC AACCATTACACCCAGAAATCACTGT CACTTTCGCTGGGAAAA
SEQ ID 1936	EVQLVESGGGVVQPGRSLRLSCAASGF TFTDAWMNWVRQAPGKGLEWIGRVK NKADGETTDYAAPVKGRITISRDDAK NTLYVQMNSLKTEDTAVYYCTADLRL STWDAYDFWGQGTMVTVSSASTKGPS VFPLAPCSRSTSESTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTKTYTCNVDHKP SNTKVDKRVESKYGPPCPPCPAPEFLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKT KPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKGQ PREPQVYTLPPSQEEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSRLTVDKSRWQEGNV FSCSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2044	GAGGTGCAGCTGGTGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACTTTCACTGATGCCTGGA TGAACTGGGTCCGCCAGGCTCCAGG GAAGGGGCTGGAGTGGATTGGCCGT GTTAAAAACAAAGCTGATGGTGAG ACAACGGACTACGCTGCACCCGTCA AAGGCAGAATCACCATCTCAAGAG ATGATGCAAAGAACACTCTGTATGT GCAAATGAACAGCCTGAAAACCGA GGACACAGCCGTGTATTATTGTACC GCTGACCTGCGACTTTCTACGTGGG ATGCTTATGATTTCTGGGGCCAAGG GACAATGGTCACCGTCTCTTCAGCA TCCACCAAGGGGCCTTCCGTGTTCC CCCTGGCCCCTTGCTCCCGCTCGAC CTCTGAATCCACCGCCGCACTCGGT TGCCTGGTCAAAGACTACTTCCCCG AGCCCGTGACTGTCTCGTGGAACTC GGGCGCCCTCACATCCGGAGTGCAT ACCTTTCCCGCCGTGTTGCAGTCCA GCGGCCTGTACAGCCTGAGCTCCGT CGTGACAGTGCCGTCCTCCTCCCTT GGAACCAAGACCTATACCTGCAACG TCGACCACAAGCCCTCCAACACCAA AGTGGACAAGCGCGTCGAATCCAA GTACGGCCCCCCTTGTCCGCCTTGTC CAGCCCCTGAGTTCCTGGGTGGTCC GTCCGTGTTCCTCTTCCCGCCCAAGC CGAAGGACACTCTGATGATTTCACG CACCCCGGAAGTCACTTGCGTGGTC GTGGACGTGTCGCAGGAAGATCCCG AAGTGCAGTTCAATTGGTACGTGGA TGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTT CAACTCTACGTACCGGGTGGTGTCC GTGCTGACCGTGCTGCACCAGGACT GGCTGAACGGAAAGGAGTACAAGT

			GCAAAGTGTCAAACAAGGGCCTCCC TTCATCCATCGAAAAGACCATCAGC AAGGCCAAGGGTCAACCTAGGGAG CCCCAGGTCTACACTTTGCCGCCTA GCCAAGAAGAAATGACTAAGAACC AAGTGTCCCTGACTTGCCTTGTCAA GGGCTTTTATCCGTCCGACATCGCC GTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACC CCACCGGTGCTCGATTCCGATGGCT CCTTCTTCCTGTACTCCCGGCTGACT GTGGACAAGTCAAGATGGCAGGAG GGAAACGTGTTCTCCTGCTCCGTGA TGCACGAAGCGCTGCACAACCATTA CACCCAGAAATCACTGTCACTTTCG CTGGGAAAA
SEQ ID 1937	QITLKESGGGLVQPGGSLRLSCTVSGF TFSNNWMTWVRQTPGKGLEWVANIK QDGTEKHYVDSVKGRFTISRDNAENSL YLQMNSLRGEDTAVYYCARNSQRSFD YWGQGTLVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTKTYTCNVDHKPSNTKVDK RVESKYGPPCPPCPAPEFLGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSQEDP EVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKC KVSNKGLPSSIEKTISKAKGQPREPQVY TLPPSQEEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGS FFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSLGK	SEQ ID 2045	CAGATCACCTTGAAGGAGTCTGGGG GAGGCTTGGTCCAGCCTGGGGGGTC CCTAAGACTCTCTTGTACAGTCTCA GGATTCACCTTTAGTAACAATTGGA TGACCTGGGTCCGCCAGACTCCAGG GAAGGGGCTGGAGTGGGTGGCCAA CATAAAGCAAGATGGAACTGAGAA ACACTATGTGGACTCTGTGAAGGGC CGATTCACCATCTCCAGAGACAACG CCGAGAACTCACTGTATCTGCAGAT GAACAGCCTGAGAGGTGAGGACAC GGCCGTGTATTATTGTGCGAGAAAC AGTCAACGTTCGTTTGACTACTGGG GCCAGGGCACCCTGGTGACCGTCTC CTCAGCATCCACCAAGGGGCCTTCC GTGTTCCCCCTGGCCCCTTGCTCCCG CTCGACCTCTGAATCCACCGCCGCA CTCGGTTGCCTGGTCAAAGACTACT TCCCCGAGCCCGTGACTGTCTCGTG GAACTCGGGCGCCCTCACATCCGGA GTGCATACCTTTCCCGCCGTGTTGC AGTCCAGCGGCCTGTACAGCCTGAG CTCCGTCGTGACAGTGCCGTCCTCC TCCCTTGGAACCAAGACCTATACCT GCAACGTCGACCACAAGCCCTCCAA CACCAAAGTGGACAAGCGCGTCGA ATCCAAGTACGGCCCCCCTTGTCCG CCTTGTCCAGCCCCTGAGTTCCTGG GTGGTCCGTCCGTGTTCCTCTTCCCG CCCAAGCCGAAGGACACTCTGATGA TTTCACGCACCCCGGAAGTCACTTG CGTGGTCGTGGACGTGTCGCAGGAA GATCCCGAAGTGCAGTTCAATTGGT ACGTGGATGGGGTCGAAGTGCACA ACGCCAAGACCAAGCCTAGGGAAG AACAGTTCAACTCTACGTACCGGGT GGTGTCCGTGCTGACCGTGCTGCAC CAGGACTGGCTGAACGGAAAGGAG TACAAGTGCAAAGTGTCAAACAAG

			GGCCTCCCTTCATCCATCGAAAAGA CCATCAGCAAGGCCAAGGGTCAACC TAGGGAGCCCCAGGTCTACACTTTG CCGCCTAGCCAAGAAGAAATGACTA AGAACCAAGTGTCCCTGACTTGCCT TGTCAAGGGCTTTTATCCGTCCGAC ATCGCCGTGGAGTGGGAGTCCAACG GACAACCGGAGAACAACTACAAGA CCACCCCACCGGTGCTCGATTCCGA TGGCTCCTTCTTCCTGTACTCCCGGC TGACTGTGGACAAGTCAAGATGGCA GGAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACT TTCGCTGGGAAAA
SEQ ID 1938	QVTLKESGGGVVQPGRSLRLSCAASGF TFSSYGMHWVRQAPGKGLEWVAVISY DGSNKYYADSVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCAKDLGDPR GGILNYWGQGTLVTVSSASTKGPSVFP LAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSN TKVDKRVESKYGPPCPPCPAPEFLGGP SVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2046	CAGGTCACCTTGAAGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTT ATATCATATGATGGAAGTAATAAAT ACTATGCAGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCTGAGGACACGG CTGTGTATTACTGTGCGAAAGATTT AGGGGATCCCCGGGGTGGTATTTTG AACTACTGGGGCCAGGGCACCCTGG TCACCGTCTCCTCAGCATCCACCAA GGGGCCTTCCGTGTTCCCCCTGGCC CCTTGCTCCCGCTCGACCTCTGAATC CACCGCCGCACTCGGTTGCCTGGTC AAAGACTACTTCCCCGAGCCCGTGA CTGTCTCGTGGAACTCGGGCGCCCT CACATCCGGAGTGCATACCTTTCCC GCCGTGTTGCAGTCCAGCGGCCTGT ACAGCCTGAGCTCCGTCGTGACAGT GCCGTCCTCCTCCCTTGGAACCAAG ACCTATACCTGCAACGTCGACCACA AGCCCTCCAACACCAAAGTGGACAA GCGCGTCGAATCCAAGTACGGCCCC CCTTGTCCGCCTTGTCCAGCCCCTGA GTTCCTGGGTGGTCCGTCCGTGTTCC TCTTCCCGCCCAAGCCGAAGGACAC TCTGATGATTTCACGCACCCCGGAA GTCACTTGCGTGGTCGTGGACGTGT CGCAGGAAGATCCCGAAGTGCAGTT CAATTGGTACGTGGATGGGGTCGAA GTGCACAACGCCAAGACCAAGCCTA GGGAAGAACAGTTCAACTCTACGTA CCGGGTGGTGTCCGTGCTGACCGTG CTGCACCAGGACTGGCTGAACGGAA AGGAGTACAAGTGCAAAGTGTCAA

			ACAAGGGCCTCCCTTCATCCATCGA AAAGACCATCAGCAAGGCCAAGGG TCAACCTAGGGAGCCCCAGGTCTAC ACTTTGCCGCCTAGCCAAGAAGAAA TGACTAAGAACCAAGTGTCCCTGAC TTGCCTTGTCAAGGGCTTTTATCCGT CCGACATCGCCGTGGAGTGGGAGTC CAACGGACAACCGGAGAACAACTA CAAGACCACCCCACCGGTGCTCGAT TCCGATGGCTCCTTCTTCCTGTACTC CCGGCTGACTGTGGACAAGTCAAGA TGGCAGGAGGGAAACGTGTTCTCCT GCTCCGTGATGCACGAAGCGCTGCA CAACCATTACACCCAGAAATCACTG TCACTTTCGCTGGGAAAA
SEQ ID 1939	EVQLVESGGGVVQPGRSLRLSCAASGF TFSSYAMHWVRQAPGKGLEWVAVISY DGSNKYYADSVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCARSSPWGEL SLYQGAFDIWGQGTMVTVSSASTKGP SVFPLAPCSRSTSESTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSG LYSLSSVVTVPSSSLGTKTYTCNVDHK PSNTKVDKRVESKYGPPCPPCPAPEFL GGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSQEDPEVQFNWYVDGVEVHNAK TKPREEQFNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKGLPSSIEKTISKAKG QPREPQVYTLPPSQEEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSRLTVDKSRWQEGN VFSCSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2047	GAGGTGCAGCTGGTGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTCAGTAGCTATGCTA TGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTT ATATCATATGATGGAAGTAATAAAT ACTACGCAGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCTGAGGACACGG CTGTGTATTACTGTGCCCGGTCGAG CCCCTGGGGGGAGTTATCGTTATAC CAGGGGGCTTTTGATATCTGGGGCC AAGGGACAATGGTCACCGTCTCTTC AGCATCCACCAAGGGGCCTTCCGTG TTCCCCCTGGCCCCTTGCTCCCGCTC GACCTCTGAATCCACCGCCGCACTC GGTTGCCTGGTCAAAGACTACTTCC CCGAGCCCGTGACTGTCTCGTGGAA CTCGGGCGCCCTCACATCCGGAGTG CATACCTTTCCCGCCGTGTTGCAGTC CAGCGGCCTGTACAGCCTGAGCTCC GTCGTGACAGTGCCGTCCTCCTCCC TTGGAACCAAGACCTATACCTGCAA CGTCGACCACAAGCCCTCCAACACC AAAGTGGACAAGCGCGTCGAATCC AAGTACGGCCCCCCTTGTCCGCCTT GTCCAGCCCCTGAGTTCCTGGGTGG TCCGTCCGTGTTCCTCTTCCCGCCCA AGCCGAAGGACACTCTGATGATTTC ACGCACCCCGGAAGTCACTTGCGTG GTCGTGGACGTGTCGCAGGAAGATC CCGAAGTGCAGTTCAATTGGTACGT GGATGGGGTCGAAGTGCACAACGC CAAGACCAAGCCTAGGGAAGAACA GTTCAACTCTACGTACCGGGTGGTG TCCGTGCTGACCGTGCTGCACCAGG ACTGGCTGAACGGAAAGGAGTACA

			AGTGCAAAGTGTCAAACAAGGGCCT CCCTTCATCCATCGAAAAGACCATC AGCAAGGCCAAGGGTCAACCTAGG GAGCCCCAGGTCTACACTTTGCCGC CTAGCCAAGAAGAAATGACTAAGA ACCAAGTGTCCCTGACTTGCCTTGT CAAGGGCTTTTATCCGTCCGACATC GCCGTGGAGTGGGAGTCCAACGGA CAACCGGAGAACAACTACAAGACC ACCCCACCGGTGCTCGATTCCGATG GCTCCTTCTTCCTGTACTCCCGGCTG ACTGTGGACAAGTCAAGATGGCAG GAGGGAAACGTGTTCTCCTGCTCCG TGATGCACGAAGCGCTGCACAACCA TTACACCCAGAAATCACTGTCACTT TCGCTGGGAAAA
SEQ ID 1940	QITLKESGGGLVQPGRSLRLSCAASGF TFDDYAMHWVRQAPGKGLEWVSAIS GSGGSTYYADSVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCAKDNDFWS GKVFDYWGQGTLVTVSSASTKGPSVF PLAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSN TKVDKRVESKYGPPCPPCPAPEFLGGP SVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2048	CAGATCACCTTGAAGGAGTCTGGGG GAGGCTTGGTACAGCCTGGCAGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTTGATGATTATGCCA TGCACTGGGTCCGGCAAGCTCCAGG GAAGGGGCTGGAGTGGGTCTCAGCT ATTAGTGGTAGTGGTGGTAGCACAT ACTACGCAGACTCCGTGAAGGGCCG GTTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCCGAGGACACGG CCGTATATTACTGTGCGAAAGATAA CGATTTTTGGAGTGGGAAAGTCTTT GACTACTGGGGCCAGGGCACCCTGG TCACCGTCTCCTCAGCATCCACCAA GGGGCCTTCCGTGTTCCCCCTGGCC CCTTGCTCCCGCTCGACCTCTGAATC CACCGCCGCACTCGGTTGCCTGGTC AAAGACTACTTCCCCGAGCCCGTGA CTGTCTCGTGGAACTCGGGCGCCCT CACATCCGGAGTGCATACCTTTCCC GCCGTGTTGCAGTCCAGCGGCCTGT ACAGCCTGAGCTCCGTCGTGACAGT GCCGTCCTCCTCCCTTGGAACCAAG ACCTATACCTGCAACGTCGACCACA AGCCCTCCAACACCAAAGTGGACAA GCGCGTCGAATCCAAGTACGGCCCC CCTTGTCCGCCTTGTCCAGCCCCTGA GTTCCTGGGTGGTCCGTCCGTGTTCC TCTTCCCGCCCAAGCCGAAGGACAC TCTGATGATTTCACGCACCCCGGAA GTCACTTGCGTGGTCGTGGACGTGT CGCAGGAAGATCCCGAAGTGCAGTT CAATTGGTACGTGGATGGGGTCGAA GTGCACAACGCCAAGACCAAGCCTA GGGAAGAACAGTTCAACTCTACGTA CCGGGTGGTGTCCGTGCTGACCGTG CTGCACCAGGACTGGCTGAACGGAA

			AGGAGTACAAGTGCAAAGTGTCAA ACAAGGGCCTCCCTTCATCCATCGA AAAGACCATCAGCAAGGCCAAGGG TCAACCTAGGGAGCCCCAGGTCTAC ACTTTGCCGCCTAGCCAAGAAGAAA TGACTAAGAACCAAGTGTCCCTGAC TTGCCTTGTCAAGGGCTTTTATCCGT CCGACATCGCCGTGGAGTGGGAGTC CAACGGACAACCGGAGAACAACTA CAAGACCACCCCACCGGTGCTCGAT TCCGATGGCTCCTTCTTCCTGTACTC CCGGCTGACTGTGGACAAGTCAAGA TGGCAGGAGGGAAACGTGTTCTCCT GCTCCGTGATGCACGAAGCGCTGCA CAACCATTACACCCAGAAATCACTG TCACTTTCGCTGGGAAAA
SEQ ID 1941	EVQLVQSGGGLVQPGGSLRLSCAASG FTFSSYSMNWVRQAPGKGLEWVSYIS STSSTIYYADSVKGRFTISRDNSKNMLF LQMNSLRAEDTAVYYCAKEGGSGWR HYFDYWGQGTLVTVSSASTKGPSVFP LAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSN TKVDKRVESKYGPPCPPCPAPEFLGGP SVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2049	GAAGTGCAGCTGGTGCAGTCTGGGG GAGGCTTGGTACAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTCAGTAGTTATAGCA TGAACTGGGTCCGCCAGGCTCCAGG GAAGGGGCTGGAGTGGGTTTCATAC ATCAGTAGTACTAGTAGTACCATAT ACTACGCAGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCC AAGAATATGCTGTTTCTACAAATGA ACAGCCTGAGAGCTGAGGACACGG CTGTGTATTACTGTGCGAAAGAAGG GGGCAGTGGCTGGCGCCACTACTTT GACTACTGGGGCCAGGGAACCCTGG TCACCGTCTCCTCAGCATCCACCAA GGGGCCTTCCGTGTTCCCCCTGGCC CCTTGCTCCCGCTCGACCTCTGAATC CACCGCCGCACTCGGTTGCCTGGTC AAAGACTACTTCCCCGAGCCCGTGA CTGTCTCGTGGAACTCGGGCGCCCT CACATCCGGAGTGCATACCTTTCCC GCCGTGTTGCAGTCCAGCGGCCTGT ACAGCCTGAGCTCCGTCGTGACAGT GCCGTCCTCCTCCCTTGGAACCAAG ACCTATACCTGCAACGTCGACCACA AGCCCTCCAACACCAAAGTGGACAA GCGCGTCGAATCCAAGTACGGCCCC CCTTGTCCGCCTTGTCCAGCCCCTGA GTTCCTGGGTGGTCCGTCCGTGTTCC TCTTCCCGCCCAAGCCGAAGGACAC TCTGATGATTTCACGCACCCCGGAA GTCACTTGCGTGGTCGTGGACGTGT CGCAGGAAGATCCCGAAGTGCAGTT CAATTGGTACGTGGATGGGGTCGAA GTGCACAACGCCAAGACCAAGCCTA GGGAAGAACAGTTCAACTCTACGTA CCGGGTGGTGTCCGTGCTGACCGTG CTGCACCAGGACTGGCTGAACGGAA AGGAGTACAAGTGCAAAGTGTCAA

			ACAAGGGCCTCCCTTCATCCATCGA AAAGACCATCAGCAAGGCCAAGGG TCAACCTAGGGAGCCCCAGGTCTAC ACTTTGCCGCCTAGCCAAGAAGAAA TGACTAAGAACCAAGTGTCCCTGAC TTGCCTTGTCAAGGGCTTTTATCCGT CCGACATCGCCGTGGAGTGGGAGTC CAACGGACAACCGGAGAACAACTA CAAGACCACCCCACCGGTGCTCGAT TCCGATGGCTCCTTCTTCCTGTACTC CCGGCTGACTGTGGACAAGTCAAGA TGGCAGGAGGGAAACGTGTTCTCCT GCTCCGTGATGCACGAAGCGCTGCA CAACCATTACACCCAGAAATCACTG TCACTTTCGCTGGGAAAA
SEQ ID 1942	QVTLKESGGGVVQPGRSLRLSCAASGF TFSSYAMHWVRQAPGKGLEWVAVISY DGSNKYYADSVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCARDYCSSTS CQNWFDPWGQGTLVTVSSASTKGPSV FPLAPCSRSTSESTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTKTYTCNVDHKP SNTKVDKRVESKYGPPCPPCPAPEFLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKT KPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKGQ PREPQVYTLPPSQEEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSRLTVDKSRWQEGNV FSCSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2050	CAGGTCACCTTGAAGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTGTCCTGTGCAGCCTCT GGATTCACCTTCAGCAGCTATGCTA TGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTT ATATCATATGATGGAAGTAATAAAT ACTACGCAGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCTGAGGACACGG CTGTGTATTACTGTGCGAGAGATTA TTGTAGTAGTACCAGCTGCCAGAAC TGGTTCGACCCCTGGGGCCAGGGCA CCCTGGTCACCGTCTCCTCAGCATC CACCAAGGGGCCTTCCGTGTTCCCC CTGGCCCCTTGCTCCCGCTCGACCTC TGAATCCACCGCCGCACTCGGTTGC CTGGTCAAAGACTACTTCCCCGAGC CCGTGACTGTCTCGTGGAACTCGGG CGCCCTCACATCCGGAGTGCATACC TTTCCCGCCGTGTTGCAGTCCAGCG GCCTGTACAGCCTGAGCTCCGTCGT GACAGTGCCGTCCTCCTCCCTTGGA ACCAAGACCTATACCTGCAACGTCG ACCACAAGCCCTCCAACACCAAAGT GGACAAGCGCGTCGAATCCAAGTAC GGCCCCCCTTGTCCGCCTTGTCCAG CCCCTGAGTTCCTGGGTGGTCCGTC CGTGTTCCTCTTCCCGCCCAAGCCG AAGGACACTCTGATGATTTCACGCA CCCCGGAAGTCACTTGCGTGGTCGT GGACGTGTCGCAGGAAGATCCCGA AGTGCAGTTCAATTGGTACGTGGAT GGGGTCGAAGTGCACAACGCCAAG ACCAAGCCTAGGGAAGAACAGTTC AACTCTACGTACCGGGTGGTGTCCG TGCTGACCGTGCTGCACCAGGACTG GCTGAACGGAAAGGAGTACAAGTG

			CAAAGTGTCAAACAAGGGCCTCCCT TCATCCATCGAAAAGACCATCAGCA AGGCCAAGGGTCAACCTAGGGAGC CCCAGGTCTACACTTTGCCGCCTAG CCAAGAAGAAATGACTAAGAACCA AGTGTCCCTGACTTGCCTTGTCAAG GGCTTTTATCCGTCCGACATCGCCG TGGAGTGGGAGTCCAACGGACAAC CGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTC CTTCTTCCTGTACTCCCGGCTGACTG TGGACAAGTCAAGATGGCAGGAGG GAAACGTGTTCTCCTGCTCCGTGAT GCACGAAGCGCTGCACAACCATTAC ACCCAGAAATCACTGTCACTTTCGC TGGGAAAA
SEQ ID 1943	QVQLVQSGGGLVQPGGSLRLSCAASG FTFSNYVMSWVRQAPGKGLEWVSAIS GIGDTTYYADSVKGRFTISRDNAKNTL YLQMNSLRAEDTAVYYCARGRVAGD AFDIWGQGTMVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTKTYTCNVDHKPSNTKV DKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQE DPEVQFNWYVDGVEVHNAKTKPREE QFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSLGK	SEQ ID 2051	CAGGTCCAGCTGGTGCAGTCTGGGG GAGGCTTGGTACAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTTAGCAACTATGTCA TGAGCTGGGTCCGCCAGGCTCCAGG GAAGGGGCTGGAGTGGGTCTCAGCT ATTAGTGGTATTGGTGATACTACAT ACTACGCGGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAACGCC AAGAACACGCTGTATCTGCAAATGA ACAGTCTGAGAGCCGAGGACACGG CTGTGTATTACTGTGCAAGAGGGCG CGTGGCGGGGGATGCTTTTGATATC TGGGGCCAAGGGACAATGGTGACC GTCTCTTCAGCATCCACCAAGGGGC CTTCCGTGTTCCCCCTGGCCCCTTGC TCCCGCTCGACCTCTGAATCCACCG CCGCACTCGGTTGCCTGGTCAAAGA CTACTTCCCCGAGCCCGTGACTGTC TCGTGGAACTCGGGCGCCCTCACAT CCGGAGTGCATACCTTTCCCGCCGT GTTGCAGTCCAGCGGCCTGTACAGC CTGAGCTCCGTCGTGACAGTGCCGT CCTCCTCCCTTGGAACCAAGACCTA TACCTGCAACGTCGACCACAAGCCC TCCAACACCAAAGTGGACAAGCGC GTCGAATCCAAGTACGGCCCCCCTT GTCCGCCTTGTCCAGCCCCTGAGTT CCTGGGTGGTCCGTCCGTGTTCCTCT TCCCGCCCAAGCCGAAGGACACTCT GATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGC AGGAAGATCCCGAAGTGCAGTTCAA TTGGTACGTGGATGGGGTCGAAGTG CACAACGCCAAGACCAAGCCTAGG GAAGAACAGTTCAACTCTACGTACC GGGTGGTGTCCGTGCTGACCGTGCT GCACCAGGACTGGCTGAACGGAAA GGAGTACAAGTGCAAAGTGTCAAA

			CAAGGGCCTCCCTTCATCCATCGAA AAGACCATCAGCAAGGCCAAGGGT CAACCTAGGGAGCCCCAGGTCTACA CTTTGCCGCCTAGCCAAGAAGAAAT GACTAAGAACCAAGTGTCCCTGACT TGCCTTGTCAAGGGCTTTTATCCGTC CGACATCGCCGTGGAGTGGGAGTCC AACGGACAACCGGAGAACAACTAC AAGACCACCCCACCGGTGCTCGATT CCGATGGCTCCTTCTTCCTGTACTCC CGGCTGACTGTGGACAAGTCAAGAT GGCAGGAGGGAAACGTGTTCTCCTG CTCCGTGATGCACGAAGCGCTGCAC AACCATTACACCCAGAAATCACTGT CACTTTCGCTGGGAAAA
SEQ ID 1944	QLQLQESGGGLVQPGGSLRLSCAASGF TFSSYAMSWVRQAPGKGLEWVSAISG SGGSTYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKDQGAAAG TLGYFDYWGQGTLVTVSSASTKGPSV FPLAPCSRSTSESTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTKTYTCNVDHKP SNTKVDKRVESKYGPPCPPCPAPEFLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKT KPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKGQ PREPQVYTLPPSQEEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSRLTVDKSRWQEGNV FSCSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2052	CAGCTGCAGCTGCAGGAGTCGGGG GGAGGCTTGGTACAGCCTGGGGGGT CCCTGAGACTCTCCTGTGCAGCCTC TGGATTCACCTTTAGCAGCTATGCC ATGAGCTGGGTCCGCCAGGCTCCAG GGAAGGGGCTGGAGTGGGTCTCAG CTATTAGTGGTAGTGGTGGTAGCAC ATACTACGCAGACTCCGTGAAGGGC CGGTTCACCATCTCCAGAGACAATT CCAAGAACACGCTGTATCTGCAAAT GAACAGCCTGAGAGCCGAGGACAC GGCCGTATATTACTGTGCGAAAGAT CAAGGGGCAGCAGCTGGTACCCTGG GGTACTTTGACTACTGGGGCCAGGG AACCCTGGTGACCGTCTCCTCAGCA TCCACCAAGGGGCCTTCCGTGTTCC CCCTGGCCCCTTGCTCCCGCTCGAC CTCTGAATCCACCGCCGCACTCGGT TGCCTGGTCAAAGACTACTTCCCCG AGCCCGTGACTGTCTCGTGGAACTC GGGCGCCCTCACATCCGGAGTGCAT ACCTTTCCCGCCGTGTTGCAGTCCA GCGGCCTGTACAGCCTGAGCTCCGT CGTGACAGTGCCGTCCTCCTCCCTT GGAACCAAGACCTATACCTGCAACG TCGACCACAAGCCCTCCAACACCAA AGTGGACAAGCGCGTCGAATCCAA GTACGGCCCCCCTTGTCCGCCTTGTC CAGCCCCTGAGTTCCTGGGTGGTCC GTCCGTGTTCCTCTTCCCGCCCAAGC CGAAGGACACTCTGATGATTTCACG CACCCCGGAAGTCACTTGCGTGGTC GTGGACGTGTCGCAGGAAGATCCCG AAGTGCAGTTCAATTGGTACGTGGA TGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTT CAACTCTACGTACCGGGTGGTGTCC GTGCTGACCGTGCTGCACCAGGACT GGCTGAACGGAAAGGAGTACAAGT

			GCAAAGTGTCAAACAAGGGCCTCCC TTCATCCATCGAAAAGACCATCAGC AAGGCCAAGGGTCAACCTAGGGAG CCCCAGGTCTACACTTTGCCGCCTA GCCAAGAAGAAATGACTAAGAACC AAGTGTCCCTGACTTGCCTTGTCAA GGGCTTTTATCCGTCCGACATCGCC GTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACC CCACCGGTGCTCGATTCCGATGGCT CCTTCTTCCTGTACTCCCGGCTGACT GTGGACAAGTCAAGATGGCAGGAG GGAAACGTGTTCTCCTGCTCCGTGA TGCACGAAGCGCTGCACAACCATTA CACCCAGAAATCACTGTCACTTTCG CTGGGAAAA
SEQ ID 1945	QVQLVQSGAEVKKPGASVKVSCKASG YTFTSYDINWVRQATGQGLEWMGWM NPNSGNTGYAQKFQGRVTMTRNTSIST AYMELSSLRSEDTAVYYCTRGIYDSSG SSNPFDSWGQGTLVTVSSASTKGPSVF PLAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSN TKVDKRVESKYGPPCPPCPAPEFLGGP SVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2053	CAGGTGCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTCTCCTGCAAGGCTTCT GGATACACCTTCACCAGTTATGATA TCAACTGGGTGCGACAGGCCACTGG ACAAGGGCTTGAGTGGATGGGATG GATGAACCCTAACAGTGGTAACACA GGCTATGCACAGAAGTTCCAGGGCA GAGTCACCATGACCAGGAACACCTC CATAAGCACAGCCTACATGGAGCTG AGCAGCCTGAGATCTGAGGACACG GCCGTGTATTACTGTACGAGAGGAA TCTATGATAGTAGTGGTTCTTCCAAT CCCTTTGACTCCTGGGGCCAGGGAA CCCTGGTGACCGTCTCCTCAGCATC CACCAAGGGGCCTTCCGTGTTCCCC CTGGCCCCTTGCTCCCGCTCGACCTC TGAATCCACCGCCGCACTCGGTTGC CTGGTCAAAGACTACTTCCCCGAGC CCGTGACTGTCTCGTGGAACTCGGG CGCCCTCACATCCGGAGTGCATACC TTTCCCGCCGTGTTGCAGTCCAGCG GCCTGTACAGCCTGAGCTCCGTCGT GACAGTGCCGTCCTCCTCCCTTGGA ACCAAGACCTATACCTGCAACGTCG ACCACAAGCCCTCCAACACCAAAGT GGACAAGCGCGTCGAATCCAAGTAC GGCCCCCCTTGTCCGCCTTGTCCAG CCCCTGAGTTCCTGGGTGGTCCGTC CGTGTTCCTCTTCCCGCCCAAGCCG AAGGACACTCTGATGATTTCACGCA CCCCGGAAGTCACTTGCGTGGTCGT GGACGTGTCGCAGGAAGATCCCGA AGTGCAGTTCAATTGGTACGTGGAT GGGGTCGAAGTGCACAACGCCAAG ACCAAGCCTAGGGAAGAACAGTTC AACTCTACGTACCGGGTGGTGTCCG TGCTGACCGTGCTGCACCAGGACTG

			GCTGAACGGAAAGGAGTACAAGTG CAAAGTGTCAAACAAGGGCCTCCCT TCATCCATCGAAAAGACCATCAGCA AGGCCAAGGGTCAACCTAGGGAGC CCCAGGTCTACACTTTGCCGCCTAG CCAAGAAGAAATGACTAAGAACCA AGTGTCCCTGACTTGCCTTGTCAAG GGCTTTTATCCGTCCGACATCGCCG TGGAGTGGGAGTCCAACGGACAAC CGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTC CTTCTTCCTGTACTCCCGGCTGACTG TGGACAAGTCAAGATGGCAGGAGG GAAACGTGTTCTCCTGCTCCGTGAT GCACGAAGCGCTGCACAACCATTAC ACCCAGAAATCACTGTCACTTTCGC TGGGAAAA
SEQ ID 1946	EVQLVQSGAEVKKPGASVKISCEASGY TFTDYAIHWVRQAPGQRLEWMGWIN AGDGGTKSSREFQGRVTITRDTSATTA YMEVSSLRSEDTAVYYCARGYCSGGS CPGTDFDYWGQGTLVTVSSASTKGPS VFPLAPCSRSTSESTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTKTYTCNVDHKP SNTKVDKRVESKYGPPCPPCPAPEFLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKT KPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKGQ PREPQVYTLPPSQEEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSRLTVDKSRWQEGNV FSCSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2054	GAGGTGCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGATTTCCTGCGAGGCTTCT GGATACACCTTCACTGATTATGCTA TACATTGGGTGCGCCAGGCCCCCGG ACAAAGACTTGAGTGGATGGGATG GATCAACGCTGGCGATGGTGGCACA AAAAGTTCACGGGAGTTCCAGGGCA GAGTCACCATTACCAGGGACACATC CGCGACCACAGCCTACATGGAGGTG AGCAGTCTGAGATCTGAAGACACGG CTGTCTATTACTGTGCGAGAGGATA TTGTAGTGGTGGTAGCTGCCCAGGA ACGGATTTTGACTACTGGGGCCAGG GAACCCTGGTCACCGTCTCCTCAGC ATCCACCAAGGGGCCTTCCGTGTTC CCCCTGGCCCCTTGCTCCCGCTCGA CCTCTGAATCCACCGCCGCACTCGG TTGCCTGGTCAAAGACTACTTCCCC GAGCCCGTGACTGTCTCGTGGAACT CGGGCGCCCTCACATCCGGAGTGCA TACCTTTCCCGCCGTGTTGCAGTCCA GCGGCCTGTACAGCCTGAGCTCCGT CGTGACAGTGCCGTCCTCCTCCCTT GGAACCAAGACCTATACCTGCAACG TCGACCACAAGCCCTCCAACACCAA AGTGGACAAGCGCGTCGAATCCAA GTACGGCCCCCCTTGTCCGCCTTGTC CAGCCCCTGAGTTCCTGGGTGGTCC GTCCGTGTTCCTCTTCCCGCCCAAGC CGAAGGACACTCTGATGATTTCACG CACCCCGGAAGTCACTTGCGTGGTC GTGGACGTGTCGCAGGAAGATCCCG AAGTGCAGTTCAATTGGTACGTGGA TGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTT CAACTCTACGTACCGGGTGGTGTCC GTGCTGACCGTGCTGCACCAGGACT

			GGCTGAACGGAAAGGAGTACAAGT GCAAAGTGTCAAACAAGGGCCTCCC TTCATCCATCGAAAAGACCATCAGC AAGGCCAAGGGTCAACCTAGGGAG CCCCAGGTCTACACTTTGCCGCCTA GCCAAGAAGAAATGACTAAGAACC AAGTGTCCCTGACTTGCCTTGTCAA GGGCTTTTATCCGTCCGACATCGCC GTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACC CCACCGGTGCTCGATTCCGATGGCT CCTTCTTCCTGTACTCCCGGCTGACT GTGGACAAGTCAAGATGGCAGGAG GGAAACGTGTTCTCCTGCTCCGTGA TGCACGAAGCGCTGCACAACCATTA CACCCAGAAATCACTGTCACTTTCG CTGGGAAAA
SEQ ID 1947	QVQLVQSGAEVKKPGASVKVSCKASG YTFTSYYMHWVRQAPGQGLEWMGIIN PSGGSTSYAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARDGVGGRD GYNFDYWGQGTLVTVSSASTKGPSVF PLAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSN TKVDKRVESKYGPPCPPCPAPEFLGGP SVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2055	CAGGTGCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTTTCCTGCAAGGCATCT GGATACACCTTCACCAGCTACTATA TGCACTGGGTGCGACAGGCCCCTGG ACAAGGGCTTGAGTGGATGGGAAT AATCAACCCTAGTGGTGGTAGCACA AGCTACGCACAGAAGTTCCAGGGCA GAGTCACCATGACCAGGGACACGTC CACGAGCACAGTCTACATGGAGCTG AGCAGCCTGAGATCTGAGGACACG GCCGTGTATTACTGTGCGAGAGATG GTGTAGGAGGGAGAGATGGCTACA ATTTTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTCTCCTCAGCATCC ACCAAGGGGCCTTCCGTGTTCCCCC TGGCCCCTTGCTCCCGCTCGACCTCT GAATCCACCGCCGCACTCGGTTGCC TGGTCAAAGACTACTTCCCCGAGCC CGTGACTGTCTCGTGGAACTCGGGC GCCCTCACATCCGGAGTGCATACCT TTCCCGCCGTGTTGCAGTCCAGCGG CCTGTACAGCCTGAGCTCCGTCGTG ACAGTGCCGTCCTCCTCCCTTGGAA CCAAGACCTATACCTGCAACGTCGA CCACAAGCCCTCCAACACCAAAGTG GACAAGCGCGTCGAATCCAAGTACG GCCCCCCTTGTCCGCCTTGTCCAGCC CCTGAGTTCCTGGGTGGTCCGTCCG TGTTCCTCTTCCCGCCCAAGCCGAA GGACACTCTGATGATTTCACGCACC CCGGAAGTCACTTGCGTGGTCGTGG ACGTGTCGCAGGAAGATCCCGAAGT GCAGTTCAATTGGTACGTGGATGGG GTCGAAGTGCACAACGCCAAGACC AAGCCTAGGGAAGAACAGTTCAACT CTACGTACCGGGTGGTGTCCGTGCT GACCGTGCTGCACCAGGACTGGCTG

			AACGGAAAGGAGTACAAGTGCAAA GTGTCAAACAAGGGCCTCCCTTCAT CCATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTACACTTTGCCGCCTAGCCAA GAAGAAATGACTAAGAACCAAGTG TCCCTGACTTGCCTTGTCAAGGGCTT TTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCCGGCTGACTGTGGACA AGTCAAGATGGCAGGAGGGAAACG TGTTCTCCTGCTCCGTGATGCACGA AGCGCTGCACAACCATTACACCCAG AAATCACTGTCACTTTCGCTGGGAA AA
SEQ ID 1948	EVQLVQSGGGLVQPGGSLRLSCAASG FTVSSNYMSWVRQAPGKGLEWVSVIY SGGSTYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARAPLAADG YFDYWGQGTLVTVSSASTKGPSVFPL APCSRSTSESTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDV SQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKGLPSSIEKTISKAKGQPRE PQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCS VMHEALHNHYTQKSLSLSLGK	SEQ ID 2056	GAAGTGCAGCTGGTGCAGTCTGGGG GAGGCTTGGTCCAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCGTCAGTAGCAACTACA TGAGCTGGGTCCGCCAGGCTCCAGG GAAGGGGCTGGAGTGGGTCTCAGTT ATTTATAGCGGTGGTAGCACATACT ACGCAGACTCCGTGAAGGGCCGATT CACCATCTCCAGAGACAATTCCAAG AACACGCTGTATCTTCAAATGAACA GCCTGAGAGCTGAGGACACGGCTGT GTATTACTGTGCGAGAGCCCCCCTA GCAGCAGATGGCTACTTTGACTACT GGGGCCAGGGAACCCTGGTCACCGT CTCCTCAGCATCCACCAAGGGGCCT TCCGTGTTCCCCCTGGCCCCTTGCTC CCGCTCGACCTCTGAATCCACCGCC GCACTCGGTTGCCTGGTCAAAGACT ACTTCCCCGAGCCCGTGACTGTCTC GTGGAACTCGGGCGCCCTCACATCC GGAGTGCATACCTTTCCCGCCGTGT TGCAGTCCAGCGGCCTGTACAGCCT GAGCTCCGTCGTGACAGTGCCGTCC TCCTCCCTTGGAACCAAGACCTATA CCTGCAACGTCGACCACAAGCCCTC CAACACCAAAGTGGACAAGCGCGT CGAATCCAAGTACGGCCCCCCTTGT CCGCCTTGTCCAGCCCCTGAGTTCCT GGGTGGTCCGTCCGTGTTCCTCTTCC CGCCCAAGCCGAAGGACACTCTGAT GATTTCACGCACCCCGGAAGTCACT TGCGTGGTCGTGGACGTGTCGCAGG AAGATCCCGAAGTGCAGTTCAATTG GTACGTGGATGGGGTCGAAGTGCAC AACGCCAAGACCAAGCCTAGGGAA GAACAGTTCAACTCTACGTACCGGG TGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGA GTACAAGTGCAAAGTGTCAAACAA

			GGGCCTCCCTTCATCCATCGAAAAG ACCATCAGCAAGGCCAAGGGTCAA CCTAGGGAGCCCCAGGTCTACACTT TGCCGCCTAGCCAAGAAGAAATGAC TAAGAACCAAGTGTCCCTGACTTGC CTTGTCAAGGGCTTTTATCCGTCCG ACATCGCCGTGGAGTGGGAGTCCAA CGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCC GATGGCTCCTTCTTCCTGTACTCCCG GCTGACTGTGGACAAGTCAAGATGG CAGGAGGGAAACGTGTTCTCCTGCT CCGTGATGCACGAAGCGCTGCACAA CCATTACACCCAGAAATCACTGTCA CTTTCGCTGGGAAAA
SEQ ID 1949	EVQLVQSGAEVKKPGSSVKVSCKASG GTFSSYAISWVRQAPGQGLEWMGGIIP IFGTANYAQKFQGRVTITADESTSTAY MELSSLRSEDTAVYYCARARGLQYLI WYFDLWGRGTLVTVSSASTKGPSVFP LAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSN TKVDKRVESKYGPPCPPCPAPEFLGGP SVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2057	GAGGTCCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGTCCTC GGTGAAGGTCTCCTGCAAGGCTTCT GGAGGCACCTTCAGCAGCTATGCTA TCAGCTGGGTGCGACAGGCCCCTGG ACAAGGGCTTGAGTGGATGGGAGG GATCATCCCTATCTTTGGTACAGCA AACTACGCACAGAAGTTCCAGGGCA GAGTCACGATTACCGCGGACGAATC CACGAGCACAGCCTACATGGAGCTG AGCAGCCTGAGATCTGAGGACACG GCCGTGTATTACTGTGCGAGAGCCC GGGGGCTACAGTACCTAATCTGGTA CTTCGATCTCTGGGGCCGTGGCACC CTGGTGACCGTCTCCTCAGCATCCA CCAAGGGGCCTTCCGTGTTCCCCCT GGCCCCTTGCTCCCGCTCGACCTCT GAATCCACCGCCGCACTCGGTTGCC TGGTCAAAGACTACTTCCCCGAGCC CGTGACTGTCTCGTGGAACTCGGGC GCCCTCACATCCGGAGTGCATACCT TTCCCGCCGTGTTGCAGTCCAGCGG CCTGTACAGCCTGAGCTCCGTCGTG ACAGTGCCGTCCTCCTCCCTTGGAA CCAAGACCTATACCTGCAACGTCGA CCACAAGCCCTCCAACACCAAAGTG GACAAGCGCGTCGAATCCAAGTACG GCCCCCCTTGTCCGCCTTGTCCAGCC CCTGAGTTCCTGGGTGGTCCGTCCG TGTTCCTCTTCCCGCCCAAGCCGAA GGACACTCTGATGATTTCACGCACC CCGGAAGTCACTTGCGTGGTCGTGG ACGTGTCGCAGGAAGATCCCGAAGT GCAGTTCAATTGGTACGTGGATGGG GTCGAAGTGCACAACGCCAAGACC AAGCCTAGGGAAGAACAGTTCAACT CTACGTACCGGGTGGTGTCCGTGCT GACCGTGCTGCACCAGGACTGGCTG AACGGAAAGGAGTACAAGTGCAAA

			GTGTCAAACAAGGGCCTCCCTTCAT CCATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTACACTTTGCCGCCTAGCCAA GAAGAAATGACTAAGAACCAAGTG TCCCTGACTTGCCTTGTCAAGGGCTT TTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCCGGCTGACTGTGGACA AGTCAAGATGGCAGGAGGGAAACG TGTTCTCCTGCTCCGTGATGCACGA AGCGCTGCACAACCATTACACCCAG AAATCACTGTCACTTTCGCTGGGAA AA
SEQ ID 1950	QVQLVQSGAEVKKPGASVKVSCKASG YTFTSYYMHWVRQAPGQGLEWMGIIN PSGGSTSYAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCASPGMVRGV ITAPLDYWGQGTLVTVSSASTKGPSVF PLAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSN TKVDKRVESKYGPPCPPCPAPEFLGGP SVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2058	CAGGTCCAGCTGGTACAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTTTCCTGCAAGGCATCT GGATACACCTTCACCAGCTACTATA TGCACTGGGTGCGACAGGCCCCTGG ACAAGGGCTTGAGTGGATGGGAAT AATCAACCCTAGTGGTGGTAGCACA AGCTACGCACAGAAGTTCCAGGGCA GAGTCACCATGACCAGGGACACGTC CACGAGCACAGTCTACATGGAGCTG AGCAGCCTGAGATCTGAGGACACG GCCGTGTATTACTGTGCGAGCCCGG GTATGGTTCGGGGAGTTATTACTGC CCCGCTTGACTACTGGGGCCAGGGC ACCCTGGTCACCGTCTCCTCAGCAT CCACCAAGGGGCCTTCCGTGTTCCC CCTGGCCCCTTGCTCCCGCTCGACCT CTGAATCCACCGCCGCACTCGGTTG CCTGGTCAAAGACTACTTCCCCGAG CCCGTGACTGTCTCGTGGAACTCGG GCGCCCTCACATCCGGAGTGCATAC CTTTCCCGCCGTGTTGCAGTCCAGC GGCCTGTACAGCCTGAGCTCCGTCG TGACAGTGCCGTCCTCCTCCCTTGG AACCAAGACCTATACCTGCAACGTC GACCACAAGCCCTCCAACACCAAAG TGGACAAGCGCGTCGAATCCAAGTA CGGCCCCCCTTGTCCGCCTTGTCCA GCCCCTGAGTTCCTGGGTGGTCCGT CCGTGTTCCTCTTCCCGCCCAAGCC GAAGGACACTCTGATGATTTCACGC ACCCCGGAAGTCACTTGCGTGGTCG TGGACGTGTCGCAGGAAGATCCCGA AGTGCAGTTCAATTGGTACGTGGAT GGGGTCGAAGTGCACAACGCCAAG ACCAAGCCTAGGGAAGAACAGTTC AACTCTACGTACCGGGTGGTGTCCG TGCTGACCGTGCTGCACCAGGACTG GCTGAACGGAAAGGAGTACAAGTG

			CAAAGTGTCAAACAAGGGCCTCCCT TCATCCATCGAAAAGACCATCAGCA AGGCCAAGGGTCAACCTAGGGAGC CCCAGGTCTACACTTTGCCGCCTAG CCAAGAAGAAATGACTAAGAACCA AGTGTCCCTGACTTGCCTTGTCAAG GGCTTTTATCCGTCCGACATCGCCG TGGAGTGGGAGTCCAACGGACAAC CGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTC CTTCTTCCTGTACTCCCGGCTGACTG TGGACAAGTCAAGATGGCAGGAGG GAAACGTGTTCTCCTGCTCCGTGAT GCACGAAGCGCTGCACAACCATTAC ACCCAGAAATCACTGTCACTTTCGC TGGGAAAA
SEQ ID 1951	EVQLVQSGGGLVKPGGSLRLSCAASG FTFSSYAISWVRQAPGQGLEWMGGIIP MYGTANYAQKFQGRVTITADESTSTA YMELSSLRSEDTALYYCAREAKWGM YYFDYWGQGTLVTVSSASTKGPSVFP LAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSN TKVDKRVESKYGPPCPPCPAPEFLGGP SVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2059	GAGGTCCAGCTGGTACAGTCTGGGG GAGGCCTGGTCAAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTCAGCAGCTATGCTA TCAGCTGGGTGCGACAGGCCCCTGG ACAAGGGCTTGAGTGGATGGGAGG GATCATCCCTATGTATGGTACAGCA AACTACGCACAGAAGTTCCAGGGCA GAGTCACGATTACCGCGGACGAATC CACGAGCACAGCCTACATGGAACTG AGCAGCCTGAGATCTGAGGACACG GCCCTCTATTACTGTGCGAGAGAAG CTAAGTGGGGAATGTACTACTTTGA CTACTGGGGCCAGGGCACCCTGGTC ACCGTCTCCTCAGCATCCACCAAGG GGCCTTCCGTGTTCCCCCTGGCCCCT TGCTCCCGCTCGACCTCTGAATCCA CCGCCGCACTCGGTTGCCTGGTCAA AGACTACTTCCCCGAGCCCGTGACT GTCTCGTGGAACTCGGGCGCCCTCA CATCCGGAGTGCATACCTTTCCCGC CGTGTTGCAGTCCAGCGGCCTGTAC AGCCTGAGCTCCGTCGTGACAGTGC CGTCCTCCTCCCTTGGAACCAAGAC CTATACCTGCAACGTCGACCACAAG CCCTCCAACACCAAAGTGGACAAGC GCGTCGAATCCAAGTACGGCCCCCC TTGTCCGCCTTGTCCAGCCCCTGAGT TCCTGGGTGGTCCGTCCGTGTTCCTC TTCCCGCCCAAGCCGAAGGACACTC TGATGATTTCACGCACCCCGGAAGT CACTTGCGTGGTCGTGGACGTGTCG CAGGAAGATCCCGAAGTGCAGTTCA ATTGGTACGTGGATGGGGTCGAAGT GCACAACGCCAAGACCAAGCCTAG GGAAGAACAGTTCAACTCTACGTAC CGGGTGGTGTCCGTGCTGACCGTGC TGCACCAGGACTGGCTGAACGGAA

			AGGAGTACAAGTGCAAAGTGTCAA ACAAGGGCCTCCCTTCATCCATCGA AAAGACCATCAGCAAGGCCAAGGG TCAACCTAGGGAGCCCCAGGTCTAC ACTTTGCCGCCTAGCCAAGAAGAAA TGACTAAGAACCAAGTGTCCCTGAC TTGCCTTGTCAAGGGCTTTTATCCGT CCGACATCGCCGTGGAGTGGGAGTC CAACGGACAACCGGAGAACAACTA CAAGACCACCCCACCGGTGCTCGAT TCCGATGGCTCCTTCTTCCTGTACTC CCGGCTGACTGTGGACAAGTCAAGA TGGCAGGAGGGAAACGTGTTCTCCT GCTCCGTGATGCACGAAGCGCTGCA CAACCATTACACCCAGAAATCACTG TCACTTTCGCTGGGAAAA
SEQ ID 1952	EVQLVESGGGVVQPGRSLRLSCAASGF TFSSYAIHWVRQAPGKGLEWVAIISDD GSKSYYADSVQGRFTISRDNSRNTVYL QMNSLRAEDTAMYYCARDRGTKWNQ LNDVFDMWGQGTMVTVSSASTKGPS VFPLAPCSRSTSESTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTKTYTCNVDHKP SNTKVDKRVESKYGPPCPPCPAPEFLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKT KPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKGQ PREPQVYTLPPSQEEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSRLTVDKSRWQEGNV FSCSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2060	GAGGTGCAGCTGGTGGAGTCCGGG GGAGGCGTGGTCCAGCCTGGGAGGT CCCTGAGACTCTCCTGTGCAGCCTC TGGATTCACCTTCAGTAGCTATGCT ATACACTGGGTCCGCCAGGCTCCAG GCAAGGGGCTGGAGTGGGTGGCAA TTATATCAGATGATGGAAGTAAGAG TTACTACGCAGACTCCGTGCAGGGC CGATTCACCATCTCCAGAGACAATT CGAGGAACACAGTATATCTGCAAAT GAACAGCCTGAGAGCTGAGGACAC GGCTATGTATTACTGTGCGAGAGAC AGGGGAACTAAATGGAACCAATTG AATGATGTTTTTGATATGTGGGGCC AAGGGACAATGGTCACCGTCTCTTC AGCATCCACCAAGGGGCCTTCCGTG TTCCCCCTGGCCCCTTGCTCCCGCTC GACCTCTGAATCCACCGCCGCACTC GGTTGCCTGGTCAAAGACTACTTCC CCGAGCCCGTGACTGTCTCGTGGAA CTCGGGCGCCCTCACATCCGGAGTG CATACCTTTCCCGCCGTGTTGCAGTC CAGCGGCCTGTACAGCCTGAGCTCC GTCGTGACAGTGCCGTCCTCCTCCC TTGGAACCAAGACCTATACCTGCAA CGTCGACCACAAGCCCTCCAACACC AAAGTGGACAAGCGCGTCGAATCC AAGTACGGCCCCCCTTGTCCGCCTT GTCCAGCCCCTGAGTTCCTGGGTGG TCCGTCCGTGTTCCTCTTCCCGCCCA AGCCGAAGGACACTCTGATGATTTC ACGCACCCCGGAAGTCACTTGCGTG GTCGTGGACGTGTCGCAGGAAGATC CCGAAGTGCAGTTCAATTGGTACGT GGATGGGGTCGAAGTGCACAACGC CAAGACCAAGCCTAGGGAAGAACA GTTCAACTCTACGTACCGGGTGGTG TCCGTGCTGACCGTGCTGCACCAGG ACTGGCTGAACGGAAAGGAGTACA

			AGTGCAAAGTGTCAAACAAGGGCCT CCCTTCATCCATCGAAAAGACCATC AGCAAGGCCAAGGGTCAACCTAGG GAGCCCCAGGTCTACACTTTGCCGC CTAGCCAAGAAGAAATGACTAAGA ACCAAGTGTCCCTGACTTGCCTTGT CAAGGGCTTTTATCCGTCCGACATC GCCGTGGAGTGGGAGTCCAACGGA CAACCGGAGAACAACTACAAGACC ACCCCACCGGTGCTCGATTCCGATG GCTCCTTCTTCCTGTACTCCCGGCTG ACTGTGGACAAGTCAAGATGGCAG GAGGGAAACGTGTTCTCCTGCTCCG TGATGCACGAAGCGCTGCACAACCA TTACACCCAGAAATCACTGTCACTT TCGCTGGGAAAA
SEQ ID 1953	QMQLVQSGAEVKKPGASVKVSCTASG YTFTSSDINWVRQATGQGLEWMGWM NPNSGNTGYAEKFQGRVTMTSDSSIST AYMELRSLTTEDTAVYYCARGGGASY TDSWGQGTLVTVSSASTKGPSVFPLAP CSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTKTYTCNVDHKPSNTKV DKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQE DPEVQFNWYVDGVEVHNAKTKPREE QFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSLGK	SEQ ID 2061	CAGATGCAGCTGGTGCAATCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTCTCCTGCACGGCTTCT GGATACACCTTCACCAGTTCTGATA TCAACTGGGTGCGACAGGCCACTGG ACAAGGGCTTGAGTGGATGGGATG GATGAACCCTAACAGTGGTAACACC GGCTATGCAGAGAAGTTCCAGGGCA GGGTCACCATGACCAGCGACTCCTC CATAAGCACCGCCTACATGGAGTTG AGAAGCCTGACCACTGAGGACACG GCCGTATATTACTGTGCGAGAGGTG GGGGTGCGAGCTATACTGACTCCTG GGGCCAGGGCACCCTGGTCACCGTC TCCTCAGCATCCACCAAGGGGCCTT CCGTGTTCCCCCTGGCCCCTTGCTCC CGCTCGACCTCTGAATCCACCGCCG CACTCGGTTGCCTGGTCAAAGACTA CTTCCCCGAGCCCGTGACTGTCTCG TGGAACTCGGGCGCCCTCACATCCG GAGTGCATACCTTTCCCGCCGTGTT GCAGTCCAGCGGCCTGTACAGCCTG AGCTCCGTCGTGACAGTGCCGTCCT CCTCCCTTGGAACCAAGACCTATAC CTGCAACGTCGACCACAAGCCCTCC AACACCAAAGTGGACAAGCGCGTC GAATCCAAGTACGGCCCCCCTTGTC CGCCTTGTCCAGCCCCTGAGTTCCT GGGTGGTCCGTCCGTGTTCCTCTTCC CGCCCAAGCCGAAGGACACTCTGAT GATTTCACGCACCCCGGAAGTCACT TGCGTGGTCGTGGACGTGTCGCAGG AAGATCCCGAAGTGCAGTTCAATTG GTACGTGGATGGGGTCGAAGTGCAC AACGCCAAGACCAAGCCTAGGGAA GAACAGTTCAACTCTACGTACCGGG TGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGA

			GTACAAGTGCAAAGTGTCAAACAA GGGCCTCCCTTCATCCATCGAAAAG ACCATCAGCAAGGCCAAGGGTCAA CCTAGGGAGCCCCAGGTCTACACTT TGCCGCCTAGCCAAGAAGAAATGAC TAAGAACCAAGTGTCCCTGACTTGC CTTGTCAAGGGCTTTTATCCGTCCG ACATCGCCGTGGAGTGGGAGTCCAA CGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCC GATGGCTCCTTCTTCCTGTACTCCCG GCTGACTGTGGACAAGTCAAGATGG CAGGAGGGAAACGTGTTCTCCTGCT CCGTGATGCACGAAGCGCTGCACAA CCATTACACCCAGAAATCACTGTCA CTTTCGCTGGGAAAA
SEQ ID 1954	QVQLVQSGGGLVQPGRSLRLSCTASGF TFGDYAMSWFRQAPGKGLEWVGFIRS KAYGGTTEYAASVKGRFTISRDDSKSI AYLQMNSLKTEDTAVYYCTAKGGYV GYSYGPFGGYWGQGTLVTVSSASTKG PSVFPLAPCSRSTSESTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTKTYTCNVDH KPSNTKVDKRVESKYGPPCPPCPAPEF LGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSQEDPEVQFNWYVDGVEVHNA KTKPREEQFNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKGLPSSIEKTISKAK GQPREPQVYTLPPSQEEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSRLTVDKSRWQEG NVFSCSVMHEALHNHYTQKSLSLSLG K	SEQ ID 2062	CAGGTCCAGCTGGTGCAGTCTGGGG GAGGCTTGGTACAGCCAGGGCGGTC CCTGAGACTCTCCTGTACAGCTTCT GGATTCACCTTTGGTGATTATGCTAT GAGCTGGTTCCGCCAGGCTCCAGGG AAGGGGCTGGAGTGGGTAGGTTTCA TTAGAAGCAAAGCTTATGGTGGGAC AACAGAATACGCCGCGTCTGTGAAA GGCAGATTCACCATCTCAAGAGATG ATTCCAAAAGCATCGCCTATCTGCA AATGAACAGCCTGAAAACCGAGGA CACAGCCGTGTATTACTGTACCGCT AAGGGGGGCTACGTCGGATACAGCT ATGGACCTTTTGGGGGCTACTGGGG CCAGGGAACCCTGGTCACCGTCTCC TCAGCATCCACCAAGGGGCCTTCCG TGTTCCCCCTGGCCCCTTGCTCCCGC TCGACCTCTGAATCCACCGCCGCAC TCGGTTGCCTGGTCAAAGACTACTT CCCCGAGCCCGTGACTGTCTCGTGG AACTCGGGCGCCCTCACATCCGGAG TGCATACCTTTCCCGCCGTGTTGCA GTCCAGCGGCCTGTACAGCCTGAGC TCCGTCGTGACAGTGCCGTCCTCCT CCCTTGGAACCAAGACCTATACCTG CAACGTCGACCACAAGCCCTCCAAC ACCAAAGTGGACAAGCGCGTCGAA TCCAAGTACGGCCCCCCTTGTCCGC CTTGTCCAGCCCCTGAGTTCCTGGG TGGTCCGTCCGTGTTCCTCTTCCCGC CCAAGCCGAAGGACACTCTGATGAT TTCACGCACCCCGGAAGTCACTTGC GTGGTCGTGGACGTGTCGCAGGAAG ATCCCGAAGTGCAGTTCAATTGGTA CGTGGATGGGGTCGAAGTGCACAAC GCCAAGACCAAGCCTAGGGAAGAA CAGTTCAACTCTACGTACCGGGTGG TGTCCGTGCTGACCGTGCTGCACCA GGACTGGCTGAACGGAAAGGAGTA

			CAAGTGCAAAGTGTCAAACAAGGG CCTCCCTTCATCCATCGAAAAGACC ATCAGCAAGGCCAAGGGTCAACCTA GGGAGCCCCAGGTCTACACTTTGCC GCCTAGCCAAGAAGAAATGACTAA GAACCAAGTGTCCCTGACTTGCCTT GTCAAGGGCTTTTATCCGTCCGACA TCGCCGTGGAGTGGGAGTCCAACGG ACAACCGGAGAACAACTACAAGAC CACCCCACCGGTGCTCGATTCCGAT GGCTCCTTCTTCCTGTACTCCCGGCT GACTGTGGACAAGTCAAGATGGCA GGAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACT TTCGCTGGGAAAA
SEQ ID 1955	QVQLVQSGGGLVQPGRSLRLSCTASGF TFGDYAMSWFRQAPGKGLEWVGFIRS KAYGGTTEYAASVKGRFTISRDDSKSI AYLQMNSLKTEDTAVYYCTRGGTMV RGFGFNYWGQGTLVTVSSASTKGPSV FPLAPCSRSTSESTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTKTYTCNVDHKP SNTKVDKRVESKYGPPCPPCPAPEFLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKT KPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKGQ PREPQVYTLPPSQEEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSRLTVDKSRWQEGNV FSCSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2063	CAGGTGCAGCTGGTGCAGTCTGGGG GAGGCTTGGTACAGCCAGGGCGGTC CCTGAGACTCTCCTGTACAGCTTCT GGATTCACCTTTGGTGATTATGCTAT GAGCTGGTTCCGCCAGGCTCCAGGG AAGGGGCTGGAGTGGGTAGGTTTCA TTAGAAGCAAAGCTTATGGTGGGAC AACAGAATACGCCGCGTCTGTGAAA GGCAGATTCACCATCTCAAGAGATG ATTCCAAAAGCATCGCCTATCTGCA AATGAACAGCCTGAAAACCGAGGA CACAGCCGTGTATTACTGTACTAGA GGGGGGACTATGGTTCGGGGTTTCG GATTTAACTACTGGGGCCAGGGAAC CCTGGTCACCGTCTCCTCAGCATCC ACCAAGGGGCCTTCCGTGTTCCCCC TGGCCCCTTGCTCCCGCTCGACCTCT GAATCCACCGCCGCACTCGGTTGCC TGGTCAAAGACTACTTCCCCGAGCC CGTGACTGTCTCGTGGAACTCGGGC GCCCTCACATCCGGAGTGCATACCT TTCCCGCCGTGTTGCAGTCCAGCGG CCTGTACAGCCTGAGCTCCGTCGTG ACAGTGCCGTCCTCCTCCCTTGGAA CCAAGACCTATACCTGCAACGTCGA CCACAAGCCCTCCAACACCAAAGTG GACAAGCGCGTCGAATCCAAGTACG GCCCCCCTTGTCCGCCTTGTCCAGCC CCTGAGTTCCTGGGTGGTCCGTCCG TGTTCCTCTTCCCGCCCAAGCCGAA GGACACTCTGATGATTTCACGCACC CCGGAAGTCACTTGCGTGGTCGTGG ACGTGTCGCAGGAAGATCCCGAAGT GCAGTTCAATTGGTACGTGGATGGG GTCGAAGTGCACAACGCCAAGACC AAGCCTAGGGAAGAACAGTTCAACT CTACGTACCGGGTGGTGTCCGTGCT GACCGTGCTGCACCAGGACTGGCTG

			AACGGAAAGGAGTACAAGTGCAAA GTGTCAAACAAGGGCCTCCCTTCAT CCATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTACACTTTGCCGCCTAGCCAA GAAGAAATGACTAAGAACCAAGTG TCCCTGACTTGCCTTGTCAAGGGCTT TTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCCGGCTGACTGTGGACA AGTCAAGATGGCAGGAGGGAAACG TGTTCTCCTGCTCCGTGATGCACGA AGCGCTGCACAACCATTACACCCAG AAATCACTGTCACTTTCGCTGGGAA AA
SEQ ID 1956	QVQLQQWGAGLLKPSETLSLTCAVYG GSFSGYYWSWIRQPPGKGLEWIGEINH SGSTNYNPSLKSRVTISVDTSKNQFSLK LSSVTAADTAVYYCARARRAMIGPLP RLVGYFDLWGRGTLVTVSSASTKGPS VFPLAPCSRSTSESTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTKTYTCNVDHKP SNTKVDKRVESKYGPPCPPCPAPEFLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKT KPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKGQ PREPQVYTLPPSQEEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSRLTVDKSRWQEGNV FSCSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2064	CAGGTGCAGCTACAGCAGTGGGGC GCAGGACTGTTGAAGCCTTCGGAGA CCCTGTCCCTCACCTGCGCTGTCTAT GGTGGGTCCTTCAGTGGTTACTACT GGAGCTGGATCCGCCAGCCCCCAGG GAAGGGGCTGGAGTGGATTGGGGA AATCAATCATAGTGGAAGCACCAAC TACAACCCGTCCCTCAAGAGTCGAG TCACCATATCAGTAGACACGTCCAA GAACCAGTTCTCCCTGAAGCTGAGC TCTGTGACCGCCGCGGACACGGCTG TGTATTACTGTGCGAGAGCCCGGCG GGCTATGATAGGGCCGCTTCCGCGA CTTGTCGGGTACTTCGATCTCTGGG GCCGTGGAACCCTGGTCACCGTCTC CTCAGCATCCACCAAGGGGCCTTCC GTGTTCCCCCTGGCCCCTTGCTCCCG CTCGACCTCTGAATCCACCGCCGCA CTCGGTTGCCTGGTCAAAGACTACT TCCCCGAGCCCGTGACTGTCTCGTG GAACTCGGGCGCCCTCACATCCGGA GTGCATACCTTTCCCGCCGTGTTGC AGTCCAGCGGCCTGTACAGCCTGAG CTCCGTCGTGACAGTGCCGTCCTCC TCCCTTGGAACCAAGACCTATACCT GCAACGTCGACCACAAGCCCTCCAA CACCAAAGTGGACAAGCGCGTCGA ATCCAAGTACGGCCCCCCTTGTCCG CCTTGTCCAGCCCCTGAGTTCCTGG GTGGTCCGTCCGTGTTCCTCTTCCCG CCCAAGCCGAAGGACACTCTGATGA TTTCACGCACCCCGGAAGTCACTTG CGTGGTCGTGGACGTGTCGCAGGAA GATCCCGAAGTGCAGTTCAATTGGT ACGTGGATGGGGTCGAAGTGCACA ACGCCAAGACCAAGCCTAGGGAAG AACAGTTCAACTCTACGTACCGGGT GGTGTCCGTGCTGACCGTGCTGCAC CAGGACTGGCTGAACGGAAAGGAG

			TACAAGTGCAAAGTGTCAAACAAG GGCCTCCCTTCATCCATCGAAAAGA CCATCAGCAAGGCCAAGGGTCAACC TAGGGAGCCCCAGGTCTACACTTTG CCGCCTAGCCAAGAAGAAATGACTA AGAACCAAGTGTCCCTGACTTGCCT TGTCAAGGGCTTTTATCCGTCCGAC ATCGCCGTGGAGTGGGAGTCCAACG GACAACCGGAGAACAACTACAAGA CCACCCCACCGGTGCTCGATTCCGA TGGCTCCTTCTTCCTGTACTCCCGGC TGACTGTGGACAAGTCAAGATGGCA GGAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACT TTCGCTGGGAAAA
SEQ ID 1957	QVQLQQWGAGLLKPSETLSLTCAVYG GSFSGYYWSWIRQPPGKGLEWIGEINH SGSTNYNPSLKSRVTISVDTSKNQFSLK LSSVTAADTAVYYCARGRPAPSWVKT RNWFDPWGQGTLVTVSSASTKGPSVF PLAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSN TKVDKRVESKYGPPCPPCPAPEFLGGP SVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2065	CAGGTGCAGCTACAGCAGTGGGGC GCAGGACTGTTGAAGCCTTCGGAGA CCCTGTCCCTCACCTGCGCTGTCTAT GGTGGGTCCTTCAGTGGTTACTACT GGAGCTGGATCCGCCAGCCCCCAGG GAAGGGGCTGGAGTGGATTGGGGA AATCAATCATAGTGGAAGCACCAAC TACAACCCGTCCCTCAAGAGTCGAG TCACCATATCAGTAGACACGTCCAA GAACCAGTTCTCCCTGAAGCTGAGC TCTGTGACCGCCGCGGACACGGCTG TGTATTACTGTGCGAGAGGCCGCCC CGCCCCATCCTGGGTTAAAACCCGT AACTGGTTCGACCCCTGGGGCCAGG GAACCCTGGTCACCGTCTCCTCAGC ATCCACCAAGGGGCCTTCCGTGTTC CCCCTGGCCCCTTGCTCCCGCTCGA CCTCTGAATCCACCGCCGCACTCGG TTGCCTGGTCAAAGACTACTTCCCC GAGCCCGTGACTGTCTCGTGGAACT CGGGCGCCCTCACATCCGGAGTGCA TACCTTTCCCGCCGTGTTGCAGTCCA GCGGCCTGTACAGCCTGAGCTCCGT CGTGACAGTGCCGTCCTCCTCCCTT GGAACCAAGACCTATACCTGCAACG TCGACCACAAGCCCTCCAACACCAA AGTGGACAAGCGCGTCGAATCCAA GTACGGCCCCCCTTGTCCGCCTTGTC CAGCCCCTGAGTTCCTGGGTGGTCC GTCCGTGTTCCTCTTCCCGCCCAAGC CGAAGGACACTCTGATGATTTCACG CACCCCGGAAGTCACTTGCGTGGTC GTGGACGTGTCGCAGGAAGATCCCG AAGTGCAGTTCAATTGGTACGTGGA TGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTT CAACTCTACGTACCGGGTGGTGTCC GTGCTGACCGTGCTGCACCAGGACT

			GGCTGAACGGAAAGGAGTACAAGT GCAAAGTGTCAAACAAGGGCCTCCC TTCATCCATCGAAAAGACCATCAGC AAGGCCAAGGGTCAACCTAGGGAG CCCCAGGTCTACACTTTGCCGCCTA GCCAAGAAGAAATGACTAAGAACC AAGTGTCCCTGACTTGCCTTGTCAA GGGCTTTTATCCGTCCGACATCGCC GTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACC CCACCGGTGCTCGATTCCGATGGCT CCTTCTTCCTGTACTCCCGGCTGACT GTGGACAAGTCAAGATGGCAGGAG GGAAACGTGTTCTCCTGCTCCGTGA TGCACGAAGCGCTGCACAACCATTA CACCCAGAAATCACTGTCACTTTCG CTGGGAAAA
SEQ ID 1958	QVQLQQSGPGLVKPSQTLSLTCAISGD SVSSNSAAWNWIRQSPSRGLEWLGRT YYRSKWYNDYAVSVKSRITINPDTSKN QFSLQLNSVTPEDTAVYYCAREASSG WNWGQGTLVTVSSASTKGPSVFPLAP CSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTKTYTCNVDHKPSNTKV DKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQE DPEVQFNWYVDGVEVHNAKTKPREE QFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSLGK	SEQ ID 2066	CAGGTACAGCTGCAGCAGTCAGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCAACAGTGC TGCTTGGAACTGGATCAGGCAGTCC CCATCGAGAGGCCTTGAGTGGCTGG GAAGGACATACTACAGGTCCAAGTG GTATAATGATTATGCAGTATCTGTG AAAAGTCGAATAACCATCAACCCAG ACACATCCAAGAACCAGTTCTCCCT GCAGCTGAACTCTGTGACTCCCGAG GACACGGCTGTGTATTACTGTGCAA GAGAGGCTAGCAGTGGCTGGAACT GGGGCCAGGGAACCCTGGTCACCGT CTCCTCAGCATCCACCAAGGGGCCT TCCGTGTTCCCCCTGGCCCCTTGCTC CCGCTCGACCTCTGAATCCACCGCC GCACTCGGTTGCCTGGTCAAAGACT ACTTCCCCGAGCCCGTGACTGTCTC GTGGAACTCGGGCGCCCTCACATCC GGAGTGCATACCTTTCCCGCCGTGT TGCAGTCCAGCGGCCTGTACAGCCT GAGCTCCGTCGTGACAGTGCCGTCC TCCTCCCTTGGAACCAAGACCTATA CCTGCAACGTCGACCACAAGCCCTC CAACACCAAAGTGGACAAGCGCGT CGAATCCAAGTACGGCCCCCCTTGT CCGCCTTGTCCAGCCCCTGAGTTCCT GGGTGGTCCGTCCGTGTTCCTCTTCC CGCCCAAGCCGAAGGACACTCTGAT GATTTCACGCACCCCGGAAGTCACT TGCGTGGTCGTGGACGTGTCGCAGG AAGATCCCGAAGTGCAGTTCAATTG GTACGTGGATGGGGTCGAAGTGCAC AACGCCAAGACCAAGCCTAGGGAA GAACAGTTCAACTCTACGTACCGGG TGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGA

			GTACAAGTGCAAAGTGTCAAACAA GGGCCTCCCTTCATCCATCGAAAAG ACCATCAGCAAGGCCAAGGGTCAA CCTAGGGAGCCCCAGGTCTACACTT TGCCGCCTAGCCAAGAAGAAATGAC TAAGAACCAAGTGTCCCTGACTTGC CTTGTCAAGGGCTTTTATCCGTCCG ACATCGCCGTGGAGTGGGAGTCCAA CGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCC GATGGCTCCTTCTTCCTGTACTCCCG GCTGACTGTGGACAAGTCAAGATGG CAGGAGGGAAACGTGTTCTCCTGCT CCGTGATGCACGAAGCGCTGCACAA CCATTACACCCAGAAATCACTGTCA CTTTCGCTGGGAAAA
SEQ ID 1959	QVQLQESGPGLVKPSQTLSLTCAISGD SVSSNNAAWNWIRQSPSRGLEWLGRT FYRSKWYNDYAVSVKSRLTVNPDTSK NQFSLRLNSVSPEDTAVYYCARGGRY TKGGYFDDWGQGTLVTVSSASTKGPS VFPLAPCSRSTSESTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTKTYTCNVDHKP SNTKVDKRVESKYGPPCPPCPAPEFLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKT KPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKGQ PREPQVYTLPPSQEEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSRLTVDKSRWQEGNV FSCSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2067	CAGGTGCAGCTGCAGGAGTCCGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCAACAATGC TGCTTGGAACTGGATCAGGCAGTCC CCATCGAGAGGCCTTGAGTGGCTGG GAAGGACATTCTACAGGTCCAAGTG GTATAATGACTATGCAGTTTCTGTG AAAAGTCGACTAACCGTCAACCCAG ACACATCCAAGAACCAGTTCTCCCT GCGGTTGAACTCTGTGAGTCCCGAG GACACGGCTGTGTATTACTGTGCAA GAGGGGGAAGATATACCAAGGGAG GGTACTTTGACGACTGGGGCCAGGG AACCCTGGTGACCGTCTCCTCAGCA TCCACCAAGGGGCCTTCCGTGTTCC CCCTGGCCCCTTGCTCCCGCTCGAC CTCTGAATCCACCGCCGCACTCGGT TGCCTGGTCAAAGACTACTTCCCCG AGCCCGTGACTGTCTCGTGGAACTC GGGCGCCCTCACATCCGGAGTGCAT ACCTTTCCCGCCGTGTTGCAGTCCA GCGGCCTGTACAGCCTGAGCTCCGT CGTGACAGTGCCGTCCTCCTCCCTT GGAACCAAGACCTATACCTGCAACG TCGACCACAAGCCCTCCAACACCAA AGTGGACAAGCGCGTCGAATCCAA GTACGGCCCCCCTTGTCCGCCTTGTC CAGCCCCTGAGTTCCTGGGTGGTCC GTCCGTGTTCCTCTTCCCGCCCAAGC CGAAGGACACTCTGATGATTTCACG CACCCCGGAAGTCACTTGCGTGGTC GTGGACGTGTCGCAGGAAGATCCCG AAGTGCAGTTCAATTGGTACGTGGA TGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTT CAACTCTACGTACCGGGTGGTGTCC GTGCTGACCGTGCTGCACCAGGACT GGCTGAACGGAAAGGAGTACAAGT

			GCAAAGTGTCAAACAAGGGCCTCCC TTCATCCATCGAAAAGACCATCAGC AAGGCCAAGGGTCAACCTAGGGAG CCCCAGGTCTACACTTTGCCGCCTA GCCAAGAAGAAATGACTAAGAACC AAGTGTCCCTGACTTGCCTTGTCAA GGGCTTTTATCCGTCCGACATCGCC GTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACC CCACCGGTGCTCGATTCCGATGGCT CCTTCTTCCTGTACTCCCGGCTGACT GTGGACAAGTCAAGATGGCAGGAG GGAAACGTGTTCTCCTGCTCCGTGA TGCACGAAGCGCTGCACAACCATTA CACCCAGAAATCACTGTCACTTTCG CTGGGAAAA
SEQ ID 1960	QVTLKESGPTLVKPTQTLTLTCTFSGFS LSTSGVGVGWIRQPPGKALEWLALIY WDDDKRYSPSLKSRLTITKDTSKNQV VLTMTNMDPVDTATYYCAHRLDSSGR GGYFDYWGQGTLVTVSSASTKGPSVF PLAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSN TKVDKRVESKYGPPCPPCPAPEFLGGP SVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2068	CAGGTCACCTTGAAGGAGTCTGGTC CTACGCTGGTGAAACCCACACAGAC CCTCACGCTGACCTGCACCTTCTCTG GGTTCTCACTCAGCACTAGTGGAGT GGGTGTGGGCTGGATCCGTCAGCCC CCAGGAAAGGCCCTGGAGTGGCTTG CACTCATTTATTGGGATGATGATAA GCGCTACAGCCCATCTCTGAAGAGC AGGCTCACCATCACCAAGGACACCT CCAAAAACCAGGTGGTCCTTACAAT GACCAACATGGACCCTGTGGACACA GCCACATATTACTGTGCACACAGAT TGGATAGCAGTGGCCGTGGTGGTTA CTTTGACTACTGGGGCCAGGGCACC CTGGTCACCGTCTCCTCAGCATCCA CCAAGGGGCCTTCCGTGTTCCCCCT GGCCCCTTGCTCCCGCTCGACCTCT GAATCCACCGCCGCACTCGGTTGCC TGGTCAAAGACTACTTCCCCGAGCC CGTGACTGTCTCGTGGAACTCGGGC GCCCTCACATCCGGAGTGCATACCT TTCCCGCCGTGTTGCAGTCCAGCGG CCTGTACAGCCTGAGCTCCGTCGTG ACAGTGCCGTCCTCCTCCCTTGGAA CCAAGACCTATACCTGCAACGTCGA CCACAAGCCCTCCAACACCAAAGTG GACAAGCGCGTCGAATCCAAGTACG GCCCCCCTTGTCCGCCTTGTCCAGCC CCTGAGTTCCTGGGTGGTCCGTCCG TGTTCCTCTTCCCGCCCAAGCCGAA GGACACTCTGATGATTTCACGCACC CCGGAAGTCACTTGCGTGGTCGTGG ACGTGTCGCAGGAAGATCCCGAAGT GCAGTTCAATTGGTACGTGGATGGG GTCGAAGTGCACAACGCCAAGACC AAGCCTAGGGAAGAACAGTTCAACT CTACGTACCGGGTGGTGTCCGTGCT GACCGTGCTGCACCAGGACTGGCTG

			AACGGAAAGGAGTACAAGTGCAAA GTGTCAAACAAGGGCCTCCCTTCAT CCATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTACACTTTGCCGCCTAGCCAA GAAGAAATGACTAAGAACCAAGTG TCCCTGACTTGCCTTGTCAAGGGCTT TTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCCGGCTGACTGTGGACA AGTCAAGATGGCAGGAGGGAAACG TGTTCTCCTGCTCCGTGATGCACGA AGCGCTGCACAACCATTACACCCAG AAATCACTGTCACTTTCGCTGGGAA AA
SEQ ID 1961	EVQLVESGGGVVQPGRSLRLSCTASGF TFSSYGMHWVRQAPGKGLEWVAVISY DGSNKYYADSVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCAKELVGTSS PYYYYYYGMDVWGQGTMVTVSSAST KGPSVFPLAPCSRSTSESTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTKTYTCN VDHKPSNTKVDKRVESKYGPPCPPCPA PEFLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSQEDPEVQFNWYVDGVEV HNAKTKPREEQFNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKGLPSSIEKTIS KAKGQPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSRLTVDKSRW QEGNVFSCSVMHEALHNHYTQKSLSL SLGK	SEQ ID 2069	GAGGTGCAGCTGGTGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTACAGCCTCT GGATTCACCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTT ATATCATATGATGGAAGTAATAAAT ACTATGCAGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCTGAGGACACGG CTGTGTATTACTGTGCGAAAGAGTT GGTGGGTACCAGCTCTCCTTATTAC TACTACTACTACGGTATGGACGTCT GGGGCCAAGGGACAATGGTCACCG TCTCTTCAGCATCCACCAAGGGGCC TTCCGTGTTCCCCCTGGCCCCTTGCT CCCGCTCGACCTCTGAATCCACCGC CGCACTCGGTTGCCTGGTCAAAGAC TACTTCCCCGAGCCCGTGACTGTCT CGTGGAACTCGGGCGCCCTCACATC CGGAGTGCATACCTTTCCCGCCGTG TTGCAGTCCAGCGGCCTGTACAGCC TGAGCTCCGTCGTGACAGTGCCGTC CTCCTCCCTTGGAACCAAGACCTAT ACCTGCAACGTCGACCACAAGCCCT CCAACACCAAAGTGGACAAGCGCG TCGAATCCAAGTACGGCCCCCCTTG TCCGCCTTGTCCAGCCCCTGAGTTCC TGGGTGGTCCGTCCGTGTTCCTCTTC CCGCCCAAGCCGAAGGACACTCTGA TGATTTCACGCACCCCGGAAGTCAC TTGCGTGGTCGTGGACGTGTCGCAG GAAGATCCCGAAGTGCAGTTCAATT GGTACGTGGATGGGGTCGAAGTGCA CAACGCCAAGACCAAGCCTAGGGA AGAACAGTTCAACTCTACGTACCGG GTGGTGTCCGTGCTGACCGTGCTGC ACCAGGACTGGCTGAACGGAAAGG

			AGTACAAGTGCAAAGTGTCAAACA AGGGCCTCCCTTCATCCATCGAAAA GACCATCAGCAAGGCCAAGGGTCA ACCTAGGGAGCCCCAGGTCTACACT TTGCCGCCTAGCCAAGAAGAAATGA CTAAGAACCAAGTGTCCCTGACTTG CCTTGTCAAGGGCTTTTATCCGTCCG ACATCGCCGTGGAGTGGGAGTCCAA CGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCC GATGGCTCCTTCTTCCTGTACTCCCG GCTGACTGTGGACAAGTCAAGATGG CAGGAGGGAAACGTGTTCTCCTGCT CCGTGATGCACGAAGCGCTGCACAA CCATTACACCCAGAAATCACTGTCA CTTTCGCTGGGAAAA
SEQ ID 1962	QLQLQESGGGLVQPGGSLRLSCAASGF TVSSNYMSWVRQAPGKGLEWVSVIYS GGSTYYADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARDYYYGSGSS PWGQGTLVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTKTYTCNVDHKPSNTKVDK RVESKYGPPCPPCPAPEFLGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSQEDP EVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKC KVSNKGLPSSIEKTISKAKGQPREPQVY TLPPSQEEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGS FFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSLGK	SEQ ID 2070	CAGCTGCAGCTGCAGGAGTCGGGG GGAGGCTTGGTCCAGCCTGGGGGGT CCCTGAGACTCTCCTGTGCAGCCTC TGGATTCACCGTCAGTAGCAACTAC ATGAGCTGGGTCCGCCAGGCTCCAG GGAAGGGGCTGGAGTGGGTCTCAGT TATTTATAGCGGTGGTAGCACATAC TACGCAGACTCCGTGAAGGGCAGAT TCACCATCTCCAGAGACAATTCCAA GAACACGCTGTATCTTCAAATGAAC AGCCTGAGAGCCGAGGACACGGCT GTGTATTACTGTGCGAGAGACTATT ACTATGGTTCGGGGAGTTCTCCCTG GGGCCAGGGAACCCTGGTCACCGTC TCCTCAGCATCCACCAAGGGGCCTT CCGTGTTCCCCCTGGCCCCTTGCTCC CGCTCGACCTCTGAATCCACCGCCG CACTCGGTTGCCTGGTCAAAGACTA CTTCCCCGAGCCCGTGACTGTCTCG TGGAACTCGGGCGCCCTCACATCCG GAGTGCATACCTTTCCCGCCGTGTT GCAGTCCAGCGGCCTGTACAGCCTG AGCTCCGTCGTGACAGTGCCGTCCT CCTCCCTTGGAACCAAGACCTATAC CTGCAACGTCGACCACAAGCCCTCC AACACCAAAGTGGACAAGCGCGTC GAATCCAAGTACGGCCCCCCTTGTC CGCCTTGTCCAGCCCCTGAGTTCCT GGGTGGTCCGTCCGTGTTCCTCTTCC CGCCCAAGCCGAAGGACACTCTGAT GATTTCACGCACCCCGGAAGTCACT TGCGTGGTCGTGGACGTGTCGCAGG AAGATCCCGAAGTGCAGTTCAATTG GTACGTGGATGGGGTCGAAGTGCAC AACGCCAAGACCAAGCCTAGGGAA GAACAGTTCAACTCTACGTACCGGG TGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGA

			GTACAAGTGCAAAGTGTCAAACAA GGGCCTCCCTTCATCCATCGAAAAG ACCATCAGCAAGGCCAAGGGTCAA CCTAGGGAGCCCCAGGTCTACACTT TGCCGCCTAGCCAAGAAGAAATGAC TAAGAACCAAGTGTCCCTGACTTGC CTTGTCAAGGGCTTTTATCCGTCCG ACATCGCCGTGGAGTGGGAGTCCAA CGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCC GATGGCTCCTTCTTCCTGTACTCCCG GCTGACTGTGGACAAGTCAAGATGG CAGGAGGGAAACGTGTTCTCCTGCT CCGTGATGCACGAAGCGCTGCACAA CCATTACACCCAGAAATCACTGTCA CTTTCGCTGGGAAAA
SEQ ID 1963	QVQLQQWGAGLLKPSETLSLTCAVYG GSFSGYYWSWIRQPPGKGLEWIGEINH SGSTNYNPSLKSRVTISVDTSKNQFSLK LSSVTAADTAVYYCARGRPYCSSTSCY PEWFDPWGQGTLVTVSSASTKGPSVFP LAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSN TKVDKRVESKYGPPCPPCPAPEFLGGP SVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2071	CAGGTGCAGCTACAGCAGTGGGGC GCAGGACTGTTGAAGCCTTCGGAGA CCCTGTCCCTCACCTGCGCTGTCTAT GGTGGGTCCTTCAGTGGTTACTACT GGAGCTGGATCCGCCAGCCCCCAGG GAAGGGGCTGGAGTGGATTGGGGA AATCAATCATAGTGGAAGCACCAAC TACAACCCGTCCCTCAAGAGTCGAG TCACCATATCAGTAGACACGTCCAA GAACCAGTTCTCCCTGAAGCTGAGC TCTGTGACCGCCGCGGACACGGCTG TGTATTACTGTGCGAGAGGCCGGCC ATATTGTAGTAGTACCAGCTGCTAC CCAGAGTGGTTCGACCCCTGGGGCC AGGGAACCCTGGTCACCGTCTCCTC AGCATCCACCAAGGGGCCTTCCGTG TTCCCCCTGGCCCCTTGCTCCCGCTC GACCTCTGAATCCACCGCCGCACTC GGTTGCCTGGTCAAAGACTACTTCC CCGAGCCCGTGACTGTCTCGTGGAA CTCGGGCGCCCTCACATCCGGAGTG CATACCTTTCCCGCCGTGTTGCAGTC CAGCGGCCTGTACAGCCTGAGCTCC GTCGTGACAGTGCCGTCCTCCTCCC TTGGAACCAAGACCTATACCTGCAA CGTCGACCACAAGCCCTCCAACACC AAAGTGGACAAGCGCGTCGAATCC AAGTACGGCCCCCCTTGTCCGCCTT GTCCAGCCCCTGAGTTCCTGGGTGG TCCGTCCGTGTTCCTCTTCCCGCCCA AGCCGAAGGACACTCTGATGATTTC ACGCACCCCGGAAGTCACTTGCGTG GTCGTGGACGTGTCGCAGGAAGATC CCGAAGTGCAGTTCAATTGGTACGT GGATGGGGTCGAAGTGCACAACGC CAAGACCAAGCCTAGGGAAGAACA GTTCAACTCTACGTACCGGGTGGTG TCCGTGCTGACCGTGCTGCACCAGG ACTGGCTGAACGGAAAGGAGTACA

			AGTGCAAAGTGTCAAACAAGGGCCT CCCTTCATCCATCGAAAAGACCATC AGCAAGGCCAAGGGTCAACCTAGG GAGCCCCAGGTCTACACTTTGCCGC CTAGCCAAGAAGAAATGACTAAGA ACCAAGTGTCCCTGACTTGCCTTGT CAAGGGCTTTTATCCGTCCGACATC GCCGTGGAGTGGGAGTCCAACGGA CAACCGGAGAACAACTACAAGACC ACCCCACCGGTGCTCGATTCCGATG GCTCCTTCTTCCTGTACTCCCGGCTG ACTGTGGACAAGTCAAGATGGCAG GAGGGAAACGTGTTCTCCTGCTCCG TGATGCACGAAGCGCTGCACAACCA TTACACCCAGAAATCACTGTCACTT TCGCTGGGAAAA
SEQ ID 1964	QVTLKESGGGVVQPGRSLRLSCAASGF TFSSYGMHWVRQAPGKGLEWVAVISY DGSNKYYADSVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCAKLRGIDYY DSSGYQRGFDYWGQGTLVTVSSASTK GPSVFPLAPCSRSTSESTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSSLGTKTYTCNV DHKPSNTKVDKRVESKYGPPCPPCPAP EFLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSQEDPEVQFNWYVDGVEVH NAKTKPREEQFNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKGLPSSIEKTISK AKGQPREPQVYTLPPSQEEMTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSRLTVDKSRWQ EGNVFSCSVMHEALHNHYTQKSLSLS LGK	SEQ ID 2072	CAGGTCACCTTGAAGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTT ATATCATATGATGGAAGTAATAAAT ACTATGCAGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCTGAGGACACGG CTGTGTATTACTGTGCGAAATTAAG GGGTATAGATTACTATGATAGTAGT GGTTACCAACGGGGGTTTGACTACT GGGGCCAGGGAACCCTGGTCACCGT CTCCTCAGCATCCACCAAGGGGCCT TCCGTGTTCCCCCTGGCCCCTTGCTC CCGCTCGACCTCTGAATCCACCGCC GCACTCGGTTGCCTGGTCAAAGACT ACTTCCCCGAGCCCGTGACTGTCTC GTGGAACTCGGGCGCCCTCACATCC GGAGTGCATACCTTTCCCGCCGTGT TGCAGTCCAGCGGCCTGTACAGCCT GAGCTCCGTCGTGACAGTGCCGTCC TCCTCCCTTGGAACCAAGACCTATA CCTGCAACGTCGACCACAAGCCCTC CAACACCAAAGTGGACAAGCGCGT CGAATCCAAGTACGGCCCCCCTTGT CCGCCTTGTCCAGCCCCTGAGTTCCT GGGTGGTCCGTCCGTGTTCCTCTTCC CGCCCAAGCCGAAGGACACTCTGAT GATTTCACGCACCCCGGAAGTCACT TGCGTGGTCGTGGACGTGTCGCAGG AAGATCCCGAAGTGCAGTTCAATTG GTACGTGGATGGGGTCGAAGTGCAC AACGCCAAGACCAAGCCTAGGGAA GAACAGTTCAACTCTACGTACCGGG TGGTGTCCGTGCTGACCGTGCTGCA

			CCAGGACTGGCTGAACGGAAAGGA GTACAAGTGCAAAGTGTCAAACAA GGGCCTCCCTTCATCCATCGAAAAG ACCATCAGCAAGGCCAAGGGTCAA CCTAGGGAGCCCCAGGTCTACACTT TGCCGCCTAGCCAAGAAGAAATGAC TAAGAACCAAGTGTCCCTGACTTGC CTTGTCAAGGGCTTTTATCCGTCCG ACATCGCCGTGGAGTGGGAGTCCAA CGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCC GATGGCTCCTTCTTCCTGTACTCCCG GCTGACTGTGGACAAGTCAAGATGG CAGGAGGGAAACGTGTTCTCCTGCT CCGTGATGCACGAAGCGCTGCACAA CCATTACACCCAGAAATCACTGTCA CTTTCGCTGGGAAAA
SEQ ID 1965	QVQLQESGPGLVKPSETLSLTCTVSGG SISSYYWSWIRQPPGKGLEWIGYIYYT GSTNYNPSLKSRVTISVDTSKNQFSLKL SSVTTADTAVYYCARGGRGDGAAFDI WGQGTMVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTKTYTCNVDHKPSNTKVDK RVESKYGPPCPPCPAPEFLGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSQEDP EVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKC KVSNKGLPSSIEKTISKAKGQPREPQVY TLPPSQEEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGS FFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSLGK	SEQ ID 2073	CAGGTGCAGCTGCAGGAGTCCGGCC CAGGACTGGTGAAGCCTTCGGAGAC CCTGTCCCTCACCTGCACTGTCTCTG GTGGCTCCATCAGTAGTTACTACTG GAGCTGGATCCGGCAGCCCCCAGGG AAGGGACTGGAGTGGATTGGCTATA TCTATTACACTGGGAGCACCAACTA CAACCCCTCCCTCAAGAGCCGAGTC ACCATATCAGTAGACACGTCCAAGA ACCAGTTCTCCCTGAAGCTGAGCTC TGTGACCACTGCGGACACGGCCGTG TATTACTGTGCGAGAGGTGGGAGGG GGGATGGGGCCGCTTTTGACATCTG GGGCCAAGGGACAATGGTCACCGTC TCTTCAGCATCCACCAAGGGGCCTT CCGTGTTCCCCCTGGCCCCTTGCTCC CGCTCGACCTCTGAATCCACCGCCG CACTCGGTTGCCTGGTCAAAGACTA CTTCCCCGAGCCCGTGACTGTCTCG TGGAACTCGGGCGCCCTCACATCCG GAGTGCATACCTTTCCCGCCGTGTT GCAGTCCAGCGGCCTGTACAGCCTG AGCTCCGTCGTGACAGTGCCGTCCT CCTCCCTTGGAACCAAGACCTATAC CTGCAACGTCGACCACAAGCCCTCC AACACCAAAGTGGACAAGCGCGTC GAATCCAAGTACGGCCCCCCTTGTC CGCCTTGTCCAGCCCCTGAGTTCCT GGGTGGTCCGTCCGTGTTCCTCTTCC CGCCCAAGCCGAAGGACACTCTGAT GATTTCACGCACCCCGGAAGTCACT TGCGTGGTCGTGGACGTGTCGCAGG AAGATCCCGAAGTGCAGTTCAATTG GTACGTGGATGGGGTCGAAGTGCAC AACGCCAAGACCAAGCCTAGGGAA GAACAGTTCAACTCTACGTACCGGG TGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGA

			GTACAAGTGCAAAGTGTCAAACAA GGGCCTCCCTTCATCCATCGAAAAG ACCATCAGCAAGGCCAAGGGTCAA CCTAGGGAGCCCCAGGTCTACACTT TGCCGCCTAGCCAAGAAGAAATGAC TAAGAACCAAGTGTCCCTGACTTGC CTTGTCAAGGGCTTTTATCCGTCCG ACATCGCCGTGGAGTGGGAGTCCAA CGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCC GATGGCTCCTTCTTCCTGTACTCCCG GCTGACTGTGGACAAGTCAAGATGG CAGGAGGGAAACGTGTTCTCCTGCT CCGTGATGCACGAAGCGCTGCACAA CCATTACACCCAGAAATCACTGTCA CTTTCGCTGGGAAAA
SEQ ID 1966	QVQLVQSGGGVVQPGRSLRLSCAASG FTFSSSAMHWVRQAPGKGLEWVAMI WHDESKKYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARPPDGG NSGRWYFDLWGRGTLVTVSSASTKGP SVFPLAPCSRSTSESTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSG LYSLSSVVTVPSSSLGTKTYTCNVDHK PSNTKVDKRVESKYGPPCPPCPAPEFL GGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSQEDPEVQFNWYVDGVEVHNAK TKPREEQFNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKGLPSSIEKTISKAKG QPREPQVYTLPPSQEEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSRLTVDKSRWQEGN VFSCSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2074	CAGGTGCAGCTGGTGCAATCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCGTCT GGATTCACCTTCAGCAGCTCTGCCA TGCACTGGGTCCGCCAGGCTCCAGG CAAGGGACTGGAGTGGGTGGCAAT GATTTGGCATGATGAGAGTAAGAAA TACTATGCAGACTCCGTGAAGGGCC GATTCACTATCTCCAGAGACAATTC CAAGAACACGCTGTATCTGCAAATG AACAGCCTGAGAGCTGAGGACACG GCTGTGTATTACTGTGCGAGACCCC CCGACGGTGGTAACTCCGGTCGCTG GTACTTCGATCTCTGGGGCCGTGGC ACCCTGGTCACCGTCTCCTCAGCAT CCACCAAGGGGCCTTCCGTGTTCCC CCTGGCCCCTTGCTCCCGCTCGACCT CTGAATCCACCGCCGCACTCGGTTG CCTGGTCAAAGACTACTTCCCCGAG CCCGTGACTGTCTCGTGGAACTCGG GCGCCCTCACATCCGGAGTGCATAC CTTTCCCGCCGTGTTGCAGTCCAGC GGCCTGTACAGCCTGAGCTCCGTCG TGACAGTGCCGTCCTCCTCCCTTGG AACCAAGACCTATACCTGCAACGTC GACCACAAGCCCTCCAACACCAAAG TGGACAAGCGCGTCGAATCCAAGTA CGGCCCCCCTTGTCCGCCTTGTCCA GCCCCTGAGTTCCTGGGTGGTCCGT CCGTGTTCCTCTTCCCGCCCAAGCC GAAGGACACTCTGATGATTTCACGC ACCCCGGAAGTCACTTGCGTGGTCG TGGACGTGTCGCAGGAAGATCCCGA AGTGCAGTTCAATTGGTACGTGGAT GGGGTCGAAGTGCACAACGCCAAG ACCAAGCCTAGGGAAGAACAGTTC AACTCTACGTACCGGGTGGTGTCCG TGCTGACCGTGCTGCACCAGGACTG GCTGAACGGAAAGGAGTACAAGTG

			CAAAGTGTCAAACAAGGGCCTCCCT TCATCCATCGAAAAGACCATCAGCA AGGCCAAGGGTCAACCTAGGGAGC CCCAGGTCTACACTTTGCCGCCTAG CCAAGAAGAAATGACTAAGAACCA AGTGTCCCTGACTTGCCTTGTCAAG GGCTTTTATCCGTCCGACATCGCCG TGGAGTGGGAGTCCAACGGACAAC CGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTC CTTCTTCCTGTACTCCCGGCTGACTG TGGACAAGTCAAGATGGCAGGAGG GAAACGTGTTCTCCTGCTCCGTGAT GCACGAAGCGCTGCACAACCATTAC ACCCAGAAATCACTGTCACTTTCGC TGGGAAAA
SEQ ID 1967	QMQLVQSGGGLVQPGGSLRLSCAASG FTFSSYAMSWVRQAPGKGLEWVSAIS GSGGSTYYADSVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCAKDKNVRK HDYGDHPYGGYFDYWGQGTLVTVSS ASTKGPSVFPLAPCSRSTSESTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVESKYGPPCP PCPAPEFLGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLT VLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTK NQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSRLTVDK SRWQEGNVFSCSVMHEALHNHYTQKS LSLSLGK	SEQ ID 2075	CAGATGCAGCTGGTGCAATCTGGGG GAGGCTTGGTACAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTTAGCAGCTATGCCA TGAGCTGGGTCCGCCAGGCTCCAGG GAAGGGGCTGGAGTGGGTCTCAGCT ATTAGTGGTAGTGGTGGTAGCACAT ACTACGCAGACTCCGTGAAGGGCCG GTTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCCGAGGACACGG CCGTATATTACTGTGCGAAAGACAA GAACGTCCGAAAACATGACTACGGT GACCACCCCTACGGGGGGTACTTTG ACTACTGGGGCCAGGGCACCCTGGT GACCGTCTCCTCAGCATCCACCAAG GGGCCTTCCGTGTTCCCCCTGGCCC CTTGCTCCCGCTCGACCTCTGAATCC ACCGCCGCACTCGGTTGCCTGGTCA AAGACTACTTCCCCGAGCCCGTGAC TGTCTCGTGGAACTCGGGCGCCCTC ACATCCGGAGTGCATACCTTTCCCG CCGTGTTGCAGTCCAGCGGCCTGTA CAGCCTGAGCTCCGTCGTGACAGTG CCGTCCTCCTCCCTTGGAACCAAGA CCTATACCTGCAACGTCGACCACAA GCCCTCCAACACCAAAGTGGACAAG CGCGTCGAATCCAAGTACGGCCCCC CTTGTCCGCCTTGTCCAGCCCCTGA GTTCCTGGGTGGTCCGTCCGTGTTCC TCTTCCCGCCCAAGCCGAAGGACAC TCTGATGATTTCACGCACCCCGGAA GTCACTTGCGTGGTCGTGGACGTGT CGCAGGAAGATCCCGAAGTGCAGTT CAATTGGTACGTGGATGGGGTCGAA GTGCACAACGCCAAGACCAAGCCTA GGGAAGAACAGTTCAACTCTACGTA CCGGGTGGTGTCCGTGCTGACCGTG CTGCACCAGGACTGGCTGAACGGAA

			AGGAGTACAAGTGCAAAGTGTCAA ACAAGGGCCTCCCTTCATCCATCGA AAAGACCATCAGCAAGGCCAAGGG TCAACCTAGGGAGCCCCAGGTCTAC ACTTTGCCGCCTAGCCAAGAAGAAA TGACTAAGAACCAAGTGTCCCTGAC TTGCCTTGTCAAGGGCTTTTATCCGT CCGACATCGCCGTGGAGTGGGAGTC CAACGGACAACCGGAGAACAACTA CAAGACCACCCCACCGGTGCTCGAT TCCGATGGCTCCTTCTTCCTGTACTC CCGGCTGACTGTGGACAAGTCAAGA TGGCAGGAGGGAAACGTGTTCTCCT GCTCCGTGATGCACGAAGCGCTGCA CAACCATTACACCCAGAAATCACTG TCACTTTCGCTGGGAAAA
SEQ ID 1968	EVQLVQSGAEVKKPGASVKVSCKASG YTFTSYAMHWVRQAPGQRLEWMGWI NAGNGNTKYSQKFQGRVTITRDTSAST AYMELSSLRSEDTAVYYCARVAGATS LWYWGQGTLVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTKTYTCNVDHKPSNTKV DKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQE DPEVQFNWYVDGVEVHNAKTKPREE QFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSLGK	SEQ ID 2076	GAGGTCCAGCTGGTACAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTTTCCTGCAAGGCTTCT GGATACACCTTCACTAGCTATGCTA TGCATTGGGTGCGCCAGGCCCCCGG ACAAAGGCTTGAGTGGATGGGATG GATCAACGCTGGCAATGGTAACACA AAATATTCACAGAAGTTCCAGGGCA GAGTCACCATTACCAGGGACACATC CGCGAGCACAGCCTACATGGAGCTG AGCAGCCTGAGATCTGAAGACACG GCTGTGTATTACTGTGCGAGAGTGG CGGGAGCTACTTCCCTATGGTACTG GGGCCAGGGCACCCTGGTCACCGTC TCCTCAGCATCCACCAAGGGGCCTT CCGTGTTCCCCCTGGCCCCTTGCTCC CGCTCGACCTCTGAATCCACCGCCG CACTCGGTTGCCTGGTCAAAGACTA CTTCCCCGAGCCCGTGACTGTCTCG TGGAACTCGGGCGCCCTCACATCCG GAGTGCATACCTTTCCCGCCGTGTT GCAGTCCAGCGGCCTGTACAGCCTG AGCTCCGTCGTGACAGTGCCGTCCT CCTCCCTTGGAACCAAGACCTATAC CTGCAACGTCGACCACAAGCCCTCC AACACCAAAGTGGACAAGCGCGTC GAATCCAAGTACGGCCCCCCTTGTC CGCCTTGTCCAGCCCCTGAGTTCCT GGGTGGTCCGTCCGTGTTCCTCTTCC CGCCCAAGCCGAAGGACACTCTGAT GATTTCACGCACCCCGGAAGTCACT TGCGTGGTCGTGGACGTGTCGCAGG AAGATCCCGAAGTGCAGTTCAATTG GTACGTGGATGGGGTCGAAGTGCAC AACGCCAAGACCAAGCCTAGGGAA GAACAGTTCAACTCTACGTACCGGG TGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGA

			GTACAAGTGCAAAGTGTCAAACAA GGGCCTCCCTTCATCCATCGAAAAG ACCATCAGCAAGGCCAAGGGTCAA CCTAGGGAGCCCCAGGTCTACACTT TGCCGCCTAGCCAAGAAGAAATGAC TAAGAACCAAGTGTCCCTGACTTGC CTTGTCAAGGGCTTTTATCCGTCCG ACATCGCCGTGGAGTGGGAGTCCAA CGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCC GATGGCTCCTTCTTCCTGTACTCCCG GCTGACTGTGGACAAGTCAAGATGG CAGGAGGGAAACGTGTTCTCCTGCT CCGTGATGCACGAAGCGCTGCACAA CCATTACACCCAGAAATCACTGTCA CTTTCGCTGGGAAAA
SEQ ID 1969	QVQLQQSGPGLVKPSQSLSLTCAISGD SVSSNSAAWNWIRQSPSRGLEWLGRT YYRSKWYNDYAVSVKSRITIKPDTSKN QFSLQLNSVTPEDTAVYYCTRLANSDG VDVWGQGTMVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTKTYTCNVDHKPSNTKV DKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQE DPEVQFNWYVDGVEVHNAKTKPREE QFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSLGK	SEQ ID 2077	CAGGTACAGCTGCAGCAGTCAGGTC CAGGACTGGTGAAGCCCTCGCAGAG CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCAACAGTGC TGCTTGGAACTGGATCAGGCAGTCC CCATCGAGAGGCCTTGAGTGGCTGG GAAGGACATACTACAGGTCCAAGTG GTATAATGATTATGCAGTATCTGTG AAGAGTCGAATAACCATCAAACCA GACACATCCAAGAACCAGTTCTCCC TGCAGCTGAACTCTGTGACTCCCGA GGACACGGCTGTGTATTACTGTACA AGGCTAGCTAATTCCGACGGTGTGG ACGTCTGGGGCCAAGGGACAATGGT CACCGTCTCCTCAGCATCCACCAAG GGGCCTTCCGTGTTCCCCCTGGCCC CTTGCTCCCGCTCGACCTCTGAATCC ACCGCCGCACTCGGTTGCCTGGTCA AAGACTACTTCCCCGAGCCCGTGAC TGTCTCGTGGAACTCGGGCGCCCTC ACATCCGGAGTGCATACCTTTCCCG CCGTGTTGCAGTCCAGCGGCCTGTA CAGCCTGAGCTCCGTCGTGACAGTG CCGTCCTCCTCCCTTGGAACCAAGA CCTATACCTGCAACGTCGACCACAA GCCCTCCAACACCAAAGTGGACAAG CGCGTCGAATCCAAGTACGGCCCCC CTTGTCCGCCTTGTCCAGCCCCTGA GTTCCTGGGTGGTCCGTCCGTGTTCC TCTTCCCGCCCAAGCCGAAGGACAC TCTGATGATTTCACGCACCCCGGAA GTCACTTGCGTGGTCGTGGACGTGT CGCAGGAAGATCCCGAAGTGCAGTT CAATTGGTACGTGGATGGGGTCGAA GTGCACAACGCCAAGACCAAGCCTA GGGAAGAACAGTTCAACTCTACGTA CCGGGTGGTGTCCGTGCTGACCGTG CTGCACCAGGACTGGCTGAACGGAA AGGAGTACAAGTGCAAAGTGTCAA

			ACAAGGGCCTCCCTTCATCCATCGA AAAGACCATCAGCAAGGCCAAGGG TCAACCTAGGGAGCCCCAGGTCTAC ACTTTGCCGCCTAGCCAAGAAGAAA TGACTAAGAACCAAGTGTCCCTGAC TTGCCTTGTCAAGGGCTTTTATCCGT CCGACATCGCCGTGGAGTGGGAGTC CAACGGACAACCGGAGAACAACTA CAAGACCACCCCACCGGTGCTCGAT TCCGATGGCTCCTTCTTCCTGTACTC CCGGCTGACTGTGGACAAGTCAAGA TGGCAGGAGGGAAACGTGTTCTCCT GCTCCGTGATGCACGAAGCGCTGCA CAACCATTACACCCAGAAATCACTG TCACTTTCGCTGGGAAAA
SEQ ID 1970	QVQLQQSGPGLVKPSQTLSLTCAISGD SVSSDSAVWTWIRQSPSRGLEWLGRT YYKSKWYNDYAASVKSRITINPDTSK NQFSLHLNSVTPEDTAVYYCARGVTR TFDYWGQGTTVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTKTYTCNVDHKPSNTKV DKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQE DPEVQFNWYVDGVEVHNAKTKPREE QFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSLGK	SEQ ID 2078	CAGGTACAGCTGCAGCAGTCAGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCGACAGTGC TGTTTGGACCTGGATCAGGCAGTCC CCATCGAGAGGCCTTGAGTGGCTGG GAAGGACATACTACAAGTCGAAGT GGTATAATGATTATGCAGCATCTGT GAAAAGTCGAATAACCATCAACCCA GACACATCCAAGAACCAGTTCTCCC TGCACCTGAACTCTGTGACTCCCGA GGACACGGCTGTGTATTACTGTGCA AGAGGTGTAACCCGGACCTTTGACT ACTGGGGCCAGGGGACCACGGTCA CCGTCTCCTCAGCATCCACCAAGGG GCCTTCCGTGTTCCCCCTGGCCCCTT GCTCCCGCTCGACCTCTGAATCCAC CGCCGCACTCGGTTGCCTGGTCAAA GACTACTTCCCCGAGCCCGTGACTG TCTCGTGGAACTCGGGCGCCCTCAC ATCCGGAGTGCATACCTTTCCCGCC GTGTTGCAGTCCAGCGGCCTGTACA GCCTGAGCTCCGTCGTGACAGTGCC GTCCTCCTCCCTTGGAACCAAGACC TATACCTGCAACGTCGACCACAAGC CCTCCAACACCAAAGTGGACAAGCG CGTCGAATCCAAGTACGGCCCCCCT TGTCCGCCTTGTCCAGCCCCTGAGTT CCTGGGTGGTCCGTCCGTGTTCCTCT TCCCGCCCAAGCCGAAGGACACTCT GATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGC AGGAAGATCCCGAAGTGCAGTTCAA TTGGTACGTGGATGGGGTCGAAGTG CACAACGCCAAGACCAAGCCTAGG GAAGAACAGTTCAACTCTACGTACC GGGTGGTGTCCGTGCTGACCGTGCT GCACCAGGACTGGCTGAACGGAAA GGAGTACAAGTGCAAAGTGTCAAA

			CAAGGGCCTCCCTTCATCCATCGAA AAGACCATCAGCAAGGCCAAGGGT CAACCTAGGGAGCCCCAGGTCTACA CTTTGCCGCCTAGCCAAGAAGAAAT GACTAAGAACCAAGTGTCCCTGACT TGCCTTGTCAAGGGCTTTTATCCGTC CGACATCGCCGTGGAGTGGGAGTCC AACGGACAACCGGAGAACAACTAC AAGACCACCCCACCGGTGCTCGATT CCGATGGCTCCTTCTTCCTGTACTCC CGGCTGACTGTGGACAAGTCAAGAT GGCAGGAGGGAAACGTGTTCTCCTG CTCCGTGATGCACGAAGCGCTGCAC AACCATTACACCCAGAAATCACTGT CACTTTCGCTGGGAAAA
SEQ ID 1971	QLQLQESGPGLVKPSQTLSLTCAISGDS VSSNSAAWNWIRQSPSRGLEWLGRTY YRSKWYNDYAVSVKSRITINPDTSKNQ FSLQLNSVTPEDTAVYYCAEGNGPFDP WGQGTLVTVSSASTKGPSVFPLAPCSR STSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTKTYTCNVDHKPSNTKVDK RVESKYGPPCPPCPAPEFLGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSQEDP EVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKC KVSNKGLPSSIEKTISKAKGQPREPQVY TLPPSQEEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGS FFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSLGK	SEQ ID 2079	CAGCTGCAGCTGCAGGAGTCGGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCAACAGTGC TGCTTGGAACTGGATCAGGCAGTCC CCATCGAGAGGCCTTGAGTGGCTGG GAAGGACATACTACAGGTCCAAGTG GTATAATGATTATGCAGTATCTGTG AAAAGTCGAATAACCATCAACCCAG ACACATCCAAGAACCAGTTCTCCCT GCAGCTGAACTCTGTGACTCCCGAG GACACGGCTGTGTATTACTGTGCAG AAGGCAATGGGCCGTTCGACCCCTG GGGCCAGGGAACCCTGGTGACCGTC TCCTCAGCATCCACCAAGGGGCCTT CCGTGTTCCCCCTGGCCCCTTGCTCC CGCTCGACCTCTGAATCCACCGCCG CACTCGGTTGCCTGGTCAAAGACTA CTTCCCCGAGCCCGTGACTGTCTCG TGGAACTCGGGCGCCCTCACATCCG GAGTGCATACCTTTCCCGCCGTGTT GCAGTCCAGCGGCCTGTACAGCCTG AGCTCCGTCGTGACAGTGCCGTCCT CCTCCCTTGGAACCAAGACCTATAC CTGCAACGTCGACCACAAGCCCTCC AACACCAAAGTGGACAAGCGCGTC GAATCCAAGTACGGCCCCCCTTGTC CGCCTTGTCCAGCCCCTGAGTTCCT GGGTGGTCCGTCCGTGTTCCTCTTCC CGCCCAAGCCGAAGGACACTCTGAT GATTTCACGCACCCCGGAAGTCACT TGCGTGGTCGTGGACGTGTCGCAGG AAGATCCCGAAGTGCAGTTCAATTG GTACGTGGATGGGGTCGAAGTGCAC AACGCCAAGACCAAGCCTAGGGAA GAACAGTTCAACTCTACGTACCGGG TGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGA GTACAAGTGCAAAGTGTCAAACAA

			GGGCCTCCCTTCATCCATCGAAAAG ACCATCAGCAAGGCCAAGGGTCAA CCTAGGGAGCCCCAGGTCTACACTT TGCCGCCTAGCCAAGAAGAAATGAC TAAGAACCAAGTGTCCCTGACTTGC CTTGTCAAGGGCTTTTATCCGTCCG ACATCGCCGTGGAGTGGGAGTCCAA CGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCC GATGGCTCCTTCTTCCTGTACTCCCG GCTGACTGTGGACAAGTCAAGATGG CAGGAGGGAAACGTGTTCTCCTGCT CCGTGATGCACGAAGCGCTGCACAA CCATTACACCCAGAAATCACTGTCA CTTTCGCTGGGAAAA
SEQ ID 1972	QITLKESGGGVVQPGRSLRLSCVASGF TFSTYPMHWVRQAPGKGLEWVAVISY DGRNEYYADSVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCATRDTPLVG VSIYWGQGTLVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTKTYTCNVDHKPSNTKV DKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQE DPEVQFNWYVDGVEVHNAKTKPREE QFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSLGK	SEQ ID 2080	CAGATCACCTTGAAGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGTAGCCTCT GGATTCACCTTCAGTACCTATCCCA TGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTT ATATCATATGATGGACGTAATGAAT ACTACGCAGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCC AAAAACACGCTGTATCTGCAAATGA ACAGTCTGCGAGCTGAAGACACGGC TGTCTATTATTGTGCGACTCGGGAT ACACCTTTGGTTGGGGTTTCGATAT ACTGGGGCCAGGGCACCCTGGTCAC CGTCTCCTCAGCATCCACCAAGGGG CCTTCCGTGTTCCCCCTGGCCCCTTG CTCCCGCTCGACCTCTGAATCCACC GCCGCACTCGGTTGCCTGGTCAAAG ACTACTTCCCCGAGCCCGTGACTGT CTCGTGGAACTCGGGCGCCCTCACA TCCGGAGTGCATACCTTTCCCGCCG TGTTGCAGTCCAGCGGCCTGTACAG CCTGAGCTCCGTCGTGACAGTGCCG TCCTCCTCCCTTGGAACCAAGACCT ATACCTGCAACGTCGACCACAAGCC CTCCAACACCAAAGTGGACAAGCGC GTCGAATCCAAGTACGGCCCCCCTT GTCCGCCTTGTCCAGCCCCTGAGTT CCTGGGTGGTCCGTCCGTGTTCCTCT TCCCGCCCAAGCCGAAGGACACTCT GATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGC AGGAAGATCCCGAAGTGCAGTTCAA TTGGTACGTGGATGGGGTCGAAGTG CACAACGCCAAGACCAAGCCTAGG GAAGAACAGTTCAACTCTACGTACC GGGTGGTGTCCGTGCTGACCGTGCT GCACCAGGACTGGCTGAACGGAAA GGAGTACAAGTGCAAAGTGTCAAA

			CAAGGGCCTCCCTTCATCCATCGAA AAGACCATCAGCAAGGCCAAGGGT CAACCTAGGGAGCCCCAGGTCTACA CTTTGCCGCCTAGCCAAGAAGAAAT GACTAAGAACCAAGTGTCCCTGACT TGCCTTGTCAAGGGCTTTTATCCGTC CGACATCGCCGTGGAGTGGGAGTCC AACGGACAACCGGAGAACAACTAC AAGACCACCCCACCGGTGCTCGATT CCGATGGCTCCTTCTTCCTGTACTCC CGGCTGACTGTGGACAAGTCAAGAT GGCAGGAGGGAAACGTGTTCTCCTG CTCCGTGATGCACGAAGCGCTGCAC AACCATTACACCCAGAAATCACTGT CACTTTCGCTGGGAAAA
SEQ ID 1973	QMQLVQSGGGLVKAGGSLRLSCSASG FTFSSYAMHWVRQAPGKGLEYVSAISS NGGSTYYADSVKGRFTISRDNSKNTLY LQMSSLRAEDTAVYYCVNRAGYGDY RHFQHWGQGTLVTVSSASTKGPSVFPL APCSRSTSESTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDV SQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKGLPSSIEKTISKAKGQPRE PQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCS VMHEALHNHYTQKSLSLSLGK	SEQ ID 2081	CAGATGCAGCTGGTGCAATCTGGGG GAGGCCTGGTCAAGGCTGGGGGGTC CCTGAGACTCTCCTGTTCAGCCTCTG GATTCACCTTCAGTAGCTATGCTAT GCACTGGGTCCGCCAGGCTCCAGGG AAGGGACTGGAATATGTTTCAGCTA TTAGTAGTAATGGGGGTAGCACATA CTACGCAGACTCAGTGAAGGGCAG ATTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTTCAAATGA GCAGTCTGAGAGCTGAGGACACGG CTGTGTATTACTGTGTGAATCGGGC GGGTTACGGTGACTACAGACACTTC CAGCACTGGGGCCAGGGCACCCTGG TCACCGTCTCCTCAGCATCCACCAA GGGGCCTTCCGTGTTCCCCCTGGCC CCTTGCTCCCGCTCGACCTCTGAATC CACCGCCGCACTCGGTTGCCTGGTC AAAGACTACTTCCCCGAGCCCGTGA CTGTCTCGTGGAACTCGGGCGCCCT CACATCCGGAGTGCATACCTTTCCC GCCGTGTTGCAGTCCAGCGGCCTGT ACAGCCTGAGCTCCGTCGTGACAGT GCCGTCCTCCTCCCTTGGAACCAAG ACCTATACCTGCAACGTCGACCACA AGCCCTCCAACACCAAAGTGGACAA GCGCGTCGAATCCAAGTACGGCCCC CCTTGTCCGCCTTGTCCAGCCCCTGA GTTCCTGGGTGGTCCGTCCGTGTTCC TCTTCCCGCCCAAGCCGAAGGACAC TCTGATGATTTCACGCACCCCGGAA GTCACTTGCGTGGTCGTGGACGTGT CGCAGGAAGATCCCGAAGTGCAGTT CAATTGGTACGTGGATGGGGTCGAA GTGCACAACGCCAAGACCAAGCCTA GGGAAGAACAGTTCAACTCTACGTA CCGGGTGGTGTCCGTGCTGACCGTG CTGCACCAGGACTGGCTGAACGGAA AGGAGTACAAGTGCAAAGTGTCAA

			ACAAGGGCCTCCCTTCATCCATCGA AAAGACCATCAGCAAGGCCAAGGG TCAACCTAGGGAGCCCCAGGTCTAC ACTTTGCCGCCTAGCCAAGAAGAAA TGACTAAGAACCAAGTGTCCCTGAC TTGCCTTGTCAAGGGCTTTTATCCGT CCGACATCGCCGTGGAGTGGGAGTC CAACGGACAACCGGAGAACAACTA CAAGACCACCCCACCGGTGCTCGAT TCCGATGGCTCCTTCTTCCTGTACTC CCGGCTGACTGTGGACAAGTCAAGA TGGCAGGAGGGAAACGTGTTCTCCT GCTCCGTGATGCACGAAGCGCTGCA CAACCATTACACCCAGAAATCACTG TCACTTTCGCTGGGAAAA
SEQ ID 1974	EVQLVQSGGGVVQPGGSLRLSCAASG FTFSSYGMHWVRQAPGKGLEWVAFIS YDGSNKYYADSVKGRFTISRDNSKNT LYLQMNSLRAEDTAVYYCATTGDRFQ EFDYWGQGTLVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTKTYTCNVDHKPSNTKV DKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQE DPEVQFNWYVDGVEVHNAKTKPREE QFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSLGK	SEQ ID 2082	GAGGTGCAGCTGGTGCAGTCTGGGG GAGGCGTGGTCCAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCGTCT GGATTCACCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCATTT ATATCATATGATGGAAGTAATAAAT ACTACGCAGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCCGAGGACACGG CCGTATATTACTGTGCGACAACAGG GGACCGCTTCCAAGAGTTTGACTAC TGGGGCCAGGGAACCCTGGTCACCG TCTCCTCAGCATCCACCAAGGGGCC TTCCGTGTTCCCCCTGGCCCCTTGCT CCCGCTCGACCTCTGAATCCACCGC CGCACTCGGTTGCCTGGTCAAAGAC TACTTCCCCGAGCCCGTGACTGTCT CGTGGAACTCGGGCGCCCTCACATC CGGAGTGCATACCTTTCCCGCCGTG TTGCAGTCCAGCGGCCTGTACAGCC TGAGCTCCGTCGTGACAGTGCCGTC CTCCTCCCTTGGAACCAAGACCTAT ACCTGCAACGTCGACCACAAGCCCT CCAACACCAAAGTGGACAAGCGCG TCGAATCCAAGTACGGCCCCCCTTG TCCGCCTTGTCCAGCCCCTGAGTTCC TGGGTGGTCCGTCCGTGTTCCTCTTC CCGCCCAAGCCGAAGGACACTCTGA TGATTTCACGCACCCCGGAAGTCAC TTGCGTGGTCGTGGACGTGTCGCAG GAAGATCCCGAAGTGCAGTTCAATT GGTACGTGGATGGGGTCGAAGTGCA CAACGCCAAGACCAAGCCTAGGGA AGAACAGTTCAACTCTACGTACCGG GTGGTGTCCGTGCTGACCGTGCTGC ACCAGGACTGGCTGAACGGAAAGG AGTACAAGTGCAAAGTGTCAAACA

			AGGGCCTCCCTTCATCCATCGAAAA GACCATCAGCAAGGCCAAGGGTCA ACCTAGGGAGCCCCAGGTCTACACT TTGCCGCCTAGCCAAGAAGAAATGA CTAAGAACCAAGTGTCCCTGACTTG CCTTGTCAAGGGCTTTTATCCGTCCG ACATCGCCGTGGAGTGGGAGTCCAA CGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCC GATGGCTCCTTCTTCCTGTACTCCCG GCTGACTGTGGACAAGTCAAGATGG CAGGAGGGAAACGTGTTCTCCTGCT CCGTGATGCACGAAGCGCTGCACAA CCATTACACCCAGAAATCACTGTCA CTTTCGCTGGGAAAA
SEQ ID 1975	QMQLVQSGGVLLQPGRSLRLSCTASG FTFAAYNINWFRQGPGGGLEWVGFIR ANADSGTTEYAASVKGRFFISRDDSRS TAYLQMTSLKTEDTAVYYCARDDRGR GDDFDYWGQGTLVTVSSASTKGPSVF PLAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSN TKVDKRVESKYGPPCPPCPAPEFLGGP SVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2083	CAGATGCAGCTGGTGCAGTCTGGGG GAGTCTTGCTTCAGCCAGGGCGGTC CCTGAGACTCTCCTGTACAGCTTCT GGATTCACCTTTGCTGCTTATAATAT CAACTGGTTCCGCCAGGGTCCTGGG GGGGGGCTGGAGTGGGTAGGTTTCA TTAGAGCCAACGCTGATAGTGGGAC AACAGAGTACGCCGCGTCTGTGAAA GGCAGATTCTTCATCTCAAGAGATG ATTCCAGAAGCACCGCCTACCTGCA AATGACTAGCCTTAAAACCGAGGAC ACAGCCGTTTATTACTGTGCCAGAG ATGATCGGGGTCGGGGAGATGACTT TGACTACTGGGGCCAGGGCACCCTG GTCACCGTCTCCTCAGCATCCACCA AGGGGCCTTCCGTGTTCCCCCTGGC CCCTTGCTCCCGCTCGACCTCTGAAT CCACCGCCGCACTCGGTTGCCTGGT CAAAGACTACTTCCCCGAGCCCGTG ACTGTCTCGTGGAACTCGGGCGCCC TCACATCCGGAGTGCATACCTTTCC CGCCGTGTTGCAGTCCAGCGGCCTG TACAGCCTGAGCTCCGTCGTGACAG TGCCGTCCTCCTCCCTTGGAACCAA GACCTATACCTGCAACGTCGACCAC AAGCCCTCCAACACCAAAGTGGACA AGCGCGTCGAATCCAAGTACGGCCC CCCTTGTCCGCCTTGTCCAGCCCCTG AGTTCCTGGGTGGTCCGTCCGTGTT CCTCTTCCCGCCCAAGCCGAAGGAC ACTCTGATGATTTCACGCACCCCGG AAGTCACTTGCGTGGTCGTGGACGT GTCGCAGGAAGATCCCGAAGTGCA GTTCAATTGGTACGTGGATGGGGTC GAAGTGCACAACGCCAAGACCAAG CCTAGGGAAGAACAGTTCAACTCTA CGTACCGGGTGGTGTCCGTGCTGAC CGTGCTGCACCAGGACTGGCTGAAC GGAAAGGAGTACAAGTGCAAAGTG

			TCAAACAAGGGCCTCCCTTCATCCA TCGAAAAGACCATCAGCAAGGCCA AGGGTCAACCTAGGGAGCCCCAGGT CTACACTTTGCCGCCTAGCCAAGAA GAAATGACTAAGAACCAAGTGTCCC TGACTTGCCTTGTCAAGGGCTTTTAT CCGTCCGACATCGCCGTGGAGTGGG AGTCCAACGGACAACCGGAGAACA ACTACAAGACCACCCCACCGGTGCT CGATTCCGATGGCTCCTTCTTCCTGT ACTCCCGGCTGACTGTGGACAAGTC AAGATGGCAGGAGGGAAACGTGTT CTCCTGCTCCGTGATGCACGAAGCG CTGCACAACCATTACACCCAGAAAT CACTGTCACTTTCGCTGGGAAAA
SEQ ID 1976	QVQLVQSGGGLVQPGGSLRLSCAASG FTFSSYGMTWVRQAPGKGLEWVSTIS GNGVGTYYPDSVKDRFTISRDSSKNTV YLQMNSLRAEDTAVYYCVKHGRAGIN WYFDLWGRGTLVTVSSASTKGPSVFP LAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSN TKVDKRVESKYGPPCPPCPAPEFLGGP SVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2084	CAGGTGCAGCTGGTGCAATCTGGGG GAGGCTTGGTACAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTTAGCAGCTATGGCA TGACGTGGGTCCGCCAGGCTCCAGG GAAGGGGCTGGAGTGGGTCTCAACT ATTAGTGGTAATGGTGTTGGCACAT ACTACCCAGACTCCGTGAAGGACCG GTTCACCATCTCCAGAGACAGTTCC AAGAACACGGTGTATCTGCAAATGA ACAGCCTGAGAGCCGAGGACACGG CCGTATATTACTGTGTGAAACATGG TAGGGCCGGAATAAACTGGTACTTC GATCTCTGGGGCCGTGGCACCCTGG TGACCGTCTCCTCAGCATCCACCAA GGGGCCTTCCGTGTTCCCCCTGGCC CCTTGCTCCCGCTCGACCTCTGAATC CACCGCCGCACTCGGTTGCCTGGTC AAAGACTACTTCCCCGAGCCCGTGA CTGTCTCGTGGAACTCGGGCGCCCT CACATCCGGAGTGCATACCTTTCCC GCCGTGTTGCAGTCCAGCGGCCTGT ACAGCCTGAGCTCCGTCGTGACAGT GCCGTCCTCCTCCCTTGGAACCAAG ACCTATACCTGCAACGTCGACCACA AGCCCTCCAACACCAAAGTGGACAA GCGCGTCGAATCCAAGTACGGCCCC CCTTGTCCGCCTTGTCCAGCCCCTGA GTTCCTGGGTGGTCCGTCCGTGTTCC TCTTCCCGCCCAAGCCGAAGGACAC TCTGATGATTTCACGCACCCCGGAA GTCACTTGCGTGGTCGTGGACGTGT CGCAGGAAGATCCCGAAGTGCAGTT CAATTGGTACGTGGATGGGGTCGAA GTGCACAACGCCAAGACCAAGCCTA GGGAAGAACAGTTCAACTCTACGTA CCGGGTGGTGTCCGTGCTGACCGTG CTGCACCAGGACTGGCTGAACGGAA AGGAGTACAAGTGCAAAGTGTCAA

			ACAAGGGCCTCCCTTCATCCATCGA AAAGACCATCAGCAAGGCCAAGGG TCAACCTAGGGAGCCCCAGGTCTAC ACTTTGCCGCCTAGCCAAGAAGAAA TGACTAAGAACCAAGTGTCCCTGAC TTGCCTTGTCAAGGGCTTTTATCCGT CCGACATCGCCGTGGAGTGGGAGTC CAACGGACAACCGGAGAACAACTA CAAGACCACCCCACCGGTGCTCGAT TCCGATGGCTCCTTCTTCCTGTACTC CCGGCTGACTGTGGACAAGTCAAGA TGGCAGGAGGGAAACGTGTTCTCCT GCTCCGTGATGCACGAAGCGCTGCA CAACCATTACACCCAGAAATCACTG TCACTTTCGCTGGGAAAA
SEQ ID 1977	QVQLQQSGPGLVKPSQTLSLTCAISGD SVSSNSAAWNWIRQSPSRGLEWLGRT YYRSKWYNDYAVSVKSRITINPDTSKN QFSLQLNSVTPEDTAVYYCARGGGLW AFDIWGQGTTVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTKTYTCNVDHKPSNTKV DKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQE DPEVQFNWYVDGVEVHNAKTKPREE QFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSLGK	SEQ ID 2085	CAGGTACAGCTGCAGCAGTCAGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCAACAGTGC TGCTTGGAACTGGATCAGGCAGTCC CCATCGAGAGGCCTTGAGTGGCTGG GAAGGACATACTACAGGTCCAAGTG GTATAATGATTATGCAGTATCTGTG AAAAGTCGAATAACCATCAACCCAG ACACATCCAAGAACCAGTTCTCCCT GCAGCTGAACTCTGTGACTCCCGAG GACACGGCTGTGTATTACTGTGCAA GAGGGGGAGGGCTTTGGGCTTTTGA TATCTGGGGCCAAGGGACCACGGTC ACCGTCTCCTCAGCATCCACCAAGG GGCCTTCCGTGTTCCCCCTGGCCCCT TGCTCCCGCTCGACCTCTGAATCCA CCGCCGCACTCGGTTGCCTGGTCAA AGACTACTTCCCCGAGCCCGTGACT GTCTCGTGGAACTCGGGCGCCCTCA CATCCGGAGTGCATACCTTTCCCGC CGTGTTGCAGTCCAGCGGCCTGTAC AGCCTGAGCTCCGTCGTGACAGTGC CGTCCTCCTCCCTTGGAACCAAGAC CTATACCTGCAACGTCGACCACAAG CCCTCCAACACCAAAGTGGACAAGC GCGTCGAATCCAAGTACGGCCCCCC TTGTCCGCCTTGTCCAGCCCCTGAGT TCCTGGGTGGTCCGTCCGTGTTCCTC TTCCCGCCCAAGCCGAAGGACACTC TGATGATTTCACGCACCCCGGAAGT CACTTGCGTGGTCGTGGACGTGTCG CAGGAAGATCCCGAAGTGCAGTTCA ATTGGTACGTGGATGGGGTCGAAGT GCACAACGCCAAGACCAAGCCTAG GGAAGAACAGTTCAACTCTACGTAC CGGGTGGTGTCCGTGCTGACCGTGC TGCACCAGGACTGGCTGAACGGAA AGGAGTACAAGTGCAAAGTGTCAA

			ACAAGGGCCTCCCTTCATCCATCGA AAAGACCATCAGCAAGGCCAAGGG TCAACCTAGGGAGCCCCAGGTCTAC ACTTTGCCGCCTAGCCAAGAAGAAA TGACTAAGAACCAAGTGTCCCTGAC TTGCCTTGTCAAGGGCTTTTATCCGT CCGACATCGCCGTGGAGTGGGAGTC CAACGGACAACCGGAGAACAACTA CAAGACCACCCCACCGGTGCTCGAT TCCGATGGCTCCTTCTTCCTGTACTC CCGGCTGACTGTGGACAAGTCAAGA TGGCAGGAGGGAAACGTGTTCTCCT GCTCCGTGATGCACGAAGCGCTGCA CAACCATTACACCCAGAAATCACTG TCACTTTCGCTGGGAAAA
SEQ ID 1978	EVQLVQSGAEVKKPGASVKVSCKASG YTFTGYYMHWVRQAPGQGLEWMGW INPNSGGTNYAQKFQGRVTMTRDTSIS TAYMELSRLRSDDTAVYYCARDKIGS CPYWGQGTLVTVSSASTKGPSVFPLAP CSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTKTYTCNVDHKPSNTKV DKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQE DPEVQFNWYVDGVEVHNAKTKPREE QFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSLGK	SEQ ID 2086	GAGGTCCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTCTCCTGCAAGGCTTCT GGATACACCTTCACCGGCTACTATA TGCACTGGGTGCGACAGGCCCCTGG ACAAGGGCTTGAGTGGATGGGATG GATCAACCCTAACAGTGGTGGCACA AACTATGCACAGAAGTTTCAGGGCA GGGTCACCATGACCAGGGACACGTC CATCAGCACAGCCTACATGGAGCTG AGCAGGCTGAGATCTGACGACACG GCCGTGTATTACTGTGCGAGAGACA AGATCGGCAGCTGTCCTTACTGGGG CCAGGGAACCCTGGTCACCGTCTCC TCAGCATCCACCAAGGGGCCTTCCG TGTTCCCCCTGGCCCCTTGCTCCCGC TCGACCTCTGAATCCACCGCCGCAC TCGGTTGCCTGGTCAAAGACTACTT CCCCGAGCCCGTGACTGTCTCGTGG AACTCGGGCGCCCTCACATCCGGAG TGCATACCTTTCCCGCCGTGTTGCA GTCCAGCGGCCTGTACAGCCTGAGC TCCGTCGTGACAGTGCCGTCCTCCT CCCTTGGAACCAAGACCTATACCTG CAACGTCGACCACAAGCCCTCCAAC ACCAAAGTGGACAAGCGCGTCGAA TCCAAGTACGGCCCCCCTTGTCCGC CTTGTCCAGCCCCTGAGTTCCTGGG TGGTCCGTCCGTGTTCCTCTTCCCGC CCAAGCCGAAGGACACTCTGATGAT TTCACGCACCCCGGAAGTCACTTGC GTGGTCGTGGACGTGTCGCAGGAAG ATCCCGAAGTGCAGTTCAATTGGTA CGTGGATGGGGTCGAAGTGCACAAC GCCAAGACCAAGCCTAGGGAAGAA CAGTTCAACTCTACGTACCGGGTGG TGTCCGTGCTGACCGTGCTGCACCA GGACTGGCTGAACGGAAAGGAGTA CAAGTGCAAAGTGTCAAACAAGGG

			CCTCCCTTCATCCATCGAAAAGACC ATCAGCAAGGCCAAGGGTCAACCTA GGGAGCCCCAGGTCTACACTTTGCC GCCTAGCCAAGAAGAAATGACTAA GAACCAAGTGTCCCTGACTTGCCTT GTCAAGGGCTTTTATCCGTCCGACA TCGCCGTGGAGTGGGAGTCCAACGG ACAACCGGAGAACAACTACAAGAC CACCCCACCGGTGCTCGATTCCGAT GGCTCCTTCTTCCTGTACTCCCGGCT GACTGTGGACAAGTCAAGATGGCA GGAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACT TTCGCTGGGAAAA
SEQ ID 1979	QVTLKESGPTLVKPTQTLTLTCTFSGFS LSTSGVGVGWIRQPPGKALEWLALIY WDDDKRYSPSLKSRLTITKDTSKNQV VLTMTNMDPVDTATYYCAHRPDSSSQ CFDYWGQGTLVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTKTYTCNVDHKPSNTKV DKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQE DPEVQFNWYVDGVEVHNAKTKPREE QFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSLGK	SEQ ID 2087	CAGGTCACCTTGAAGGAGTCTGGTC CTACGCTGGTGAAACCCACACAGAC CCTCACGCTGACCTGCACCTTCTCTG GGTTCTCACTCAGCACTAGTGGAGT GGGTGTGGGCTGGATCCGTCAGCCC CCAGGAAAGGCCCTGGAGTGGCTTG CACTCATTTATTGGGATGATGATAA GCGCTACAGCCCATCTCTGAAGAGC AGGCTCACCATCACCAAGGACACCT CCAAAAACCAGGTGGTCCTTACAAT GACCAACATGGACCCTGTGGACACA GCCACATATTACTGTGCACACAGAC CGGATAGCAGCAGTCAATGTTTTGA CTACTGGGGCCAGGGAACCCTGGTC ACCGTCTCCTCAGCATCCACCAAGG GGCCTTCCGTGTTCCCCCTGGCCCCT TGCTCCCGCTCGACCTCTGAATCCA CCGCCGCACTCGGTTGCCTGGTCAA AGACTACTTCCCCGAGCCCGTGACT GTCTCGTGGAACTCGGGCGCCCTCA CATCCGGAGTGCATACCTTTCCCGC CGTGTTGCAGTCCAGCGGCCTGTAC AGCCTGAGCTCCGTCGTGACAGTGC CGTCCTCCTCCCTTGGAACCAAGAC CTATACCTGCAACGTCGACCACAAG CCCTCCAACACCAAAGTGGACAAGC GCGTCGAATCCAAGTACGGCCCCCC TTGTCCGCCTTGTCCAGCCCCTGAGT TCCTGGGTGGTCCGTCCGTGTTCCTC TTCCCGCCCAAGCCGAAGGACACTC TGATGATTTCACGCACCCCGGAAGT CACTTGCGTGGTCGTGGACGTGTCG CAGGAAGATCCCGAAGTGCAGTTCA ATTGGTACGTGGATGGGGTCGAAGT GCACAACGCCAAGACCAAGCCTAG GGAAGAACAGTTCAACTCTACGTAC CGGGTGGTGTCCGTGCTGACCGTGC TGCACCAGGACTGGCTGAACGGAA AGGAGTACAAGTGCAAAGTGTCAA

			ACAAGGGCCTCCCTTCATCCATCGA AAAGACCATCAGCAAGGCCAAGGG TCAACCTAGGGAGCCCCAGGTCTAC ACTTTGCCGCCTAGCCAAGAAGAAA TGACTAAGAACCAAGTGTCCCTGAC TTGCCTTGTCAAGGGCTTTTATCCGT CCGACATCGCCGTGGAGTGGGAGTC CAACGGACAACCGGAGAACAACTA CAAGACCACCCCACCGGTGCTCGAT TCCGATGGCTCCTTCTTCCTGTACTC CCGGCTGACTGTGGACAAGTCAAGA TGGCAGGAGGGAAACGTGTTCTCCT GCTCCGTGATGCACGAAGCGCTGCA CAACCATTACACCCAGAAATCACTG TCACTTTCGCTGGGAAAA
SEQ ID 1980	QVTLKESGGGVVQPGRSLRLSCAASGF TFSSYAMHWVRQAPGKGLEWVAVISY DGSNKYYADSVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCARSSGWSLP EDYWGQGTLVTVSSASTKGPSVFPLAP CSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTKTYTCNVDHKPSNTKV DKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQE DPEVQFNWYVDGVEVHNAKTKPREE QFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSLGK	SEQ ID 2088	CAGGTCACCTTGAAGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTCAGTAGCTATGCTA TGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTT ATATCATATGATGGAAGTAATAAAT ACTACGCAGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCTGAGGACACGG CTGTGTATTACTGTGCGAGAAGCAG TGGCTGGTCACTGCCTGAAGACTAC TGGGGCCAGGGAACCCTGGTCACCG TCTCCTCAGCATCCACCAAGGGGCC TTCCGTGTTCCCCCTGGCCCCTTGCT CCCGCTCGACCTCTGAATCCACCGC CGCACTCGGTTGCCTGGTCAAAGAC TACTTCCCCGAGCCCGTGACTGTCT CGTGGAACTCGGGCGCCCTCACATC CGGAGTGCATACCTTTCCCGCCGTG TTGCAGTCCAGCGGCCTGTACAGCC TGAGCTCCGTCGTGACAGTGCCGTC CTCCTCCCTTGGAACCAAGACCTAT ACCTGCAACGTCGACCACAAGCCCT CCAACACCAAAGTGGACAAGCGCG TCGAATCCAAGTACGGCCCCCCTTG TCCGCCTTGTCCAGCCCCTGAGTTCC TGGGTGGTCCGTCCGTGTTCCTCTTC CCGCCCAAGCCGAAGGACACTCTGA TGATTTCACGCACCCCGGAAGTCAC TTGCGTGGTCGTGGACGTGTCGCAG GAAGATCCCGAAGTGCAGTTCAATT GGTACGTGGATGGGGTCGAAGTGCA CAACGCCAAGACCAAGCCTAGGGA AGAACAGTTCAACTCTACGTACCGG GTGGTGTCCGTGCTGACCGTGCTGC ACCAGGACTGGCTGAACGGAAAGG AGTACAAGTGCAAAGTGTCAAACA

			AGGGCCTCCCTTCATCCATCGAAAA GACCATCAGCAAGGCCAAGGGTCA ACCTAGGGAGCCCCAGGTCTACACT TTGCCGCCTAGCCAAGAAGAAATGA CTAAGAACCAAGTGTCCCTGACTTG CCTTGTCAAGGGCTTTTATCCGTCCG ACATCGCCGTGGAGTGGGAGTCCAA CGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCC GATGGCTCCTTCTTCCTGTACTCCCG GCTGACTGTGGACAAGTCAAGATGG CAGGAGGGAAACGTGTTCTCCTGCT CCGTGATGCACGAAGCGCTGCACAA CCATTACACCCAGAAATCACTGTCA CTTTCGCTGGGAAAA
SEQ ID 1981	QVQLVQSGAEVKKPGASVKVSCKVSG YTLTELSMHWVRQAPGKGLEWMGGF DPEDGETIYAQKFQGRVTMTEDTSTDT AYMELSSLRSEDTAVYYCATDVNPEL LGAGFDYWGQGTLVTVSSASTKGPSV FPLAPCSRSTSESTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTKTYTCNVDHKP SNTKVDKRVESKYGPPCPPCPAPEFLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKT KPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKGQ PREPQVYTLPPSQEEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSRLTVDKSRWQEGNV FSCSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2089	CAGGTCCAGCTGGTACAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTCTCCTGCAAGGTTTCC GGATACACCCTCACTGAATTATCCA TGCACTGGGTGCGACAGGCTCCTGG AAAAGGGCTTGAGTGGATGGGAGG TTTTGATCCTGAAGATGGTGAAACA ATCTACGCACAGAAGTTCCAGGGCA GAGTCACCATGACCGAGGACACATC TACAGACACAGCCTACATGGAGCTG AGCAGCCTGAGATCTGAGGACACG GCCGTGTATTACTGTGCAACGGATG TGAACCCGGAGCTACTGGGGGCGG GATTTGACTACTGGGGCCAGGGCAC CCTGGTCACCGTCTCCTCAGCATCC ACCAAGGGGCCTTCCGTGTTCCCCC TGGCCCCTTGCTCCCGCTCGACCTCT GAATCCACCGCCGCACTCGGTTGCC TGGTCAAAGACTACTTCCCCGAGCC CGTGACTGTCTCGTGGAACTCGGGC GCCCTCACATCCGGAGTGCATACCT TTCCCGCCGTGTTGCAGTCCAGCGG CCTGTACAGCCTGAGCTCCGTCGTG ACAGTGCCGTCCTCCTCCCTTGGAA CCAAGACCTATACCTGCAACGTCGA CCACAAGCCCTCCAACACCAAAGTG GACAAGCGCGTCGAATCCAAGTACG GCCCCCCTTGTCCGCCTTGTCCAGCC CCTGAGTTCCTGGGTGGTCCGTCCG TGTTCCTCTTCCCGCCCAAGCCGAA GGACACTCTGATGATTTCACGCACC CCGGAAGTCACTTGCGTGGTCGTGG ACGTGTCGCAGGAAGATCCCGAAGT GCAGTTCAATTGGTACGTGGATGGG GTCGAAGTGCACAACGCCAAGACC AAGCCTAGGGAAGAACAGTTCAACT CTACGTACCGGGTGGTGTCCGTGCT GACCGTGCTGCACCAGGACTGGCTG AACGGAAAGGAGTACAAGTGCAAA

			GTGTCAAACAAGGGCCTCCCTTCAT CCATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTACACTTTGCCGCCTAGCCAA GAAGAAATGACTAAGAACCAAGTG TCCCTGACTTGCCTTGTCAAGGGCTT TTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCCGGCTGACTGTGGACA AGTCAAGATGGCAGGAGGGAAACG TGTTCTCCTGCTCCGTGATGCACGA AGCGCTGCACAACCATTACACCCAG AAATCACTGTCACTTTCGCTGGGAA AA
SEQ ID 1982	QVTLKESGGGLVQPGGSLRLSCAASGF TFSDQYMDWVRQAPGKGLEWVGRVR NKANSYTTEYAASVKGRFTISRDDSKN SLYLQMNSLNTEDTAMYFCASSLNSG GYRCFHHWGQGTLVTVSSASTKGPSV FPLAPCSRSTSESTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTKTYTCNVDHKP SNTKVDKRVESKYGPPCPPCPAPEFLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKT KPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKGQ PREPQVYTLPPSQEEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSRLTVDKSRWQEGNV FSCSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2090	CAGGTCACCTTGAAGGAGTCTGGGG GAGGCTTGGTCCAGCCTGGAGGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTCAGTGACCAGTACA TGGACTGGGTCCGCCAGGCTCCAGG GAAGGGGCTGGAGTGGGTTGGCCGT GTTAGAAACAAAGCTAACAGTTACA CCACAGAATACGCCGCGTCTGTGAA AGGCAGATTCACCATCTCAAGAGAT GATTCAAAGAACTCACTGTATCTGC AAATGAATAGTCTGAACACCGAGG ACACGGCCATGTATTTCTGTGCTAG TAGTCTCAATAGTGGGGGCTACCGA TGCTTCCATCACTGGGGCCAGGGCA CCCTGGTGACCGTCTCCTCAGCATC CACCAAGGGGCCTTCCGTGTTCCCC CTGGCCCCTTGCTCCCGCTCGACCTC TGAATCCACCGCCGCACTCGGTTGC CTGGTCAAAGACTACTTCCCCGAGC CCGTGACTGTCTCGTGGAACTCGGG CGCCCTCACATCCGGAGTGCATACC TTTCCCGCCGTGTTGCAGTCCAGCG GCCTGTACAGCCTGAGCTCCGTCGT GACAGTGCCGTCCTCCTCCCTTGGA ACCAAGACCTATACCTGCAACGTCG ACCACAAGCCCTCCAACACCAAAGT GGACAAGCGCGTCGAATCCAAGTAC GGCCCCCCTTGTCCGCCTTGTCCAG CCCCTGAGTTCCTGGGTGGTCCGTC CGTGTTCCTCTTCCCGCCCAAGCCG AAGGACACTCTGATGATTTCACGCA CCCCGGAAGTCACTTGCGTGGTCGT GGACGTGTCGCAGGAAGATCCCGA AGTGCAGTTCAATTGGTACGTGGAT GGGGTCGAAGTGCACAACGCCAAG ACCAAGCCTAGGGAAGAACAGTTC AACTCTACGTACCGGGTGGTGTCCG TGCTGACCGTGCTGCACCAGGACTG GCTGAACGGAAAGGAGTACAAGTG

			CAAAGTGTCAAACAAGGGCCTCCCT TCATCCATCGAAAAGACCATCAGCA AGGCCAAGGGTCAACCTAGGGAGC CCCAGGTCTACACTTTGCCGCCTAG CCAAGAAGAAATGACTAAGAACCA AGTGTCCCTGACTTGCCTTGTCAAG GGCTTTTATCCGTCCGACATCGCCG TGGAGTGGGAGTCCAACGGACAAC CGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTC CTTCTTCCTGTACTCCCGGCTGACTG TGGACAAGTCAAGATGGCAGGAGG GAAACGTGTTCTCCTGCTCCGTGAT GCACGAAGCGCTGCACAACCATTAC ACCCAGAAATCACTGTCACTTTCGC TGGGAAAA
SEQ ID 1983	QVQLVQSGGGLVQPGGSLRLSCSASGF TFSSYAMHWVRQAPGKGLEYVSAISS NGGSTYYADSVKGRFTISRDNSKNTLY LQMSSLRAEDTAVYYCVKAPRGVVPA AMRGGYWGQGTLVTVSSASTKGPSVF PLAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSN TKVDKRVESKYGPPCPPCPAPEFLGGP SVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2091	CAGGTCCAGCTGGTGCAGTCTGGGG GAGGCTTGGTCCAGCCTGGGGGGTC CCTGAGACTCTCCTGTTCAGCCTCTG GATTCACCTTCAGTAGCTATGCTAT GCACTGGGTCCGCCAGGCTCCAGGG AAGGGACTGGAATATGTTTCAGCTA TTAGTAGTAATGGGGGTAGCACATA CTACGCAGACTCAGTGAAGGGCAG ATTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTTCAAATGA GCAGTCTGAGAGCTGAGGACACGG CTGTGTATTACTGTGTGAAAGCGCC GAGGGGTGTAGTACCAGCTGCTATG CGGGGGGGCTACTGGGGCCAGGGA ACCCTGGTCACCGTCTCCTCAGCAT CCACCAAGGGGCCTTCCGTGTTCCC CCTGGCCCCTTGCTCCCGCTCGACCT CTGAATCCACCGCCGCACTCGGTTG CCTGGTCAAAGACTACTTCCCCGAG CCCGTGACTGTCTCGTGGAACTCGG GCGCCCTCACATCCGGAGTGCATAC CTTTCCCGCCGTGTTGCAGTCCAGC GGCCTGTACAGCCTGAGCTCCGTCG TGACAGTGCCGTCCTCCTCCCTTGG AACCAAGACCTATACCTGCAACGTC GACCACAAGCCCTCCAACACCAAAG TGGACAAGCGCGTCGAATCCAAGTA CGGCCCCCCTTGTCCGCCTTGTCCA GCCCCTGAGTTCCTGGGTGGTCCGT CCGTGTTCCTCTTCCCGCCCAAGCC GAAGGACACTCTGATGATTTCACGC ACCCCGGAAGTCACTTGCGTGGTCG TGGACGTGTCGCAGGAAGATCCCGA AGTGCAGTTCAATTGGTACGTGGAT GGGGTCGAAGTGCACAACGCCAAG ACCAAGCCTAGGGAAGAACAGTTC AACTCTACGTACCGGGTGGTGTCCG TGCTGACCGTGCTGCACCAGGACTG GCTGAACGGAAAGGAGTACAAGTG

			CAAAGTGTCAAACAAGGGCCTCCCT TCATCCATCGAAAAGACCATCAGCA AGGCCAAGGGTCAACCTAGGGAGC CCCAGGTCTACACTTTGCCGCCTAG CCAAGAAGAAATGACTAAGAACCA AGTGTCCCTGACTTGCCTTGTCAAG GGCTTTTATCCGTCCGACATCGCCG TGGAGTGGGAGTCCAACGGACAAC CGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTC CTTCTTCCTGTACTCCCGGCTGACTG TGGACAAGTCAAGATGGCAGGAGG GAAACGTGTTCTCCTGCTCCGTGAT GCACGAAGCGCTGCACAACCATTAC ACCCAGAAATCACTGTCACTTTCGC TGGGAAAA
SEQ ID 1984	QVQLQESGGGLVQPGRSLRLSCTASGF TFGDYAMSWFRQAPGKGLEWVGFIRS KAYGGTTEYAASVKGRFTISRDDSKSI AYLQMNSLKTEDTAVYYCTRLVGNSG SYYPFGYWGQGTLVTVSSASTKGPSVF PLAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSN TKVDKRVESKYGPPCPPCPAPEFLGGP SVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2092	CAGGTGCAGCTGCAGGAGTCGGGG GGAGGCTTGGTACAGCCAGGGCGGT CCCTGAGACTCTCCTGTACAGCTTCT GGATTCACCTTTGGTGATTATGCTAT GAGCTGGTTCCGCCAGGCTCCAGGG AAGGGGCTGGAGTGGGTAGGTTTCA TTAGAAGCAAAGCTTATGGTGGGAC AACAGAATACGCCGCGTCTGTGAAA GGCAGATTCACCATCTCAAGAGATG ATTCCAAAAGCATCGCCTATCTGCA AATGAACAGCCTGAAAACCGAGGA CACAGCCGTGTATTACTGTACTAGA TTGGTGGGCAATAGTGGGAGCTACT ATCCGTTTGGGTACTGGGGCCAGGG AACCCTGGTGACCGTCTCCTCAGCA TCCACCAAGGGGCCTTCCGTGTTCC CCCTGGCCCCTTGCTCCCGCTCGAC CTCTGAATCCACCGCCGCACTCGGT TGCCTGGTCAAAGACTACTTCCCCG AGCCCGTGACTGTCTCGTGGAACTC GGGCGCCCTCACATCCGGAGTGCAT ACCTTTCCCGCCGTGTTGCAGTCCA GCGGCCTGTACAGCCTGAGCTCCGT CGTGACAGTGCCGTCCTCCTCCCTT GGAACCAAGACCTATACCTGCAACG TCGACCACAAGCCCTCCAACACCAA AGTGGACAAGCGCGTCGAATCCAA GTACGGCCCCCCTTGTCCGCCTTGTC CAGCCCCTGAGTTCCTGGGTGGTCC GTCCGTGTTCCTCTTCCCGCCCAAGC CGAAGGACACTCTGATGATTTCACG CACCCCGGAAGTCACTTGCGTGGTC GTGGACGTGTCGCAGGAAGATCCCG AAGTGCAGTTCAATTGGTACGTGGA TGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTT CAACTCTACGTACCGGGTGGTGTCC GTGCTGACCGTGCTGCACCAGGACT GGCTGAACGGAAAGGAGTACAAGT

			GCAAAGTGTCAAACAAGGGCCTCCC TTCATCCATCGAAAAGACCATCAGC AAGGCCAAGGGTCAACCTAGGGAG CCCCAGGTCTACACTTTGCCGCCTA GCCAAGAAGAAATGACTAAGAACC AAGTGTCCCTGACTTGCCTTGTCAA GGGCTTTTATCCGTCCGACATCGCC GTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACC CCACCGGTGCTCGATTCCGATGGCT CCTTCTTCCTGTACTCCCGGCTGACT GTGGACAAGTCAAGATGGCAGGAG GGAAACGTGTTCTCCTGCTCCGTGA TGCACGAAGCGCTGCACAACCATTA CACCCAGAAATCACTGTCACTTTCG CTGGGAAAA
SEQ ID 1985	QVQLQQWGAGLLKPSETLSLTCAVYG GSFSGYYWSWIRQPPGKGLEWIGEINH SGSTNYNPSLKSRVTISVDTSKNQFSLK LSSVTAADTAVYYCARGRSLPYRGLA PRSFGGYYFDYWGQGTLVTVSSASTK GPSVFPLAPCSRSTSESTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSSLGTKTYTCNV DHKPSNTKVDKRVESKYGPPCPPCPAP EFLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSQEDPEVQFNWYVDGVEVH NAKTKPREEQFNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKGLPSSIEKTISK AKGQPREPQVYTLPPSQEEMTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSRLTVDKSRWQ EGNVFSCSVMHEALHNHYTQKSLSLS LGK	SEQ ID 2093	CAGGTGCAGCTACAGCAGTGGGGC GCAGGACTGTTGAAGCCTTCGGAGA CCCTGTCCCTCACCTGCGCTGTCTAT GGTGGGTCCTTCAGTGGTTACTACT GGAGCTGGATCCGCCAGCCCCCAGG GAAGGGGCTGGAGTGGATTGGGGA AATCAATCATAGTGGAAGCACCAAC TACAACCCGTCCCTCAAGAGTCGAG TCACCATATCAGTAGACACGTCCAA GAACCAGTTCTCCCTGAAGCTGAGC TCGGTGACCGCCGCGGACACGGCTG TGTATTACTGTGCGAGAGGCCGGTC CCTTCCCTACCGGGGGTTGGCTCCT AGATCTTTCGGAGGATACTACTTTG ACTACTGGGGCCAGGGAACCCTGGT CACCGTCTCCTCAGCATCCACCAAG GGGCCTTCCGTGTTCCCCCTGGCCC CTTGCTCCCGCTCGACCTCTGAATCC ACCGCCGCACTCGGTTGCCTGGTCA AAGACTACTTCCCCGAGCCCGTGAC TGTCTCGTGGAACTCGGGCGCCCTC ACATCCGGAGTGCATACCTTTCCCG CCGTGTTGCAGTCCAGCGGCCTGTA CAGCCTGAGCTCCGTCGTGACAGTG CCGTCCTCCTCCCTTGGAACCAAGA CCTATACCTGCAACGTCGACCACAA GCCCTCCAACACCAAAGTGGACAAG CGCGTCGAATCCAAGTACGGCCCCC CTTGTCCGCCTTGTCCAGCCCCTGA GTTCCTGGGTGGTCCGTCCGTGTTCC TCTTCCCGCCCAAGCCGAAGGACAC TCTGATGATTTCACGCACCCCGGAA GTCACTTGCGTGGTCGTGGACGTGT CGCAGGAAGATCCCGAAGTGCAGTT CAATTGGTACGTGGATGGGGTCGAA GTGCACAACGCCAAGACCAAGCCTA GGGAAGAACAGTTCAACTCTACGTA CCGGGTGGTGTCCGTGCTGACCGTG

			CTGCACCAGGACTGGCTGAACGGAA AGGAGTACAAGTGCAAAGTGTCAA ACAAGGGCCTCCCTTCATCCATCGA AAAGACCATCAGCAAGGCCAAGGG TCAACCTAGGGAGCCCCAGGTCTAC ACTTTGCCGCCTAGCCAAGAAGAAA TGACTAAGAACCAAGTGTCCCTGAC TTGCCTTGTCAAGGGCTTTTATCCGT CCGACATCGCCGTGGAGTGGGAGTC CAACGGACAACCGGAGAACAACTA CAAGACCACCCCACCGGTGCTCGAT TCCGATGGCTCCTTCTTCCTGTACTC CCGGCTGACTGTGGACAAGTCAAGA TGGCAGGAGGGAAACGTGTTCTCCT GCTCCGTGATGCACGAAGCGCTGCA CAACCATTACACCCAGAAATCACTG TCACTTTCGCTGGGAAAA
SEQ ID 1986	QVQLQESGGGLVRPGGSLRLSCGDSGF NFSGYEMNWVRQAPGKGLEWVSYVS TSGSTRYYADSVKGRFTISRDNAKNTL YLQMNSLRVEDTAVYYCARGRTHWG PQDFDYWGQGTLVTVSSASTKGPSVFP LAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSN TKVDKRVESKYGPPCPPCPAPEFLGGP SVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2094	CAGGTGCAGCTGCAGGAGTCGGGG GGAGGCTTGGTACGGCCTGGAGGGT CCCTGAGACTCTCCTGTGGAGACTC TGGATTCAACTTCAGTGGATATGAA ATGAACTGGGTCCGCCAGGCTCCAG GGAAGGGGCTGGAGTGGGTTTCATA CGTCAGTACTAGTGGTAGTACCAGA TACTACGCAGACTCTGTGAAGGGCC GATTTACCATCTCCAGAGACAACGC CAAGAACACCCTGTATTTGCAAATG AACAGTCTGAGAGTCGAGGACACG GCTGTGTATTACTGTGCAAGAGGAC GGACTCACTGGGGCCCCCAGGACTT TGACTACTGGGGCCAGGGAACCCTG GTCACCGTCTCCTCAGCATCCACCA AGGGGCCTTCCGTGTTCCCCCTGGC CCCTTGCTCCCGCTCGACCTCTGAAT CCACCGCCGCACTCGGTTGCCTGGT CAAAGACTACTTCCCCGAGCCCGTG ACTGTCTCGTGGAACTCGGGCGCCC TCACATCCGGAGTGCATACCTTTCC CGCCGTGTTGCAGTCCAGCGGCCTG TACAGCCTGAGCTCCGTCGTGACAG TGCCGTCCTCCTCCCTTGGAACCAA GACCTATACCTGCAACGTCGACCAC AAGCCCTCCAACACCAAAGTGGACA AGCGCGTCGAATCCAAGTACGGCCC CCCTTGTCCGCCTTGTCCAGCCCCTG AGTTCCTGGGTGGTCCGTCCGTGTT CCTCTTCCCGCCCAAGCCGAAGGAC ACTCTGATGATTTCACGCACCCCGG AAGTCACTTGCGTGGTCGTGGACGT GTCGCAGGAAGATCCCGAAGTGCA GTTCAATTGGTACGTGGATGGGGTC GAAGTGCACAACGCCAAGACCAAG CCTAGGGAAGAACAGTTCAACTCTA CGTACCGGGTGGTGTCCGTGCTGAC CGTGCTGCACCAGGACTGGCTGAAC

			GGAAAGGAGTACAAGTGCAAAGTG TCAAACAAGGGCCTCCCTTCATCCA TCGAAAAGACCATCAGCAAGGCCA AGGGTCAACCTAGGGAGCCCCAGGT CTACACTTTGCCGCCTAGCCAAGAA GAAATGACTAAGAACCAAGTGTCCC TGACTTGCCTTGTCAAGGGCTTTTAT CCGTCCGACATCGCCGTGGAGTGGG AGTCCAACGGACAACCGGAGAACA ACTACAAGACCACCCCACCGGTGCT CGATTCCGATGGCTCCTTCTTCCTGT ACTCCCGGCTGACTGTGGACAAGTC AAGATGGCAGGAGGGAAACGTGTT CTCCTGCTCCGTGATGCACGAAGCG CTGCACAACCATTACACCCAGAAAT CACTGTCACTTTCGCTGGGAAAA
SEQ ID 1987	QVQLQESGGGLVQPGGSLRLSCAASG FTFSSYAMSWVRQAPGKGLEWVSAIS GSGGSTYYADSVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCAKGGMYYY GSGSSYFDYWGQGTLVTVSSASTKGPS VFPLAPCSRSTSESTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTKTYTCNVDHKP SNTKVDKRVESKYGPPCPPCPAPEFLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKT KPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKGQ PREPQVYTLPPSQEEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSRLTVDKSRWQEGNV FSCSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2095	CAGGTGCAGCTGCAGGAGTCGGGG GGAGGCTTGGTACAGCCTGGGGGGT CCCTGAGACTCTCCTGTGCAGCCTC TGGATTCACCTTTAGCAGCTATGCC ATGAGCTGGGTCCGCCAGGCTCCAG GGAAGGGGCTGGAGTGGGTCTCAG CTATTAGTGGTAGTGGTGGTAGCAC ATACTACGCAGACTCCGTGAAGGGC CGGTTCACCATCTCCAGAGACAATT CCAAGAACACGCTGTATCTGCAAAT GAACAGCCTGAGAGCCGAGGACAC GGCCGTATATTACTGTGCGAAAGGA GGAATGTATTACTATGGTTCGGGGA GCTCGTACTTTGACTACTGGGGCCA GGGAACCCTGGTGACCGTCTCCTCA GCATCCACCAAGGGGCCTTCCGTGT TCCCCCTGGCCCCTTGCTCCCGCTCG ACCTCTGAATCCACCGCCGCACTCG GTTGCCTGGTCAAAGACTACTTCCC CGAGCCCGTGACTGTCTCGTGGAAC TCGGGCGCCCTCACATCCGGAGTGC ATACCTTTCCCGCCGTGTTGCAGTCC AGCGGCCTGTACAGCCTGAGCTCCG TCGTGACAGTGCCGTCCTCCTCCCTT GGAACCAAGACCTATACCTGCAACG TCGACCACAAGCCCTCCAACACCAA AGTGGACAAGCGCGTCGAATCCAA GTACGGCCCCCCTTGTCCGCCTTGTC CAGCCCCTGAGTTCCTGGGTGGTCC GTCCGTGTTCCTCTTCCCGCCCAAGC CGAAGGACACTCTGATGATTTCACG CACCCCGGAAGTCACTTGCGTGGTC GTGGACGTGTCGCAGGAAGATCCCG AAGTGCAGTTCAATTGGTACGTGGA TGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTT CAACTCTACGTACCGGGTGGTGTCC GTGCTGACCGTGCTGCACCAGGACT GGCTGAACGGAAAGGAGTACAAGT

			GCAAAGTGTCAAACAAGGGCCTCCC TTCATCCATCGAAAAGACCATCAGC AAGGCCAAGGGTCAACCTAGGGAG CCCCAGGTCTACACTTTGCCGCCTA GCCAAGAAGAAATGACTAAGAACC AAGTGTCCCTGACTTGCCTTGTCAA GGGCTTTTATCCGTCCGACATCGCC GTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACC CCACCGGTGCTCGATTCCGATGGCT CCTTCTTCCTGTACTCCCGGCTGACT GTGGACAAGTCAAGATGGCAGGAG GGAAACGTGTTCTCCTGCTCCGTGA TGCACGAAGCGCTGCACAACCATTA CACCCAGAAATCACTGTCACTTTCG CTGGGAAAA
SEQ ID 1988	QVQLVQSGGGLVQPGGSLRLSCAASG FTFSSYAMSWVRQAPGKGLEWVSGIS GSGGSTYYADSVKGRFTISRDNSKNM LFLQMNSPRAEDTAVYYCAKKIAAAG KQPVDYWGQGTLVTVSSASTKGPSVF PLAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSN TKVDKRVESKYGPPCPPCPAPEFLGGP SVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2096	CAGGTGCAGCTGGTGCAATCTGGGG GAGGCTTGGTACAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTTAGCAGCTATGCCA TGAGCTGGGTCCGCCAGGCTCCAGG GAAGGGGCTGGAATGGGTCTCAGGT ATTAGTGGTAGTGGTGGTAGCACAT ACTACGCAGACTCCGTGAAGGGCCG GTTCACCATCTCCAGAGACAATTCC AAGAACATGCTGTTTCTGCAAATGA ACAGCCCGAGAGCCGAGGACACGG CCGTATATTACTGTGCGAAGAAAAT AGCAGCAGCTGGTAAGCAACCTGTT GACTACTGGGGCCAGGGAACCCTGG TCACCGTCTCCTCAGCATCCACCAA GGGGCCTTCCGTGTTCCCCCTGGCC CCTTGCTCCCGCTCGACCTCTGAATC CACCGCCGCACTCGGTTGCCTGGTC AAAGACTACTTCCCCGAGCCCGTGA CTGTCTCGTGGAACTCGGGCGCCCT CACATCCGGAGTGCATACCTTTCCC GCCGTGTTGCAGTCCAGCGGCCTGT ACAGCCTGAGCTCCGTCGTGACAGT GCCGTCCTCCTCCCTTGGAACCAAG ACCTATACCTGCAACGTCGACCACA AGCCCTCCAACACCAAAGTGGACAA GCGCGTCGAATCCAAGTACGGCCCC CCTTGTCCGCCTTGTCCAGCCCCTGA GTTCCTGGGTGGTCCGTCCGTGTTCC TCTTCCCGCCCAAGCCGAAGGACAC TCTGATGATTTCACGCACCCCGGAA GTCACTTGCGTGGTCGTGGACGTGT CGCAGGAAGATCCCGAAGTGCAGTT CAATTGGTACGTGGATGGGGTCGAA GTGCACAACGCCAAGACCAAGCCTA GGGAAGAACAGTTCAACTCTACGTA CCGGGTGGTGTCCGTGCTGACCGTG CTGCACCAGGACTGGCTGAACGGAA

			AGGAGTACAAGTGCAAAGTGTCAA ACAAGGGCCTCCCTTCATCCATCGA AAAGACCATCAGCAAGGCCAAGGG TCAACCTAGGGAGCCCCAGGTCTAC ACTTTGCCGCCTAGCCAAGAAGAAA TGACTAAGAACCAAGTGTCCCTGAC TTGCCTTGTCAAGGGCTTTTATCCGT CCGACATCGCCGTGGAGTGGGAGTC CAACGGACAACCGGAGAACAACTA CAAGACCACCCCACCGGTGCTCGAT TCCGATGGCTCCTTCTTCCTGTACTC CCGGCTGACTGTGGACAAGTCAAGA TGGCAGGAGGGAAACGTGTTCTCCT GCTCCGTGATGCACGAAGCGCTGCA CAACCATTACACCCAGAAATCACTG TCACTTTCGCTGGGAAAA
SEQ ID 1989	QVQLQQWGAGLLKPSETLSLTCAVYG GSFSGYYWSWIRQPPGKGLEWIGEINH SGSTNYNPSLKSRVTISVDTSKNQFSLK LSSVTAADTAVYYCARRKVYDYVWG SYRLPGSVSYYFDYWGQGTLVTVSSA STKGPSVFPLAPCSRSTSESTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTKTYTC NVDHKPSNTKVDKRVESKYGPPCPPCP APEFLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSQEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKGLPSSIEKTI SKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSRLTVDKSR WQEGNVFSCSVMHEALHNHYTQKSLS LSLGK	SEQ ID 2097	CAGGTGCAGCTACAGCAGTGGGGC GCAGGACTGTTGAAGCCTTCGGAGA CCCTGTCCCTCACCTGCGCTGTCTAT GGTGGGTCCTTCAGTGGTTACTACT GGAGCTGGATCCGCCAGCCCCCAGG GAAGGGGCTGGAGTGGATTGGGGA AATCAATCATAGTGGAAGCACCAAC TACAACCCGTCCCTCAAGAGTCGAG TCACCATATCAGTAGACACGTCCAA GAACCAGTTCTCCCTGAAGCTGAGC TCTGTGACCGCCGCGGACACGGCTG TGTATTACTGTGCGAGAAGGAAGGT GTATGATTACGTTTGGGGGAGTTAT CGCCTCCCCGGGTCGGTATCGTACT ACTTTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTCTCCTCAGCATCC ACCAAGGGGCCTTCCGTGTTCCCCC TGGCCCCTTGCTCCCGCTCGACCTCT GAATCCACCGCCGCACTCGGTTGCC TGGTCAAAGACTACTTCCCCGAGCC CGTGACTGTCTCGTGGAACTCGGGC GCCCTCACATCCGGAGTGCATACCT TTCCCGCCGTGTTGCAGTCCAGCGG CCTGTACAGCCTGAGCTCCGTCGTG ACAGTGCCGTCCTCCTCCCTTGGAA CCAAGACCTATACCTGCAACGTCGA CCACAAGCCCTCCAACACCAAAGTG GACAAGCGCGTCGAATCCAAGTACG GCCCCCCTTGTCCGCCTTGTCCAGCC CCTGAGTTCCTGGGTGGTCCGTCCG TGTTCCTCTTCCCGCCCAAGCCGAA GGACACTCTGATGATTTCACGCACC CCGGAAGTCACTTGCGTGGTCGTGG ACGTGTCGCAGGAAGATCCCGAAGT GCAGTTCAATTGGTACGTGGATGGG GTCGAAGTGCACAACGCCAAGACC AAGCCTAGGGAAGAACAGTTCAACT CTACGTACCGGGTGGTGTCCGTGCT GACCGTGCTGCACCAGGACTGGCTG

			AACGGAAAGGAGTACAAGTGCAAA GTGTCAAACAAGGGCCTCCCTTCAT CCATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTACACTTTGCCGCCTAGCCAA GAAGAAATGACTAAGAACCAAGTG TCCCTGACTTGCCTTGTCAAGGGCTT TTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCCGGCTGACTGTGGACA AGTCAAGATGGCAGGAGGGAAACG TGTTCTCCTGCTCCGTGATGCACGA AGCGCTGCACAACCATTACACCCAG AAATCACTGTCACTTTCGCTGGGAA AA
SEQ ID 1990	QVQLVQSGAEVKKPGESLKISCKGSGY SFTSYWIGWVRQMPGKGLEWMGIIYP GDSDTRYSPSFQGQVTISADKSISTAYL QWSSLKASDTAMYYCARLPGRAARPD YWGQGTLVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTKTYTCNVDHKPSNTKVDK RVESKYGPPCPPCPAPEFLGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSQEDP EVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKC KVSNKGLPSSIEKTISKAKGQPREPQVY TLPPSQEEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGS FFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSLGK	SEQ ID 2098	CAGGTCCAGCTGGTACAGTCTGGAG CAGAGGTGAAAAAGCCCGGGGAGT CTCTGAAGATCTCCTGTAAGGGTTC TGGATACAGCTTTACCAGCTACTGG ATCGGCTGGGTGCGCCAGATGCCCG GGAAAGGCCTGGAGTGGATGGGGA TCATCTATCCTGGTGACTCTGATACC AGATACAGCCCGTCCTTCCAAGGCC AGGTCACCATCTCAGCCGACAAGTC CATCAGCACCGCCTACCTGCAGTGG AGCAGCCTGAAGGCCTCGGACACCG CCATGTATTACTGTGCGAGACTCCC GGGGAGAGCAGCTCGTCCAGACTAC TGGGGCCAGGGCACCCTGGTCACCG TCTCCTCAGCATCCACCAAGGGGCC TTCCGTGTTCCCCCTGGCCCCTTGCT CCCGCTCGACCTCTGAATCCACCGC CGCACTCGGTTGCCTGGTCAAAGAC TACTTCCCCGAGCCCGTGACTGTCT CGTGGAACTCGGGCGCCCTCACATC CGGAGTGCATACCTTTCCCGCCGTG TTGCAGTCCAGCGGCCTGTACAGCC TGAGCTCCGTCGTGACAGTGCCGTC CTCCTCCCTTGGAACCAAGACCTAT ACCTGCAACGTCGACCACAAGCCCT CCAACACCAAAGTGGACAAGCGCG TCGAATCCAAGTACGGCCCCCCTTG TCCGCCTTGTCCAGCCCCTGAGTTCC TGGGTGGTCCGTCCGTGTTCCTCTTC CCGCCCAAGCCGAAGGACACTCTGA TGATTTCACGCACCCCGGAAGTCAC TTGCGTGGTCGTGGACGTGTCGCAG GAAGATCCCGAAGTGCAGTTCAATT GGTACGTGGATGGGGTCGAAGTGCA CAACGCCAAGACCAAGCCTAGGGA AGAACAGTTCAACTCTACGTACCGG GTGGTGTCCGTGCTGACCGTGCTGC ACCAGGACTGGCTGAACGGAAAGG

			AGTACAAGTGCAAAGTGTCAAACA AGGGCCTCCCTTCATCCATCGAAAA GACCATCAGCAAGGCCAAGGGTCA ACCTAGGGAGCCCCAGGTCTACACT TTGCCGCCTAGCCAAGAAGAAATGA CTAAGAACCAAGTGTCCCTGACTTG CCTTGTCAAGGGCTTTTATCCGTCCG ACATCGCCGTGGAGTGGGAGTCCAA CGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCC GATGGCTCCTTCTTCCTGTACTCCCG GCTGACTGTGGACAAGTCAAGATGG CAGGAGGGAAACGTGTTCTCCTGCT CCGTGATGCACGAAGCGCTGCACAA CCATTACACCCAGAAATCACTGTCA CTTTCGCTGGGAAAA
SEQ ID 1991	QVTLKESGGGVVQPGRSLRLSCAASGF TFSSYAMHWVRQAPGKGLEWVAVISY DGSNKYYADSVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCARGPGAVA GTKPKYYFDYWGQGTLVTVSSASTKG PSVFPLAPCSRSTSESTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTKTYTCNVDH KPSNTKVDKRVESKYGPPCPPCPAPEF LGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSQEDPEVQFNWYVDGVEVHNA KTKPREEQFNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKGLPSSIEKTISKAK GQPREPQVYTLPPSQEEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSRLTVDKSRWQEG NVFSCSVMHEALHNHYTQKSLSLSLG K	SEQ ID 2099	CAGGTCACCTTGAAGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTCAGTAGCTATGCTA TGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTT ATATCATATGATGGAAGTAATAAAT ACTACGCAGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCTGAGGACACGG CTGTGTATTACTGTGCGAGAGGCCC CGGGGCAGTGGCTGGTACTAAGCCA AAGTACTACTTTGACTACTGGGGCC AGGGAACCCTGGTCACCGTCTCCTC AGCATCCACCAAGGGGCCTTCCGTG TTCCCCCTGGCCCCTTGCTCCCGCTC GACCTCTGAATCCACCGCCGCACTC GGTTGCCTGGTCAAAGACTACTTCC CCGAGCCCGTGACTGTCTCGTGGAA CTCGGGCGCCCTCACATCCGGAGTG CATACCTTTCCCGCCGTGTTGCAGTC CAGCGGCCTGTACAGCCTGAGCTCC GTCGTGACAGTGCCGTCCTCCTCCC TTGGAACCAAGACCTATACCTGCAA CGTCGACCACAAGCCCTCCAACACC AAAGTGGACAAGCGCGTCGAATCC AAGTACGGCCCCCCTTGTCCGCCTT GTCCAGCCCCTGAGTTCCTGGGTGG TCCGTCCGTGTTCCTCTTCCCGCCCA AGCCGAAGGACACTCTGATGATTTC ACGCACCCCGGAAGTCACTTGCGTG GTCGTGGACGTGTCGCAGGAAGATC CCGAAGTGCAGTTCAATTGGTACGT GGATGGGGTCGAAGTGCACAACGC CAAGACCAAGCCTAGGGAAGAACA GTTCAACTCTACGTACCGGGTGGTG TCCGTGCTGACCGTGCTGCACCAGG ACTGGCTGAACGGAAAGGAGTACA

			AGTGCAAAGTGTCAAACAAGGGCCT CCCTTCATCCATCGAAAAGACCATC AGCAAGGCCAAGGGTCAACCTAGG GAGCCCCAGGTCTACACTTTGCCGC CTAGCCAAGAAGAAATGACTAAGA ACCAAGTGTCCCTGACTTGCCTTGT CAAGGGCTTTTATCCGTCCGACATC GCCGTGGAGTGGGAGTCCAACGGA CAACCGGAGAACAACTACAAGACC ACCCCACCGGTGCTCGATTCCGATG GCTCCTTCTTCCTGTACTCCCGGCTG ACTGTGGACAAGTCAAGATGGCAG GAGGGAAACGTGTTCTCCTGCTCCG TGATGCACGAAGCGCTGCACAACCA TTACACCCAGAAATCACTGTCACTT TCGCTGGGAAAA
SEQ ID 1992	EVQLVQSGGGVVQPGRSLRLSCAASG FTFSSYAMHWVRQAPGKGLEWVAVIS YDGSNKYYADSVKGRFTISRDNSKNT LYLQMNSLRAEDTAVYYCARATYYY DSSGYRFDYWGQGTLVTVSSASTKGP SVFPLAPCSRSTSESTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSG LYSLSSVVTVPSSSLGTKTYTCNVDHK PSNTKVDKRVESKYGPPCPPCPAPEFL GGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSQEDPEVQFNWYVDGVEVHNAK TKPREEQFNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKGLPSSIEKTISKAKG QPREPQVYTLPPSQEEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSRLTVDKSRWQEGN VFSCSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2100	GAGGTCCAGCTGGTGCAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTCAGTAGCTATGCTA TGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTT ATATCATATGATGGAAGTAATAAAT ACTACGCAGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCTGAGGACACGG CTGTGTATTACTGTGCGAGGGCCAC GTATTACTATGATAGTAGTGGTTAT AGGTTTGACTACTGGGGCCAGGGAA CCCTGGTCACCGTCTCCTCAGCATC CACCAAGGGGCCTTCCGTGTTCCCC CTGGCCCCTTGCTCCCGCTCGACCTC TGAATCCACCGCCGCACTCGGTTGC CTGGTCAAAGACTACTTCCCCGAGC CCGTGACTGTCTCGTGGAACTCGGG CGCCCTCACATCCGGAGTGCATACC TTTCCCGCCGTGTTGCAGTCCAGCG GCCTGTACAGCCTGAGCTCCGTCGT GACAGTGCCGTCCTCCTCCCTTGGA ACCAAGACCTATACCTGCAACGTCG ACCACAAGCCCTCCAACACCAAAGT GGACAAGCGCGTCGAATCCAAGTAC GGCCCCCCTTGTCCGCCTTGTCCAG CCCCTGAGTTCCTGGGTGGTCCGTC CGTGTTCCTCTTCCCGCCCAAGCCG AAGGACACTCTGATGATTTCACGCA CCCCGGAAGTCACTTGCGTGGTCGT GGACGTGTCGCAGGAAGATCCCGA AGTGCAGTTCAATTGGTACGTGGAT GGGGTCGAAGTGCACAACGCCAAG ACCAAGCCTAGGGAAGAACAGTTC AACTCTACGTACCGGGTGGTGTCCG TGCTGACCGTGCTGCACCAGGACTG

			GCTGAACGGAAAGGAGTACAAGTG CAAAGTGTCAAACAAGGGCCTCCCT TCATCCATCGAAAAGACCATCAGCA AGGCCAAGGGTCAACCTAGGGAGC CCCAGGTCTACACTTTGCCGCCTAG CCAAGAAGAAATGACTAAGAACCA AGTGTCCCTGACTTGCCTTGTCAAG GGCTTTTATCCGTCCGACATCGCCG TGGAGTGGGAGTCCAACGGACAAC CGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTC CTTCTTCCTGTACTCCCGGCTGACTG TGGACAAGTCAAGATGGCAGGAGG GAAACGTGTTCTCCTGCTCCGTGAT GCACGAAGCGCTGCACAACCATTAC ACCCAGAAATCACTGTCACTTTCGC TGGGAAAA
SEQ ID 1993	EVQLVQSGGGLVEPGGSLRLSCAASRF TFSDAWMSWVRQAPGKGLEWVGRIK SKISGGTTDYAAPVQGRFTISRDDSKN TLYLQMDSLKTEDTAVYYCANRNLGY WGQGTLVTVSSASTKGPSVFPLAPCSR STSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTKTYTCNVDHKPSNTKVDK RVESKYGPPCPPCPAPEFLGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSQEDP EVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKC KVSNKGLPSSIEKTISKAKGQPREPQVY TLPPSQEEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGS FFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSLGK	SEQ ID 2101	GAGGTCCAGCTGGTACAGTCTGGGG GAGGCTTGGTAGAACCGGGGGGGT CCCTTAGACTCTCCTGTGCAGCCTCT CGATTCACTTTCAGTGACGCCTGGA TGAGCTGGGTCCGCCAGGCTCCAGG TAAGGGGCTGGAGTGGGTTGGCCGT ATTAAAAGCAAAATAAGTGGTGGG ACAACAGACTACGCTGCACCCGTGC AAGGCAGATTCACCATCTCAAGAGA TGATTCAAAAAACACGCTGTATCTG CAAATGGACAGCCTGAAAACCGAG GACACAGCCGTGTATTACTGTGCGA ACCGAAACTTAGGCTACTGGGGCCA GGGCACCCTGGTGACCGTCTCCTCA GCATCCACCAAGGGGCCTTCCGTGT TCCCCCTGGCCCCTTGCTCCCGCTCG ACCTCTGAATCCACCGCCGCACTCG GTTGCCTGGTCAAAGACTACTTCCC CGAGCCCGTGACTGTCTCGTGGAAC TCGGGCGCCCTCACATCCGGAGTGC ATACCTTTCCCGCCGTGTTGCAGTCC AGCGGCCTGTACAGCCTGAGCTCCG TCGTGACAGTGCCGTCCTCCTCCCTT GGAACCAAGACCTATACCTGCAACG TCGACCACAAGCCCTCCAACACCAA AGTGGACAAGCGCGTCGAATCCAA GTACGGCCCCCCTTGTCCGCCTTGTC CAGCCCCTGAGTTCCTGGGTGGTCC GTCCGTGTTCCTCTTCCCGCCCAAGC CGAAGGACACTCTGATGATTTCACG CACCCCGGAAGTCACTTGCGTGGTC GTGGACGTGTCGCAGGAAGATCCCG AAGTGCAGTTCAATTGGTACGTGGA TGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTT CAACTCTACGTACCGGGTGGTGTCC GTGCTGACCGTGCTGCACCAGGACT GGCTGAACGGAAAGGAGTACAAGT GCAAAGTGTCAAACAAGGGCCTCCC

			TTCATCCATCGAAAAGACCATCAGC AAGGCCAAGGGTCAACCTAGGGAG CCCCAGGTCTACACTTTGCCGCCTA GCCAAGAAGAAATGACTAAGAACC AAGTGTCCCTGACTTGCCTTGTCAA GGGCTTTTATCCGTCCGACATCGCC GTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACC CCACCGGTGCTCGATTCCGATGGCT CCTTCTTCCTGTACTCCCGGCTGACT GTGGACAAGTCAAGATGGCAGGAG GGAAACGTGTTCTCCTGCTCCGTGA TGCACGAAGCGCTGCACAACCATTA CACCCAGAAATCACTGTCACTTTCG CTGGGAAAA
SEQ ID 1994	EVQLVQSGAEVKKPGASVKVSCKASG YTFTSYAMHWVRQAPGQRLEWMGWI NAGNGNTKYSQKFQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARARYYD SSGYIAPSGYFDYWGQGTLVTVSSAST KGPSVFPLAPCSRSTSESTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTKTYTCN VDHKPSNTKVDKRVESKYGPPCPPCPA PEFLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSQEDPEVQFNWYVDGVEV HNAKTKPREEQFNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKGLPSSIEKTIS KAKGQPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSRLTVDKSRW QEGNVFSCSVMHEALHNHYTQKSLSL SLGK	SEQ ID 2102	GAGGTCCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTTTCCTGCAAGGCTTCT GGATACACCTTCACTAGCTATGCTA TGCATTGGGTGCGCCAGGCCCCCGG ACAAAGGCTTGAGTGGATGGGATG GATCAACGCTGGCAATGGTAACACA AAATATTCACAGAAGTTCCAGGGCA GAGTCACCATGACCACAGACACATC CACGAGCACAGCCTACATGGAGCTG AGGAGCCTGAGATCTGACGACACG GCCGTGTATTACTGTGCGAGAGCTC GTTACTATGATAGTAGTGGTTATAT TGCCCCATCGGGTTACTTTGACTACT GGGGCCAGGGAACCCTGGTCACCGT CTCCTCAGCATCCACCAAGGGGCCT TCCGTGTTCCCCCTGGCCCCTTGCTC CCGCTCGACCTCTGAATCCACCGCC GCACTCGGTTGCCTGGTCAAAGACT ACTTCCCCGAGCCCGTGACTGTCTC GTGGAACTCGGGCGCCCTCACATCC GGAGTGCATACCTTTCCCGCCGTGT TGCAGTCCAGCGGCCTGTACAGCCT GAGCTCCGTCGTGACAGTGCCGTCC TCCTCCCTTGGAACCAAGACCTATA CCTGCAACGTCGACCACAAGCCCTC CAACACCAAAGTGGACAAGCGCGT CGAATCCAAGTACGGCCCCCCTTGT CCGCCTTGTCCAGCCCCTGAGTTCCT GGGTGGTCCGTCCGTGTTCCTCTTCC CGCCCAAGCCGAAGGACACTCTGAT GATTTCACGCACCCCGGAAGTCACT TGCGTGGTCGTGGACGTGTCGCAGG AAGATCCCGAAGTGCAGTTCAATTG GTACGTGGATGGGGTCGAAGTGCAC AACGCCAAGACCAAGCCTAGGGAA GAACAGTTCAACTCTACGTACCGGG TGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGA

			GTACAAGTGCAAAGTGTCAAACAA GGGCCTCCCTTCATCCATCGAAAAG ACCATCAGCAAGGCCAAGGGTCAA CCTAGGGAGCCCCAGGTCTACACTT TGCCGCCTAGCCAAGAAGAAATGAC TAAGAACCAAGTGTCCCTGACTTGC CTTGTCAAGGGCTTTTATCCGTCCG ACATCGCCGTGGAGTGGGAGTCCAA CGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCC GATGGCTCCTTCTTCCTGTACTCCCG GCTGACTGTGGACAAGTCAAGATGG CAGGAGGGAAACGTGTTCTCCTGCT CCGTGATGCACGAAGCGCTGCACAA CCATTACACCCAGAAATCACTGTCA CTTTCGCTGGGAAAA
SEQ ID 1995	QVQLVQSGAEVKKPGASVKVSCKASG YTFTSYAMHWVRQAPGQRLEWMGWI NAGNGNTKYSQKFQGRVTITRDTSAST AYMELSSLRSEDTAVYYCARDGPAVD GAEYFQHWGQGTLVTVSSASTKGPSV FPLAPCSRSTSESTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTKTYTCNVDHKP SNTKVDKRVESKYGPPCPPCPAPEFLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKT KPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKGQ PREPQVYTLPPSQEEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSRLTVDKSRWQEGNV FSCSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2103	CAGGTGCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTTTCCTGCAAGGCTTCT GGATACACCTTCACTAGCTATGCTA TGCATTGGGTGCGCCAGGCCCCCGG ACAAAGGCTTGAGTGGATGGGATG GATCAACGCTGGCAATGGTAACACA AAATATTCACAGAAGTTCCAGGGCA GAGTCACCATTACCAGGGACACATC CGCGAGCACAGCCTACATGGAGCTG AGCAGCCTGAGATCTGAAGACACG GCTGTGTATTACTGTGCGAGAGATG GCCCCGCCGTTGATGGTGCTGAATA CTTCCAGCACTGGGGCCAGGGCACC CTGGTCACCGTCTCCTCAGCATCCA CCAAGGGGCCTTCCGTGTTCCCCCT GGCCCCTTGCTCCCGCTCGACCTCT GAATCCACCGCCGCACTCGGTTGCC TGGTCAAAGACTACTTCCCCGAGCC CGTGACTGTCTCGTGGAACTCGGGC GCCCTCACATCCGGAGTGCATACCT TTCCCGCCGTGTTGCAGTCCAGCGG CCTGTACAGCCTGAGCTCCGTCGTG ACAGTGCCGTCCTCCTCCCTTGGAA CCAAGACCTATACCTGCAACGTCGA CCACAAGCCCTCCAACACCAAAGTG GACAAGCGCGTCGAATCCAAGTACG GCCCCCCTTGTCCGCCTTGTCCAGCC CCTGAGTTCCTGGGTGGTCCGTCCG TGTTCCTCTTCCCGCCCAAGCCGAA GGACACTCTGATGATTTCACGCACC CCGGAAGTCACTTGCGTGGTCGTGG ACGTGTCGCAGGAAGATCCCGAAGT GCAGTTCAATTGGTACGTGGATGGG GTCGAAGTGCACAACGCCAAGACC AAGCCTAGGGAAGAACAGTTCAACT CTACGTACCGGGTGGTGTCCGTGCT GACCGTGCTGCACCAGGACTGGCTG

			AACGGAAAGGAGTACAAGTGCAAA GTGTCAAACAAGGGCCTCCCTTCAT CCATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTACACTTTGCCGCCTAGCCAA GAAGAAATGACTAAGAACCAAGTG TCCCTGACTTGCCTTGTCAAGGGCTT TTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCCGGCTGACTGTGGACA AGTCAAGATGGCAGGAGGGAAACG TGTTCTCCTGCTCCGTGATGCACGA AGCGCTGCACAACCATTACACCCAG AAATCACTGTCACTTTCGCTGGGAA AA
SEQ ID 1996	QLQLQESGPGLVKPSQTLSLTCAISGDS VSSNSAAWNWIRQSPSRGLEWLGRTY YRSKWYNDYAVSLKSRITINPDTSKNQ FSLQLNSVTPEDTAVYYCASLASGSPP PGDYWGQGTLVTVSSASTKGPSVFPL APCSRSTSESTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDV SQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKGLPSSIEKTISKAKGQPRE PQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCS VMHEALHNHYTQKSLSLSLGK	SEQ ID 2104	CAGCTGCAGCTGCAGGAGTCGGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCAACAGTGC TGCTTGGAACTGGATCAGGCAGTCC CCATCGCGAGGCCTTGAGTGGCTGG GAAGGACTTACTACAGGTCCAAGTG GTATAATGATTATGCAGTATCTCTG AAAAGTCGAATAACCATCAACCCGG ACACATCCAAGAACCAGTTCTCCCT GCAGCTGAACTCTGTGACTCCCGAG GACACGGCTGTATATTACTGTGCAA GTTTGGCGAGTGGTTCCCCCCCTCC GGGGGACTACTGGGGCCAGGGAAC CCTGGTGACCGTCTCCTCAGCATCC ACCAAGGGGCCTTCCGTGTTCCCCC TGGCCCCTTGCTCCCGCTCGACCTCT GAATCCACCGCCGCACTCGGTTGCC TGGTCAAAGACTACTTCCCCGAGCC CGTGACTGTCTCGTGGAACTCGGGC GCCCTCACATCCGGAGTGCATACCT TTCCCGCCGTGTTGCAGTCCAGCGG CCTGTACAGCCTGAGCTCCGTCGTG ACAGTGCCGTCCTCCTCCCTTGGAA CCAAGACCTATACCTGCAACGTCGA CCACAAGCCCTCCAACACCAAAGTG GACAAGCGCGTCGAATCCAAGTACG GCCCCCCTTGTCCGCCTTGTCCAGCC CCTGAGTTCCTGGGTGGTCCGTCCG TGTTCCTCTTCCCGCCCAAGCCGAA GGACACTCTGATGATTTCACGCACC CCGGAAGTCACTTGCGTGGTCGTGG ACGTGTCGCAGGAAGATCCCGAAGT GCAGTTCAATTGGTACGTGGATGGG GTCGAAGTGCACAACGCCAAGACC AAGCCTAGGGAAGAACAGTTCAACT CTACGTACCGGGTGGTGTCCGTGCT GACCGTGCTGCACCAGGACTGGCTG AACGGAAAGGAGTACAAGTGCAAA

			GTGTCAAACAAGGGCCTCCCTTCAT CCATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTACACTTTGCCGCCTAGCCAA GAAGAAATGACTAAGAACCAAGTG TCCCTGACTTGCCTTGTCAAGGGCTT TTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCCGGCTGACTGTGGACA AGTCAAGATGGCAGGAGGGAAACG TGTTCTCCTGCTCCGTGATGCACGA AGCGCTGCACAACCATTACACCCAG AAATCACTGTCACTTTCGCTGGGAA AA
SEQ ID 1997	QVTLKESGGGVVQPGRSLRLSCAASGF TFSTYGMHWVRQAPGKGLEWVALISY DGSKKYYANSVKGRFTISRDNSKNTL YLQMKSLRAEDTAMYYCAKGPIVGAT MDYWGQGALVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTKTYTCNVDHKPSNTKV DKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQE DPEVQFNWYVDGVEVHNAKTKPREE QFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSLGK	SEQ ID 2105	CAGGTCACCTTGAAGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTCAGTACCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCACTT ATATCATATGATGGAAGTAAAAAAT ACTATGCAAACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCC AAGAACACGTTGTATCTGCAAATGA AAAGTCTGAGAGCTGAGGACACGG CTATGTATTACTGTGCGAAAGGCCC TATAGTGGGAGCGACTATGGACTAC TGGGGCCAGGGAGCCCTGGTCACCG TCTCCTCAGCATCCACCAAGGGGCC TTCCGTGTTCCCCCTGGCCCCTTGCT CCCGCTCGACCTCTGAATCCACCGC CGCACTCGGTTGCCTGGTCAAAGAC TACTTCCCCGAGCCCGTGACTGTCT CGTGGAACTCGGGCGCCCTCACATC CGGAGTGCATACCTTTCCCGCCGTG TTGCAGTCCAGCGGCCTGTACAGCC TGAGCTCCGTCGTGACAGTGCCGTC CTCCTCCCTTGGAACCAAGACCTAT ACCTGCAACGTCGACCACAAGCCCT CCAACACCAAAGTGGACAAGCGCG TCGAATCCAAGTACGGCCCCCCTTG TCCGCCTTGTCCAGCCCCTGAGTTCC TGGGTGGTCCGTCCGTGTTCCTCTTC CCGCCCAAGCCGAAGGACACTCTGA TGATTTCACGCACCCCGGAAGTCAC TTGCGTGGTCGTGGACGTGTCGCAG GAAGATCCCGAAGTGCAGTTCAATT GGTACGTGGATGGGGTCGAAGTGCA CAACGCCAAGACCAAGCCTAGGGA AGAACAGTTCAACTCTACGTACCGG GTGGTGTCCGTGCTGACCGTGCTGC ACCAGGACTGGCTGAACGGAAAGG AGTACAAGTGCAAAGTGTCAAACA

			AGGGCCTCCCTTCATCCATCGAAAA GACCATCAGCAAGGCCAAGGGTCA ACCTAGGGAGCCCCAGGTCTACACT TTGCCGCCTAGCCAAGAAGAAATGA CTAAGAACCAAGTGTCCCTGACTTG CCTTGTCAAGGGCTTTTATCCGTCCG ACATCGCCGTGGAGTGGGAGTCCAA CGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCC GATGGCTCCTTCTTCCTGTACTCCCG GCTGACTGTGGACAAGTCAAGATGG CAGGAGGGAAACGTGTTCTCCTGCT CCGTGATGCACGAAGCGCTGCACAA CCATTACACCCAGAAATCACTGTCA CTTTCGCTGGGAAAA
SEQ ID 1998	EVQLVQSGAEVKKPGSSVKVSCKASG GTFSSYAISWVRQAPGQGLEWMGWIS AYNGNTNYAQKLQGRVTMTTDTSTST AYMELRSLRSDDTAVYYCARWYGDY GLDYWGQGTLVTVSSASTKGPSVFPL APCSRSTSESTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDV SQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKGLPSSIEKTISKAKGQPRE PQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCS VMHEALHNHYTQKSLSLSLGK	SEQ ID 2106	GAGGTGCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGTCCTC GGTGAAGGTCTCCTGCAAGGCTTCT GGAGGCACCTTCAGCAGCTATGCTA TCAGCTGGGTGCGACAGGCCCCTGG ACAAGGGCTTGAGTGGATGGGATG GATCAGCGCTTACAATGGTAACACA AACTATGCACAGAAGCTCCAGGGCA GAGTCACCATGACCACAGACACATC CACGAGCACAGCCTACATGGAGCTG AGGAGCCTGAGATCTGACGACACG GCCGTGTATTACTGTGCGAGATGGT ACGGTGACTACGGCCTTGACTACTG GGGCCAGGGAACCCTGGTCACCGTC TCCTCAGCATCCACCAAGGGGCCTT CCGTGTTCCCCCTGGCCCCTTGCTCC CGCTCGACCTCTGAATCCACCGCCG CACTCGGTTGCCTGGTCAAAGACTA CTTCCCCGAGCCCGTGACTGTCTCG TGGAACTCGGGCGCCCTCACATCCG GAGTGCATACCTTTCCCGCCGTGTT GCAGTCCAGCGGCCTGTACAGCCTG AGCTCCGTCGTGACAGTGCCGTCCT CCTCCCTTGGAACCAAGACCTATAC CTGCAACGTCGACCACAAGCCCTCC AACACCAAAGTGGACAAGCGCGTC GAATCCAAGTACGGCCCCCCTTGTC CGCCTTGTCCAGCCCCTGAGTTCCT GGGTGGTCCGTCCGTGTTCCTCTTCC CGCCCAAGCCGAAGGACACTCTGAT GATTTCACGCACCCCGGAAGTCACT TGCGTGGTCGTGGACGTGTCGCAGG AAGATCCCGAAGTGCAGTTCAATTG GTACGTGGATGGGGTCGAAGTGCAC AACGCCAAGACCAAGCCTAGGGAA GAACAGTTCAACTCTACGTACCGGG TGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGA GTACAAGTGCAAAGTGTCAAACAA

			GGGCCTCCCTTCATCCATCGAAAAG ACCATCAGCAAGGCCAAGGGTCAA CCTAGGGAGCCCCAGGTCTACACTT TGCCGCCTAGCCAAGAAGAAATGAC TAAGAACCAAGTGTCCCTGACTTGC CTTGTCAAGGGCTTTTATCCGTCCG ACATCGCCGTGGAGTGGGAGTCCAA CGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCC GATGGCTCCTTCTTCCTGTACTCCCG GCTGACTGTGGACAAGTCAAGATGG CAGGAGGGAAACGTGTTCTCCTGCT CCGTGATGCACGAAGCGCTGCACAA CCATTACACCCAGAAATCACTGTCA CTTTCGCTGGGAAAA
SEQ ID 1999	EVQLVQSGAEVKKPGASVKVSCKASG YTFTSYAMHWVRQAPGQRLAWMGWI NAGNGNTKYSEKFEGRVTITRDTSAST AYMELSSLRSEDTAVYYCARVAKYYY ESGGYRASNWFDPWGQGTLVTVSSAS TKGPSVFPLAPCSRSTSESTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTKTYTCN VDHKPSNTKVDKRVESKYGPPCPPCPA PEFLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSQEDPEVQFNWYVDGVEV HNAKTKPREEQFNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKGLPSSIEKTIS KAKGQPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSRLTVDKSRW QEGNVFSCSVMHEALHNHYTQKSLSL SLGK	SEQ ID 2107	GAGGTCCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTTTCCTGCAAGGCTTCT GGATACACCTTCACTAGCTATGCTA TGCATTGGGTGCGCCAGGCCCCCGG ACAAAGGCTTGCGTGGATGGGATGG ATCAACGCTGGCAATGGTAACACAA AATATTCAGAGAAGTTCGAAGGCAG AGTCACCATCACCAGGGACACATCC GCGAGCACAGCCTACATGGAGCTGA GCAGCCTGAGATCTGAAGACACGGC TGTGTATTACTGTGCGAGGGTCGCC AAATATTATTACGAGAGTGGTGGTT ATCGGGCCTCCAACTGGTTCGACCC CTGGGGCCAGGGCACCCTGGTCACC GTCTCCTCAGCATCCACCAAGGGGC CTTCCGTGTTCCCCCTGGCCCCTTGC TCCCGCTCGACCTCTGAATCCACCG CCGCACTCGGTTGCCTGGTCAAAGA CTACTTCCCCGAGCCCGTGACTGTC TCGTGGAACTCGGGCGCCCTCACAT CCGGAGTGCATACCTTTCCCGCCGT GTTGCAGTCCAGCGGCCTGTACAGC CTGAGCTCCGTCGTGACAGTGCCGT CCTCCTCCCTTGGAACCAAGACCTA TACCTGCAACGTCGACCACAAGCCC TCCAACACCAAAGTGGACAAGCGC GTCGAATCCAAGTACGGCCCCCCTT GTCCGCCTTGTCCAGCCCCTGAGTT CCTGGGTGGTCCGTCCGTGTTCCTCT TCCCGCCCAAGCCGAAGGACACTCT GATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGC AGGAAGATCCCGAAGTGCAGTTCAA TTGGTACGTGGATGGGGTCGAAGTG CACAACGCCAAGACCAAGCCTAGG GAAGAACAGTTCAACTCTACGTACC GGGTGGTGTCCGTGCTGACCGTGCT GCACCAGGACTGGCTGAACGGAAA

			GGAGTACAAGTGCAAAGTGTCAAA CAAGGGCCTCCCTTCATCCATCGAA AAGACCATCAGCAAGGCCAAGGGT CAACCTAGGGAGCCCCAGGTCTACA CTTTGCCGCCTAGCCAAGAAGAAAT GACTAAGAACCAAGTGTCCCTGACT TGCCTTGTCAAGGGCTTTTATCCGTC CGACATCGCCGTGGAGTGGGAGTCC AACGGACAACCGGAGAACAACTAC AAGACCACCCCACCGGTGCTCGATT CCGATGGCTCCTTCTTCCTGTACTCC CGGCTGACTGTGGACAAGTCAAGAT GGCAGGAGGGAAACGTGTTCTCCTG CTCCGTGATGCACGAAGCGCTGCAC AACCATTACACCCAGAAATCACTGT CACTTTCGCTGGGAAAA
SEQ ID 2000	QVQLQESGPGLVKPSQTLSLTCAISGD SVSSNSAAWNWIRQSPSRGLEWLGRT YYRSKWYNDYAVSVKSRITINPDTSKN QFSLQLNSVTPEDTAVYYCARAPPPTV GWYAPVFDYWGQGTLVTVSSASTKGP SVFPLAPCSRSTSESTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSG LYSLSSVVTVPSSSLGTKTYTCNVDHK PSNTKVDKRVESKYGPPCPPCPAPEFL GGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSQEDPEVQFNWYVDGVEVHNAK TKPREEQFNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKGLPSSIEKTISKAKG QPREPQVYTLPPSQEEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSRLTVDKSRWQEGN VFSCSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2108	CAGGTGCAGCTGCAGGAGTCAGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCAACAGTGC TGCTTGGAACTGGATCAGGCAGTCC CCATCGAGAGGCCTTGAGTGGCTGG GAAGGACATACTACAGGTCCAAGTG GTATAATGATTATGCAGTATCTGTG AAAAGTCGAATAACCATCAACCCAG ACACATCCAAGAACCAGTTCTCCCT GCAGCTGAACTCTGTGACTCCCGAG GACACGGCTGTGTATTACTGTGCAA GAGCGCCCCCTCCGACTGTTGGCTG GTACGCCCCCGTCTTTGACTACTGG GGCCAGGGAACCCTGGTCACCGTCT CCTCAGCATCCACCAAGGGGCCTTC CGTGTTCCCCCTGGCCCCTTGCTCCC GCTCGACCTCTGAATCCACCGCCGC ACTCGGTTGCCTGGTCAAAGACTAC TTCCCCGAGCCCGTGACTGTCTCGT GGAACTCGGGCGCCCTCACATCCGG AGTGCATACCTTTCCCGCCGTGTTG CAGTCCAGCGGCCTGTACAGCCTGA GCTCCGTCGTGACAGTGCCGTCCTC CTCCCTTGGAACCAAGACCTATACC TGCAACGTCGACCACAAGCCCTCCA ACACCAAAGTGGACAAGCGCGTCG AATCCAAGTACGGCCCCCCTTGTCC GCCTTGTCCAGCCCCTGAGTTCCTG GGTGGTCCGTCCGTGTTCCTCTTCCC GCCCAAGCCGAAGGACACTCTGATG ATTTCACGCACCCCGGAAGTCACTT GCGTGGTCGTGGACGTGTCGCAGGA AGATCCCGAAGTGCAGTTCAATTGG TACGTGGATGGGGTCGAAGTGCACA ACGCCAAGACCAAGCCTAGGGAAG AACAGTTCAACTCTACGTACCGGGT GGTGTCCGTGCTGACCGTGCTGCAC

			CAGGACTGGCTGAACGGAAAGGAG TACAAGTGCAAAGTGTCAAACAAG GGCCTCCCTTCATCCATCGAAAAGA CCATCAGCAAGGCCAAGGGTCAACC TAGGGAGCCCCAGGTCTACACTTTG CCGCCTAGCCAAGAAGAAATGACTA AGAACCAAGTGTCCCTGACTTGCCT TGTCAAGGGCTTTTATCCGTCCGAC ATCGCCGTGGAGTGGGAGTCCAACG GACAACCGGAGAACAACTACAAGA CCACCCCACCGGTGCTCGATTCCGA TGGCTCCTTCTTCCTGTACTCCCGGC TGACTGTGGACAAGTCAAGATGGCA GGAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACT TTCGCTGGGAAAA
SEQ ID 2001	QLQLQESGGGLVQPGGSLRLSCSASGI SFRDYWMHWIRQTPGKGLVWVSRINP DGSSTSYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKVTGRRVG AHDYWGQGTLVTVSSASTKGPSVFPL APCSRSTSESTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDV SQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKGLPSSIEKTISKAKGQPRE PQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCS VMHEALHNHYTQKSLSLSLGK	SEQ ID 2109	CAGCTGCAGCTGCAGGAGTCCGGGG GAGGCTTAGTTCAGCCGGGGGGGTC CCTGAGACTCTCCTGCTCAGCCTCT GGAATCAGCTTCAGAGATTACTGGA TGCACTGGATCCGCCAAACTCCAGG GAAGGGGCTGGTGTGGGTCTCACGT ATTAATCCTGATGGGAGTAGCACAA GCTACGCGGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCTGAGGACACGG CTGTGTATTACTGTGCGAAAGTTAC GGGACGGAGAGTGGGAGCCCATGA CTACTGGGGCCAGGGAACCCTGGTC ACCGTCTCCTCAGCATCCACCAAGG GGCCTTCCGTGTTCCCCCTGGCCCCT TGCTCCCGCTCGACCTCTGAATCCA CCGCCGCACTCGGTTGCCTGGTCAA AGACTACTTCCCCGAGCCCGTGACT GTCTCGTGGAACTCGGGCGCCCTCA CATCCGGAGTGCATACCTTTCCCGC CGTGTTGCAGTCCAGCGGCCTGTAC AGCCTGAGCTCCGTCGTGACAGTGC CGTCCTCCTCCCTTGGAACCAAGAC CTATACCTGCAACGTCGACCACAAG CCCTCCAACACCAAAGTGGACAAGC GCGTCGAATCCAAGTACGGCCCCCC TTGTCCGCCTTGTCCAGCCCCTGAGT TCCTGGGTGGTCCGTCCGTGTTCCTC TTCCCGCCCAAGCCGAAGGACACTC TGATGATTTCACGCACCCCGGAAGT CACTTGCGTGGTCGTGGACGTGTCG CAGGAAGATCCCGAAGTGCAGTTCA ATTGGTACGTGGATGGGGTCGAAGT GCACAACGCCAAGACCAAGCCTAG GGAAGAACAGTTCAACTCTACGTAC CGGGTGGTGTCCGTGCTGACCGTGC TGCACCAGGACTGGCTGAACGGAA

			AGGAGTACAAGTGCAAAGTGTCAA ACAAGGGCCTCCCTTCATCCATCGA AAAGACCATCAGCAAGGCCAAGGG TCAACCTAGGGAGCCCCAGGTCTAC ACTTTGCCGCCTAGCCAAGAAGAAA TGACTAAGAACCAAGTGTCCCTGAC TTGCCTTGTCAAGGGCTTTTATCCGT CCGACATCGCCGTGGAGTGGGAGTC CAACGGACAACCGGAGAACAACTA CAAGACCACCCCACCGGTGCTCGAT TCCGATGGCTCCTTCTTCCTGTACTC CCGGCTGACTGTGGACAAGTCAAGA TGGCAGGAGGGAAACGTGTTCTCCT GCTCCGTGATGCACGAAGCGCTGCA CAACCATTACACCCAGAAATCACTG TCACTTTCGCTGGGAAAA
SEQ ID 2002	QVQLVQSGAEVKKPGASVKVSCKASG YTFTGYYMHWVRQAPGQGLEWMGW INPNSGGTNYAQKFQGRVTMTRDTSIS TAYMELSRLRSDDTAVYYCAFAQPGA ETLNFDLWGRGTLVTVSSASTKGPSVF PLAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSN TKVDKRVESKYGPPCPPCPAPEFLGGP SVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2110	CAGGTGCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTCTCCTGCAAGGCTTCT GGATACACCTTCACCGGCTACTATA TGCACTGGGTGCGACAGGCCCCTGG ACAAGGGCTTGAGTGGATGGGATG GATCAACCCTAACAGTGGTGGCACA AACTATGCACAGAAGTTTCAGGGCA GGGTCACCATGACCAGGGACACGTC CATCAGCACAGCCTACATGGAGCTG AGCAGGCTGAGATCTGACGACACG GCCGTGTATTACTGTGCCTTTGCCCA GCCGGGCGCTGAGACGTTGAACTTC GATCTCTGGGGCCGTGGCACCCTGG TCACCGTCTCCTCAGCATCCACCAA GGGGCCTTCCGTGTTCCCCCTGGCC CCTTGCTCCCGCTCGACCTCTGAATC CACCGCCGCACTCGGTTGCCTGGTC AAAGACTACTTCCCCGAGCCCGTGA CTGTCTCGTGGAACTCGGGCGCCCT CACATCCGGAGTGCATACCTTTCCC GCCGTGTTGCAGTCCAGCGGCCTGT ACAGCCTGAGCTCCGTCGTGACAGT GCCGTCCTCCTCCCTTGGAACCAAG ACCTATACCTGCAACGTCGACCACA AGCCCTCCAACACCAAAGTGGACAA GCGCGTCGAATCCAAGTACGGCCCC CCTTGTCCGCCTTGTCCAGCCCCTGA GTTCCTGGGTGGTCCGTCCGTGTTCC TCTTCCCGCCCAAGCCGAAGGACAC TCTGATGATTTCACGCACCCCGGAA GTCACTTGCGTGGTCGTGGACGTGT CGCAGGAAGATCCCGAAGTGCAGTT CAATTGGTACGTGGATGGGGTCGAA GTGCACAACGCCAAGACCAAGCCTA GGGAAGAACAGTTCAACTCTACGTA CCGGGTGGTGTCCGTGCTGACCGTG CTGCACCAGGACTGGCTGAACGGAA AGGAGTACAAGTGCAAAGTGTCAA

			ACAAGGGCCTCCCTTCATCCATCGA AAAGACCATCAGCAAGGCCAAGGG TCAACCTAGGGAGCCCCAGGTCTAC ACTTTGCCGCCTAGCCAAGAAGAAA TGACTAAGAACCAAGTGTCCCTGAC TTGCCTTGTCAAGGGCTTTTATCCGT CCGACATCGCCGTGGAGTGGGAGTC CAACGGACAACCGGAGAACAACTA CAAGACCACCCCACCGGTGCTCGAT TCCGATGGCTCCTTCTTCCTGTACTC CCGGCTGACTGTGGACAAGTCAAGA TGGCAGGAGGGAAACGTGTTCTCCT GCTCCGTGATGCACGAAGCGCTGCA CAACCATTACACCCAGAAATCACTG TCACTTTCGCTGGGAAAA
SEQ ID 2003	QVQLQQSGPGLVKPSQTLSLTCAISGD SVSSKSAAWNWIRQSPSRGLEWLGRT YYRSKWNNDYALSVKSRITINPDTSKN QFSLQLKSVTPEDTALYYCVRQVAGG MDVWGQGTTVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTKTYTCNVDHKPSNTKV DKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQE DPEVQFNWYVDGVEVHNAKTKPREE QFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSLGK	SEQ ID 2111	CAGGTACAGCTGCAGCAGTCAGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCAAAAGTGC TGCTTGGAACTGGATCAGGCAGTCC CCATCGAGAGGCCTTGAGTGGCTGG GAAGGACATACTACAGGTCCAAATG GAATAATGATTATGCATTATCTGTG AAAAGTCGAATAACCATCAACCCAG ACACATCCAAGAACCAGTTCTCCCT GCAGCTGAAGTCTGTGACTCCCGAG GACACGGCTCTGTATTACTGTGTAA GACAAGTCGCGGGCGGTATGGACGT CTGGGGCCAAGGGACCACGGTCACC GTCTCCTCAGCATCCACCAAGGGGC CTTCCGTGTTCCCCCTGGCCCCTTGC TCCCGCTCGACCTCTGAATCCACCG CCGCACTCGGTTGCCTGGTCAAAGA CTACTTCCCCGAGCCCGTGACTGTC TCGTGGAACTCGGGCGCCCTCACAT CCGGAGTGCATACCTTTCCCGCCGT GTTGCAGTCCAGCGGCCTGTACAGC CTGAGCTCCGTCGTGACAGTGCCGT CCTCCTCCCTTGGAACCAAGACCTA TACCTGCAACGTCGACCACAAGCCC TCCAACACCAAAGTGGACAAGCGC GTCGAATCCAAGTACGGCCCCCCTT GTCCGCCTTGTCCAGCCCCTGAGTT CCTGGGTGGTCCGTCCGTGTTCCTCT TCCCGCCCAAGCCGAAGGACACTCT GATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGC AGGAAGATCCCGAAGTGCAGTTCAA TTGGTACGTGGATGGGGTCGAAGTG CACAACGCCAAGACCAAGCCTAGG GAAGAACAGTTCAACTCTACGTACC GGGTGGTGTCCGTGCTGACCGTGCT GCACCAGGACTGGCTGAACGGAAA GGAGTACAAGTGCAAAGTGTCAAA

			CAAGGGCCTCCCTTCATCCATCGAA AAGACCATCAGCAAGGCCAAGGGT CAACCTAGGGAGCCCCAGGTCTACA CTTTGCCGCCTAGCCAAGAAGAAAT GACTAAGAACCAAGTGTCCCTGACT TGCCTTGTCAAGGGCTTTTATCCGTC CGACATCGCCGTGGAGTGGGAGTCC AACGGACAACCGGAGAACAACTAC AAGACCACCCCACCGGTGCTCGATT CCGATGGCTCCTTCTTCCTGTACTCC CGGCTGACTGTGGACAAGTCAAGAT GGCAGGAGGGAAACGTGTTCTCCTG CTCCGTGATGCACGAAGCGCTGCAC AACCATTACACCCAGAAATCACTGT CACTTTCGCTGGGAAAA
SEQ ID 2004	QVQLVQSGGGLVQPGRSLRLSCTASGF TFGDYAMSWFRQAPGKGLEWVSAISG SGGSTYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKGSVYSGSY YMLIDYWGQGTLVTVSSASTKGPSVFP LAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSN TKVDKRVESKYGPPCPPCPAPEFLGGP SVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2112	CAGGTGCAGCTGGTGCAATCTGGGG GAGGCTTGGTACAGCCAGGGCGGTC CCTGAGACTCTCCTGTACAGCTTCT GGATTCACCTTTGGTGATTATGCTAT GAGCTGGTTCCGCCAGGCTCCAGGG AAGGGGCTGGAGTGGGTCTCAGCTA TTAGTGGTAGTGGTGGTAGCACATA CTATGCAGACTCCGTGAAGGGCCGA TTCACCATCTCCAGAGACAATTCCA AGAACACGCTGTATCTGCAAATGAA CAGCCTGAGAGCTGAGGACACGGCT GTGTATTACTGTGCGAAAGGATCGG TATATAGTGGGAGCTACTATATGCT CATTGACTACTGGGGCCAGGGCACC CTGGTCACCGTCTCCTCAGCATCCA CCAAGGGGCCTTCCGTGTTCCCCCT GGCCCCTTGCTCCCGCTCGACCTCT GAATCCACCGCCGCACTCGGTTGCC TGGTCAAAGACTACTTCCCCGAGCC CGTGACTGTCTCGTGGAACTCGGGC GCCCTCACATCCGGAGTGCATACCT TTCCCGCCGTGTTGCAGTCCAGCGG CCTGTACAGCCTGAGCTCCGTCGTG ACAGTGCCGTCCTCCTCCCTTGGAA CCAAGACCTATACCTGCAACGTCGA CCACAAGCCCTCCAACACCAAAGTG GACAAGCGCGTCGAATCCAAGTACG GCCCCCCTTGTCCGCCTTGTCCAGCC CCTGAGTTCCTGGGTGGTCCGTCCG TGTTCCTCTTCCCGCCCAAGCCGAA GGACACTCTGATGATTTCACGCACC CCGGAAGTCACTTGCGTGGTCGTGG ACGTGTCGCAGGAAGATCCCGAAGT GCAGTTCAATTGGTACGTGGATGGG GTCGAAGTGCACAACGCCAAGACC AAGCCTAGGGAAGAACAGTTCAACT CTACGTACCGGGTGGTGTCCGTGCT GACCGTGCTGCACCAGGACTGGCTG AACGGAAAGGAGTACAAGTGCAAA

			GTGTCAAACAAGGGCCTCCCTTCAT CCATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTACACTTTGCCGCCTAGCCAA GAAGAAATGACTAAGAACCAAGTG TCCCTGACTTGCCTTGTCAAGGGCTT TTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCCGGCTGACTGTGGACA AGTCAAGATGGCAGGAGGGAAACG TGTTCTCCTGCTCCGTGATGCACGA AGCGCTGCACAACCATTACACCCAG AAATCACTGTCACTTTCGCTGGGAA AA
SEQ ID 2005	QVQLQQSGPGLVRPSQTLSLTCVISGD SVSSGSAAWNWIRQSPSRGLEWLGRT YYRAKWYNEYAGSVKSRITISPDTSKN QFSLQLNSVTPEDTAVYFCTRQDKDNT RYSGLGVWGQGTTVTVSSASTKGPSV FPLAPCSRSTSESTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTKTYTCNVDHKP SNTKVDKRVESKYGPPCPPCPAPEFLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKT KPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKGQ PREPQVYTLPPSQEEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSRLTVDKSRWQEGNV FSCSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2113	CAGGTACAGCTGCAGCAGTCAGGTC CAGGACTGGTGAGGCCCTCGCAGAC CCTCTCACTCACCTGTGTCATCTCCG GGGACAGTGTCTCTAGCGGCAGTGC TGCTTGGAACTGGATCAGGCAGTCC CCATCGAGAGGCCTTGAGTGGCTGG GAAGGACATATTATAGGGCCAAGTG GTATAATGAATATGCAGGGTCTGTG AAAAGCCGAATAACCATCAGTCCGG ACACATCCAAGAACCAGTTCTCCCT GCAACTGAACTCTGTGACTCCCGAG GACACGGCTGTGTATTTCTGTACAA GACAAGACAAAGACAACACGAGAT ATTCCGGTTTGGGCGTCTGGGGCCA AGGGACCACGGTGACCGTCTCCTCA GCATCCACCAAGGGGCCTTCCGTGT TCCCCCTGGCCCCTTGCTCCCGCTCG ACCTCTGAATCCACCGCCGCACTCG GTTGCCTGGTCAAAGACTACTTCCC CGAGCCCGTGACTGTCTCGTGGAAC TCGGGCGCCCTCACATCCGGAGTGC ATACCTTTCCCGCCGTGTTGCAGTCC AGCGGCCTGTACAGCCTGAGCTCCG TCGTGACAGTGCCGTCCTCCTCCCTT GGAACCAAGACCTATACCTGCAACG TCGACCACAAGCCCTCCAACACCAA AGTGGACAAGCGCGTCGAATCCAA GTACGGCCCCCCTTGTCCGCCTTGTC CAGCCCCTGAGTTCCTGGGTGGTCC GTCCGTGTTCCTCTTCCCGCCCAAGC CGAAGGACACTCTGATGATTTCACG CACCCCGGAAGTCACTTGCGTGGTC GTGGACGTGTCGCAGGAAGATCCCG AAGTGCAGTTCAATTGGTACGTGGA TGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTT CAACTCTACGTACCGGGTGGTGTCC GTGCTGACCGTGCTGCACCAGGACT GGCTGAACGGAAAGGAGTACAAGT

			GCAAAGTGTCAAACAAGGGCCTCCC TTCATCCATCGAAAAGACCATCAGC AAGGCCAAGGGTCAACCTAGGGAG CCCCAGGTCTACACTTTGCCGCCTA GCCAAGAAGAAATGACTAAGAACC AAGTGTCCCTGACTTGCCTTGTCAA GGGCTTTTATCCGTCCGACATCGCC GTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACC CCACCGGTGCTCGATTCCGATGGCT CCTTCTTCCTGTACTCCCGGCTGACT GTGGACAAGTCAAGATGGCAGGAG GGAAACGTGTTCTCCTGCTCCGTGA TGCACGAAGCGCTGCACAACCATTA CACCCAGAAATCACTGTCACTTTCG CTGGGAAAA
SEQ ID 2006	EVQLVETGGGLVQPGGSLRLSCAASEF TLRNYGVSWVRQAPGKGLEWVSGMS GSGYSTYYADSVKGRFTISRDSSKNTL FLQMDSLRAEDTAIYYCARGPRMWSS GIDAFDIWGHGTMVTVSSASTKGPSVF PLAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSN TKVDKRVESKYGPPCPPCPAPEFLGGP SVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2114	GAGGTGCAGCTGGTGGAGACCGGG GGAGGCTTAGTTCAGCCTGGGGGGT CCCTGAGACTCTCCTGTGCAGCCTC TGAATTCACCCTTAGGAACTATGGC GTGAGCTGGGTCCGCCAGGCTCCAG GGAAGGGGCTGGAGTGGGTCTCAG GTATGAGTGGTAGTGGTTATAGTAC ATACTACGCAGACTCCGTGAAGGGC CGGTTCACCATCTCCAGAGACAGTT CCAAGAACACGCTGTTTCTGCAAAT GGACAGCCTGAGAGCCGAGGACAC GGCCATATATTACTGTGCGAGAGGG CCCCGAATGTGGAGCAGTGGCATTG ATGCTTTTGATATCTGGGGCCACGG GACAATGGTGACCGTCTCTTCAGCA TCCACCAAGGGGCCTTCCGTGTTCC CCCTGGCCCCTTGCTCCCGCTCGAC CTCTGAATCCACCGCCGCACTCGGT TGCCTGGTCAAAGACTACTTCCCCG AGCCCGTGACTGTCTCGTGGAACTC GGGCGCCCTCACATCCGGAGTGCAT ACCTTTCCCGCCGTGTTGCAGTCCA GCGGCCTGTACAGCCTGAGCTCCGT CGTGACAGTGCCGTCCTCCTCCCTT GGAACCAAGACCTATACCTGCAACG TCGACCACAAGCCCTCCAACACCAA AGTGGACAAGCGCGTCGAATCCAA GTACGGCCCCCCTTGTCCGCCTTGTC CAGCCCCTGAGTTCCTGGGTGGTCC GTCCGTGTTCCTCTTCCCGCCCAAGC CGAAGGACACTCTGATGATTTCACG CACCCCGGAAGTCACTTGCGTGGTC GTGGACGTGTCGCAGGAAGATCCCG AAGTGCAGTTCAATTGGTACGTGGA TGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTT CAACTCTACGTACCGGGTGGTGTCC GTGCTGACCGTGCTGCACCAGGACT

			GGCTGAACGGAAAGGAGTACAAGT GCAAAGTGTCAAACAAGGGCCTCCC TTCATCCATCGAAAAGACCATCAGC AAGGCCAAGGGTCAACCTAGGGAG CCCCAGGTCTACACTTTGCCGCCTA GCCAAGAAGAAATGACTAAGAACC AAGTGTCCCTGACTTGCCTTGTCAA GGGCTTTTATCCGTCCGACATCGCC GTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACC CCACCGGTGCTCGATTCCGATGGCT CCTTCTTCCTGTACTCCCGGCTGACT GTGGACAAGTCAAGATGGCAGGAG GGAAACGTGTTCTCCTGCTCCGTGA TGCACGAAGCGCTGCACAACCATTA CACCCAGAAATCACTGTCACTTTCG CTGGGAAAA
SEQ ID 2007	QVQLQQWGAGLLKPSETLSLTCAVYG GSVSGYYWSWIRQPPGKGLEWMGEIH HSGSTNYNPSLKSRVTISLDTPKNQFSL KLSSVTAADTAVYYCARRDWAGKRV WGQGTLVTVSSASTKGPSVFPLAPCSR STSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTKTYTCNVDHKPSNTKVDK RVESKYGPPCPPCPAPEFLGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSQEDP EVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKC KVSNKGLPSSIEKTISKAKGQPREPQVY TLPPSQEEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGS FFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSLGK	SEQ ID 2115	CAGGTGCAGCTACAGCAGTGGGGC GCAGGACTGTTGAAGCCTTCGGAGA CCCTGTCCCTCACCTGCGCTGTCTAT GGTGGGTCCGTCAGTGGTTACTACT GGAGCTGGATCCGCCAGCCCCCAGG GAAGGGGCTGGAGTGGATGGGGGA AATCCATCATAGTGGAAGCACCAAC TACAACCCGTCCCTCAAGAGTCGAG TCACCATATCACTAGACACGCCCAA GAACCAGTTCTCCCTGAAGCTAAGC TCTGTGACCGCCGCGGACACGGCTG TATATTACTGTGCGAGACGGGATTG GGCAGGAAAAAGGGTCTGGGGCCA GGGAACCCTGGTCACCGTCTCCTCA GCATCCACCAAGGGGCCTTCCGTGT TCCCCCTGGCCCCTTGCTCCCGCTCG ACCTCTGAATCCACCGCCGCACTCG GTTGCCTGGTCAAAGACTACTTCCC CGAGCCCGTGACTGTCTCGTGGAAC TCGGGCGCCCTCACATCCGGAGTGC ATACCTTTCCCGCCGTGTTGCAGTCC AGCGGCCTGTACAGCCTGAGCTCCG TCGTGACAGTGCCGTCCTCCTCCCTT GGAACCAAGACCTATACCTGCAACG TCGACCACAAGCCCTCCAACACCAA AGTGGACAAGCGCGTCGAATCCAA GTACGGCCCCCCTTGTCCGCCTTGTC CAGCCCCTGAGTTCCTGGGTGGTCC GTCCGTGTTCCTCTTCCCGCCCAAGC CGAAGGACACTCTGATGATTTCACG CACCCCGGAAGTCACTTGCGTGGTC GTGGACGTGTCGCAGGAAGATCCCG AAGTGCAGTTCAATTGGTACGTGGA TGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTT CAACTCTACGTACCGGGTGGTGTCC GTGCTGACCGTGCTGCACCAGGACT GGCTGAACGGAAAGGAGTACAAGT

			GCAAAGTGTCAAACAAGGGCCTCCC TTCATCCATCGAAAAGACCATCAGC AAGGCCAAGGGTCAACCTAGGGAG CCCCAGGTCTACACTTTGCCGCCTA GCCAAGAAGAAATGACTAAGAACC AAGTGTCCCTGACTTGCCTTGTCAA GGGCTTTTATCCGTCCGACATCGCC GTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACC CCACCGGTGCTCGATTCCGATGGCT CCTTCTTCCTGTACTCCCGGCTGACT GTGGACAAGTCAAGATGGCAGGAG GGAAACGTGTTCTCCTGCTCCGTGA TGCACGAAGCGCTGCACAACCATTA CACCCAGAAATCACTGTCACTTTCG CTGGGAAAA
SEQ ID 2008	QVQLQQSGPGLLKPSQTLSLTCAISGD SVSSNTATWNWIRQSPSRGLEWLGRT YYRSKWYKDNALSVKSRITINPDTSKN QFSLQLNSVTPEDTAVYYCAGGRAGIA AFDIWGQGTTVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTKTYTCNVDHKPSNTKV DKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQE DPEVQFNWYVDGVEVHNAKTKPREE QFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSLGK	SEQ ID 2116	CAGGTACAGCTGCAGCAGTCAGGTC CAGGACTATTAAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCAACACTGC TACTTGGAACTGGATCAGGCAGTCC CCATCGAGAGGCCTTGAGTGGCTGG GAAGGACATACTACAGGTCCAAGTG GTATAAGGATAATGCACTGTCTGTG AAAAGTCGAATAACCATCAACCCAG ACACATCCAAGAACCAGTTCTCCCT GCAGCTGAACTCTGTGACTCCCGAG GACACGGCTGTGTATTACTGTGCAG GAGGTCGGGCTGGTATTGCCGCTTT TGATATCTGGGGCCAAGGGACCACG GTCACCGTCTCCTCAGCATCCACCA AGGGGCCTTCCGTGTTCCCCCTGGC CCCTTGCTCCCGCTCGACCTCTGAAT CCACCGCCGCACTCGGTTGCCTGGT CAAAGACTACTTCCCCGAGCCCGTG ACTGTCTCGTGGAACTCGGGCGCCC TCACATCCGGAGTGCATACCTTTCC CGCCGTGTTGCAGTCCAGCGGCCTG TACAGCCTGAGCTCCGTCGTGACAG TGCCGTCCTCCTCCCTTGGAACCAA GACCTATACCTGCAACGTCGACCAC AAGCCCTCCAACACCAAAGTGGACA AGCGCGTCGAATCCAAGTACGGCCC CCCTTGTCCGCCTTGTCCAGCCCCTG AGTTCCTGGGTGGTCCGTCCGTGTT CCTCTTCCCGCCCAAGCCGAAGGAC ACTCTGATGATTTCACGCACCCCGG AAGTCACTTGCGTGGTCGTGGACGT GTCGCAGGAAGATCCCGAAGTGCA GTTCAATTGGTACGTGGATGGGGTC GAAGTGCACAACGCCAAGACCAAG CCTAGGGAAGAACAGTTCAACTCTA CGTACCGGGTGGTGTCCGTGCTGAC CGTGCTGCACCAGGACTGGCTGAAC GGAAAGGAGTACAAGTGCAAAGTG

			TCAAACAAGGGCCTCCCTTCATCCA TCGAAAAGACCATCAGCAAGGCCA AGGGTCAACCTAGGGAGCCCCAGGT CTACACTTTGCCGCCTAGCCAAGAA GAAATGACTAAGAACCAAGTGTCCC TGACTTGCCTTGTCAAGGGCTTTTAT CCGTCCGACATCGCCGTGGAGTGGG AGTCCAACGGACAACCGGAGAACA ACTACAAGACCACCCCACCGGTGCT CGATTCCGATGGCTCCTTCTTCCTGT ACTCCCGGCTGACTGTGGACAAGTC AAGATGGCAGGAGGGAAACGTGTT CTCCTGCTCCGTGATGCACGAAGCG CTGCACAACCATTACACCCAGAAAT CACTGTCACTTTCGCTGGGAAAA
SEQ ID 2009	QVQLVQSGGGLIQPGGSLRLSCAASGF TVSSNYMSWVRQAPGKGLEWVSLIYS DGRTNYADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCAKGALQGEWR RFDYWGQGTLVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTKTYTCNVDHKPSNTKV DKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQE DPEVQFNWYVDGVEVHNAKTKPREE QFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSLGK	SEQ ID 2117	CAGGTGCAGCTGGTGCAATCTGGAG GAGGCTTGATCCAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGGTTCACCGTCAGTAGCAACTACA TGAGCTGGGTCCGCCAGGCTCCAGG GAAGGGGCTGGAATGGGTCTCACTT ATTTATAGTGATGGTCGCACAAACT ATGCAGACTCCGTGAAGGGCCGATT CACCATCTCCAGAGACAATTCCAAG AACACGCTGTATCTGCAAATGAACA GCCTGAGAGCCGAGGACACGGCCG TATATTACTGTGCGAAGGGGGCCCT ACAGGGCGAATGGCGGAGATTTGA CTACTGGGGCCAGGGCACCCTGGTC ACCGTCTCCTCAGCATCCACCAAGG GGCCTTCCGTGTTCCCCCTGGCCCCT TGCTCCCGCTCGACCTCTGAATCCA CCGCCGCACTCGGTTGCCTGGTCAA AGACTACTTCCCCGAGCCCGTGACT GTCTCGTGGAACTCGGGCGCCCTCA CATCCGGAGTGCATACCTTTCCCGC CGTGTTGCAGTCCAGCGGCCTGTAC AGCCTGAGCTCCGTCGTGACAGTGC CGTCCTCCTCCCTTGGAACCAAGAC CTATACCTGCAACGTCGACCACAAG CCCTCCAACACCAAAGTGGACAAGC GCGTCGAATCCAAGTACGGCCCCCC TTGTCCGCCTTGTCCAGCCCCTGAGT TCCTGGGTGGTCCGTCCGTGTTCCTC TTCCCGCCCAAGCCGAAGGACACTC TGATGATTTCACGCACCCCGGAAGT CACTTGCGTGGTCGTGGACGTGTCG CAGGAAGATCCCGAAGTGCAGTTCA ATTGGTACGTGGATGGGGTCGAAGT GCACAACGCCAAGACCAAGCCTAG GGAAGAACAGTTCAACTCTACGTAC CGGGTGGTGTCCGTGCTGACCGTGC TGCACCAGGACTGGCTGAACGGAA AGGAGTACAAGTGCAAAGTGTCAA

			ACAAGGGCCTCCCTTCATCCATCGA AAAGACCATCAGCAAGGCCAAGGG TCAACCTAGGGAGCCCCAGGTCTAC ACTTTGCCGCCTAGCCAAGAAGAAA TGACTAAGAACCAAGTGTCCCTGAC TTGCCTTGTCAAGGGCTTTTATCCGT CCGACATCGCCGTGGAGTGGGAGTC CAACGGACAACCGGAGAACAACTA CAAGACCACCCCACCGGTGCTCGAT TCCGATGGCTCCTTCTTCCTGTACTC CCGGCTGACTGTGGACAAGTCAAGA TGGCAGGAGGGAAACGTGTTCTCCT GCTCCGTGATGCACGAAGCGCTGCA CAACCATTACACCCAGAAATCACTG TCACTTTCGCTGGGAAAA
SEQ ID 2010	QVQLQQSGPGLVKPSQTLSLTCAISGD SVSSNSAAWNWIRQSPSRGLEWLGRT YYRSKWYNDYAVSVKSRITINPDTSKN QFSLQLNSVTPEDTAVYYCTRTNQGY GGNSGVFDYWGQGTLVTVSSASTKGP SVFPLAPCSRSTSESTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSG LYSLSSVVTVPSSSLGTKTYTCNVDHK PSNTKVDKRVESKYGPPCPPCPAPEFL GGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSQEDPEVQFNWYVDGVEVHNAK TKPREEQFNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKGLPSSIEKTISKAKG QPREPQVYTLPPSQEEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSRLTVDKSRWQEGN VFSCSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2118	CAGGTGCAGCTACAGCAGTCAGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCAACAGTGC TGCTTGGAACTGGATCAGGCAGTCC CCATCGAGAGGCCTTGAGTGGCTGG GAAGGACATATTACAGGTCCAAGTG GTATAATGATTATGCAGTATCTGTG AAAAGTCGAATAACCATCAACCCAG ACACATCCAAGAACCAGTTCTCCCT GCAGCTGAACTCTGTGACTCCCGAG GACACGGCTGTGTATTACTGTACAA GAACCAACCAGGGATACGGTGGTA ACTCCGGGGTATTTGACTACTGGGG CCAGGGAACCCTGGTCACCGTCTCC TCAGCATCCACCAAGGGGCCTTCCG TGTTCCCCCTGGCCCCTTGCTCCCGC TCGACCTCTGAATCCACCGCCGCAC TCGGTTGCCTGGTCAAAGACTACTT CCCCGAGCCCGTGACTGTCTCGTGG AACTCGGGCGCCCTCACATCCGGAG TGCATACCTTTCCCGCCGTGTTGCA GTCCAGCGGCCTGTACAGCCTGAGC TCCGTCGTGACAGTGCCGTCCTCCT CCCTTGGAACCAAGACCTATACCTG CAACGTCGACCACAAGCCCTCCAAC ACCAAAGTGGACAAGCGCGTCGAA TCCAAGTACGGCCCCCCTTGTCCGC CTTGTCCAGCCCCTGAGTTCCTGGG TGGTCCGTCCGTGTTCCTCTTCCCGC CCAAGCCGAAGGACACTCTGATGAT TTCACGCACCCCGGAAGTCACTTGC GTGGTCGTGGACGTGTCGCAGGAAG ATCCCGAAGTGCAGTTCAATTGGTA CGTGGATGGGGTCGAAGTGCACAAC GCCAAGACCAAGCCTAGGGAAGAA CAGTTCAACTCTACGTACCGGGTGG TGTCCGTGCTGACCGTGCTGCACCA GGACTGGCTGAACGGAAAGGAGTA

			CAAGTGCAAAGTGTCAAACAAGGG CCTCCCTTCATCCATCGAAAAGACC ATCAGCAAGGCCAAGGGTCAACCTA GGGAGCCCCAGGTCTACACTTTGCC GCCTAGCCAAGAAGAAATGACTAA GAACCAAGTGTCCCTGACTTGCCTT GTCAAGGGCTTTTATCCGTCCGACA TCGCCGTGGAGTGGGAGTCCAACGG ACAACCGGAGAACAACTACAAGAC CACCCCACCGGTGCTCGATTCCGAT GGCTCCTTCTTCCTGTACTCCCGGCT GACTGTGGACAAGTCAAGATGGCA GGAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACT TTCGCTGGGAAAA
SEQ ID 2011	QVQLQQSGPGLVKPSQTLSLTCAISGD SVSGNSAAWNWIRQSPSRGLEWLGRT YYRSKWYNDYAVSVKSRITINPDTSKN QFSLQLNSVTPEDTAVYYCARIVGGAV DCWGQGTLVTVSSASTKGPSVFPLAPC SRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTKTYTCNVDHKPSNTKVD KRVESKYGPPCPPCPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSQED PEVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKC KVSNKGLPSSIEKTISKAKGQPREPQVY TLPPSQEEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGS FFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSLGK	SEQ ID 2119	CAGGTGCAGCTACAGCAGTCAGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTGGCAACAGTGC TGCTTGGAACTGGATCAGGCAGTCC CCATCGAGAGGCCTTGAGTGGCTGG GAAGGACATACTACAGGTCCAAGTG GTATAATGATTATGCAGTATCTGTG AAAAGTCGAATAACCATCAACCCAG ACACATCCAAGAACCAGTTCTCCCT GCAGTTGAATTCTGTGACTCCCGAG GACACGGCTGTGTATTACTGTGCGA GGATAGTGGGAGGTGCCGTTGACTG CTGGGGCCAGGGAACCCTGGTGACC GTCTCCTCAGCATCCACCAAGGGGC CTTCCGTGTTCCCCCTGGCCCCTTGC TCCCGCTCGACCTCTGAATCCACCG CCGCACTCGGTTGCCTGGTCAAAGA CTACTTCCCCGAGCCCGTGACTGTC TCGTGGAACTCGGGCGCCCTCACAT CCGGAGTGCATACCTTTCCCGCCGT GTTGCAGTCCAGCGGCCTGTACAGC CTGAGCTCCGTCGTGACAGTGCCGT CCTCCTCCCTTGGAACCAAGACCTA TACCTGCAACGTCGACCACAAGCCC TCCAACACCAAAGTGGACAAGCGC GTCGAATCCAAGTACGGCCCCCCTT GTCCGCCTTGTCCAGCCCCTGAGTT CCTGGGTGGTCCGTCCGTGTTCCTCT TCCCGCCCAAGCCGAAGGACACTCT GATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGC AGGAAGATCCCGAAGTGCAGTTCAA TTGGTACGTGGATGGGGTCGAAGTG CACAACGCCAAGACCAAGCCTAGG GAAGAACAGTTCAACTCTACGTACC GGGTGGTGTCCGTGCTGACCGTGCT GCACCAGGACTGGCTGAACGGAAA

			GGAGTACAAGTGCAAAGTGTCAAA CAAGGGCCTCCCTTCATCCATCGAA AAGACCATCAGCAAGGCCAAGGGT CAACCTAGGGAGCCCCAGGTCTACA CTTTGCCGCCTAGCCAAGAAGAAAT GACTAAGAACCAAGTGTCCCTGACT TGCCTTGTCAAGGGCTTTTATCCGTC CGACATCGCCGTGGAGTGGGAGTCC AACGGACAACCGGAGAACAACTAC AAGACCACCCCACCGGTGCTCGATT CCGATGGCTCCTTCTTCCTGTACTCC CGGCTGACTGTGGACAAGTCAAGAT GGCAGGAGGGAAACGTGTTCTCCTG CTCCGTGATGCACGAAGCGCTGCAC AACCATTACACCCAGAAATCACTGT CACTTTCGCTGGGAAAA
SEQ ID 2012	EVQLVQSGAEVKKPGASVKVSCKASG YTFTSYAMHWVRQAPGQRLEWMGWI NAGNGNTKYSQKFQGRVTITRDTSAST AYMELSSLRSEDTAVYYCARVRVGAT TVYDSWFDPWGQGTLVTVSSASTKGP SVFPLAPCSRSTSESTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSG LYSLSSVVTVPSSSLGTKTYTCNVDHK PSNTKVDKRVESKYGPPCPPCPAPEFL GGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSQEDPEVQFNWYVDGVEVHNAK TKPREEQFNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKGLPSSIEKTISKAKG QPREPQVYTLPPSQEEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSRLTVDKSRWQEGN VFSCSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2120	GAGGTGCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTTTCCTGCAAGGCTTCT GGATACACCTTCACTAGCTATGCTA TGCATTGGGTGCGCCAGGCCCCCGG ACAAAGGCTTGAGTGGATGGGATG GATCAACGCTGGCAATGGTAACACA AAATATTCACAGAAGTTCCAGGGCA GAGTCACCATTACCAGGGACACATC CGCGAGCACAGCCTACATGGAGCTG AGCAGCCTGAGATCTGAAGACACG GCTGTGTATTACTGTGCGAGAGTTA GAGTGGGAGCTACTACTGTTTACGA CAGCTGGTTCGACCCCTGGGGCCAG GGAACCCTGGTGACCGTCTCCTCAG CATCCACCAAGGGGCCTTCCGTGTT CCCCCTGGCCCCTTGCTCCCGCTCG ACCTCTGAATCCACCGCCGCACTCG GTTGCCTGGTCAAAGACTACTTCCC CGAGCCCGTGACTGTCTCGTGGAAC TCGGGCGCCCTCACATCCGGAGTGC ATACCTTTCCCGCCGTGTTGCAGTCC AGCGGCCTGTACAGCCTGAGCTCCG TCGTGACAGTGCCGTCCTCCTCCCTT GGAACCAAGACCTATACCTGCAACG TCGACCACAAGCCCTCCAACACCAA AGTGGACAAGCGCGTCGAATCCAA GTACGGCCCCCCTTGTCCGCCTTGTC CAGCCCCTGAGTTCCTGGGTGGTCC GTCCGTGTTCCTCTTCCCGCCCAAGC CGAAGGACACTCTGATGATTTCACG CACCCCGGAAGTCACTTGCGTGGTC GTGGACGTGTCGCAGGAAGATCCCG AAGTGCAGTTCAATTGGTACGTGGA TGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTT CAACTCTACGTACCGGGTGGTGTCC GTGCTGACCGTGCTGCACCAGGACT GGCTGAACGGAAAGGAGTACAAGT

			GCAAAGTGTCAAACAAGGGCCTCCC TTCATCCATCGAAAAGACCATCAGC AAGGCCAAGGGTCAACCTAGGGAG CCCCAGGTCTACACTTTGCCGCCTA GCCAAGAAGAAATGACTAAGAACC AAGTGTCCCTGACTTGCCTTGTCAA GGGCTTTTATCCGTCCGACATCGCC GTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACC CCACCGGTGCTCGATTCCGATGGCT CCTTCTTCCTGTACTCCCGGCTGACT GTGGACAAGTCAAGATGGCAGGAG GGAAACGTGTTCTCCTGCTCCGTGA TGCACGAAGCGCTGCACAACCATTA CACCCAGAAATCACTGTCACTTTCG CTGGGAAAA
SEQ ID 2013	QVQLVQSGGGLVQPGGSLRLSCAASG FTFSSYAMSWVRQAPGKGLEWVSAIS GSGGSTYYADSVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCAKDGGSSPY YDSSGLLPWYFDLWGRGTLVTVSSAS TKGPSVFPLAPCSRSTSESTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTKTYTCN VDHKPSNTKVDKRVESKYGPPCPPCPA PEFLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSQEDPEVQFNWYVDGVEV HNAKTKPREEQFNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKGLPSSIEKTIS KAKGQPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSRLTVDKSRW QEGNVFSCSVMHEALHNHYTQKSLSL SLGK	SEQ ID 2121	CAGGTGCAGCTGGTGCAGTCTGGGG GAGGCTTGGTACAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTTAGCAGCTATGCCA TGAGCTGGGTCCGCCAGGCTCCAGG GAAGGGGCTGGAGTGGGTCTCAGCT ATTAGTGGTAGTGGTGGTAGCACAT ACTACGCAGACTCCGTGAAGGGCCG GTTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCCGAGGACACGG CCGTATATTACTGTGCGAAAGATGG GGGGTCCAGCCCATACTATGATAGT AGTGGTTTACTACCCTGGTACTTCG ATCTCTGGGGCCGTGGCACCCTGGT CACCGTCTCCTCAGCATCCACCAAG GGGCCTTCCGTGTTCCCCCTGGCCC CTTGCTCCCGCTCGACCTCTGAATCC ACCGCCGCACTCGGTTGCCTGGTCA AAGACTACTTCCCCGAGCCCGTGAC TGTCTCGTGGAACTCGGGCGCCCTC ACATCCGGAGTGCATACCTTTCCCG CCGTGTTGCAGTCCAGCGGCCTGTA CAGCCTGAGCTCCGTCGTGACAGTG CCGTCCTCCTCCCTTGGAACCAAGA CCTATACCTGCAACGTCGACCACAA GCCCTCCAACACCAAAGTGGACAAG CGCGTCGAATCCAAGTACGGCCCCC CTTGTCCGCCTTGTCCAGCCCCTGA GTTCCTGGGTGGTCCGTCCGTGTTCC TCTTCCCGCCCAAGCCGAAGGACAC TCTGATGATTTCACGCACCCCGGAA GTCACTTGCGTGGTCGTGGACGTGT CGCAGGAAGATCCCGAAGTGCAGTT CAATTGGTACGTGGATGGGGTCGAA GTGCACAACGCCAAGACCAAGCCTA GGGAAGAACAGTTCAACTCTACGTA CCGGGTGGTGTCCGTGCTGACCGTG

			CTGCACCAGGACTGGCTGAACGGAA AGGAGTACAAGTGCAAAGTGTCAA ACAAGGGCCTCCCTTCATCCATCGA AAAGACCATCAGCAAGGCCAAGGG TCAACCTAGGGAGCCCCAGGTCTAC ACTTTGCCGCCTAGCCAAGAAGAAA TGACTAAGAACCAAGTGTCCCTGAC TTGCCTTGTCAAGGGCTTTTATCCGT CCGACATCGCCGTGGAGTGGGAGTC CAACGGACAACCGGAGAACAACTA CAAGACCACCCCACCGGTGCTCGAT TCCGATGGCTCCTTCTTCCTGTACTC CCGGCTGACTGTGGACAAGTCAAGA TGGCAGGAGGGAAACGTGTTCTCCT GCTCCGTGATGCACGAAGCGCTGCA CAACCATTACACCCAGAAATCACTG TCACTTTCGCTGGGAAAA
SEQ ID 2014	QVQLQESGGGLVQPGGSLRLSCAASG FTFSSYAMHWVRQAPGKGLEYVSAISS NGGSTYYANSVKGRFTISRDNSKNTLY LQMGSLRAEDMAVYYCARAKFWTYY FDYWGQGTLVTVSSASTKGPSVFPLAP CSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTKTYTCNVDHKPSNTKV DKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQE DPEVQFNWYVDGVEVHNAKTKPREE QFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSLGK	SEQ ID 2122	CAGGTGCAGCTGCAGGAGTCGGGG GGAGGCTTGGTCCAGCCTGGGGGGT CCCTGAGACTCTCCTGTGCAGCCTC TGGATTCACCTTCAGTAGCTATGCT ATGCACTGGGTCCGCCAGGCTCCAG GGAAGGGACTGGAATATGTTTCAGC TATTAGTAGTAATGGGGGTAGCACA TATTATGCAAACTCTGTGAAGGGCA GATTCACCATCTCCAGAGACAATTC CAAGAACACGCTGTATCTTCAAATG GGCAGCCTGAGAGCTGAGGACATG GCTGTGTATTACTGTGCGAGAGCTA AGTTTTGGACATACTACTTTGACTA CTGGGGCCAGGGAACCCTGGTGACC GTCTCCTCAGCATCCACCAAGGGGC CTTCCGTGTTCCCCCTGGCCCCTTGC TCCCGCTCGACCTCTGAATCCACCG CCGCACTCGGTTGCCTGGTCAAAGA CTACTTCCCCGAGCCCGTGACTGTC TCGTGGAACTCGGGCGCCCTCACAT CCGGAGTGCATACCTTTCCCGCCGT GTTGCAGTCCAGCGGCCTGTACAGC CTGAGCTCCGTCGTGACAGTGCCGT CCTCCTCCCTTGGAACCAAGACCTA TACCTGCAACGTCGACCACAAGCCC TCCAACACCAAAGTGGACAAGCGC GTCGAATCCAAGTACGGCCCCCCTT GTCCGCCTTGTCCAGCCCCTGAGTT CCTGGGTGGTCCGTCCGTGTTCCTCT TCCCGCCCAAGCCGAAGGACACTCT GATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGC AGGAAGATCCCGAAGTGCAGTTCAA TTGGTACGTGGATGGGGTCGAAGTG CACAACGCCAAGACCAAGCCTAGG GAAGAACAGTTCAACTCTACGTACC GGGTGGTGTCCGTGCTGACCGTGCT GCACCAGGACTGGCTGAACGGAAA

			GGAGTACAAGTGCAAAGTGTCAAA CAAGGGCCTCCCTTCATCCATCGAA AAGACCATCAGCAAGGCCAAGGGT CAACCTAGGGAGCCCCAGGTCTACA CTTTGCCGCCTAGCCAAGAAGAAAT GACTAAGAACCAAGTGTCCCTGACT TGCCTTGTCAAGGGCTTTTATCCGTC CGACATCGCCGTGGAGTGGGAGTCC AACGGACAACCGGAGAACAACTAC AAGACCACCCCACCGGTGCTCGATT CCGATGGCTCCTTCTTCCTGTACTCC CGGCTGACTGTGGACAAGTCAAGAT GGCAGGAGGGAAACGTGTTCTCCTG CTCCGTGATGCACGAAGCGCTGCAC AACCATTACACCCAGAAATCACTGT CACTTTCGCTGGGAAAA
SEQ ID 2015	QVQLQQWGAGLLKPSETLSLTCAVYG GSFSGYYWSWIRQPPGKGLEWIGEINH SGSTNYNPSLKSRVTISVDTSKNQFSLK LSSVTAADTAVYYCARGGGSGSYYKR FFDYWGQGTLVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTKTYTCNVDHKPSNTKV DKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQE DPEVQFNWYVDGVEVHNAKTKPREE QFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSLGK	SEQ ID 2123	CAGGTGCAGCTACAGCAGTGGGGC GCAGGACTGTTGAAGCCTTCGGAGA CCCTGTCCCTCACCTGCGCTGTCTAT GGTGGGTCCTTCAGTGGTTACTACT GGAGCTGGATCCGCCAGCCCCCAGG GAAGGGGCTGGAGTGGATTGGGGA AATCAATCATAGTGGAAGCACCAAC TACAACCCGTCCCTCAAGAGTCGAG TCACCATATCAGTAGACACGTCCAA GAACCAGTTCTCCCTGAAGCTGAGC TCTGTGACCGCCGCGGACACGGCTG TGTATTACTGTGCGAGAGGCGGTGG TTCGGGGAGTTATTATAAGAGGTTC TTTGACTACTGGGGCCAGGGAACCC TGGTCACCGTCTCCTCAGCATCCAC CAAGGGGCCTTCCGTGTTCCCCCTG GCCCCTTGCTCCCGCTCGACCTCTG AATCCACCGCCGCACTCGGTTGCCT GGTCAAAGACTACTTCCCCGAGCCC GTGACTGTCTCGTGGAACTCGGGCG CCCTCACATCCGGAGTGCATACCTT TCCCGCCGTGTTGCAGTCCAGCGGC CTGTACAGCCTGAGCTCCGTCGTGA CAGTGCCGTCCTCCTCCCTTGGAAC CAAGACCTATACCTGCAACGTCGAC CACAAGCCCTCCAACACCAAAGTGG ACAAGCGCGTCGAATCCAAGTACGG CCCCCCTTGTCCGCCTTGTCCAGCCC CTGAGTTCCTGGGTGGTCCGTCCGT GTTCCTCTTCCCGCCCAAGCCGAAG GACACTCTGATGATTTCACGCACCC CGGAAGTCACTTGCGTGGTCGTGGA CGTGTCGCAGGAAGATCCCGAAGTG CAGTTCAATTGGTACGTGGATGGGG TCGAAGTGCACAACGCCAAGACCA AGCCTAGGGAAGAACAGTTCAACTC TACGTACCGGGTGGTGTCCGTGCTG ACCGTGCTGCACCAGGACTGGCTGA ACGGAAAGGAGTACAAGTGCAAAG

			TGTCAAACAAGGGCCTCCCTTCATC CATCGAAAAGACCATCAGCAAGGC CAAGGGTCAACCTAGGGAGCCCCA GGTCTACACTTTGCCGCCTAGCCAA GAAGAAATGACTAAGAACCAAGTG TCCCTGACTTGCCTTGTCAAGGGCTT TTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCCGGCTGACTGTGGACA AGTCAAGATGGCAGGAGGGAAACG TGTTCTCCTGCTCCGTGATGCACGA AGCGCTGCACAACCATTACACCCAG AAATCACTGTCACTTTCGCTGGGAA AA
SEQ ID 2016	EVQLVQSGAEVRKPGASVKVSCKASG YTFTSYAISWVRQAPGQGLEWMGWIS AYDGNTNYAQKLQGRVTMTTDTSTST AYMEVRSLRSDDTAVYYCARDGTVR RVVGATTPGNFDYRGQGTLVTVSSAS TKGPSVFPLAPCSRSTSESTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTKTYTCN VDHKPSNTKVDKRVESKYGPPCPPCPA PEFLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSQEDPEVQFNWYVDGVEV HNAKTKPREEQFNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKGLPSSIEKTIS KAKGQPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSRLTVDKSRW QEGNVFSCSVMHEALHNHYTQKSLSL SLGK	SEQ ID 2124	GAGGTGCAGCTGGTGCAGTCTGGAG CTGAGGTGAGGAAGCCTGGGGCCTC AGTGAAGGTCTCCTGCAAGGCTTCT GGTTACACATTTACCAGTTATGCCA TCAGCTGGGTGCGACAGGCCCCTGG ACAAGGGCTTGAGTGGATGGGGTG GATCAGCGCTTACGACGGTAACACA AACTATGCACAGAAGCTCCAGGGCA GAGTCACCATGACCACAGACACATC CACGAGCACAGCCTACATGGAGGTG AGGAGCCTGAGATCTGACGACACG GCCGTGTATTACTGTGCGAGAGATG GTACGGTCCGAAGGGTAGTGGGAG CTACTACCCCTGGAAACTTTGACTA CAGGGGCCAGGGAACCCTGGTCACC GTCTCCTCAGCATCCACCAAGGGGC CTTCCGTGTTCCCCCTGGCCCCTTGC TCCCGCTCGACCTCTGAATCCACCG CCGCACTCGGTTGCCTGGTCAAAGA CTACTTCCCCGAGCCCGTGACTGTC TCGTGGAACTCGGGCGCCCTCACAT CCGGAGTGCATACCTTTCCCGCCGT GTTGCAGTCCAGCGGCCTGTACAGC CTGAGCTCCGTCGTGACAGTGCCGT CCTCCTCCCTTGGAACCAAGACCTA TACCTGCAACGTCGACCACAAGCCC TCCAACACCAAAGTGGACAAGCGC GTCGAATCCAAGTACGGCCCCCCTT GTCCGCCTTGTCCAGCCCCTGAGTT CCTGGGTGGTCCGTCCGTGTTCCTCT TCCCGCCCAAGCCGAAGGACACTCT GATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGC AGGAAGATCCCGAAGTGCAGTTCAA TTGGTACGTGGATGGGGTCGAAGTG CACAACGCCAAGACCAAGCCTAGG GAAGAACAGTTCAACTCTACGTACC GGGTGGTGTCCGTGCTGACCGTGCT GCACCAGGACTGGCTGAACGGAAA

			GGAGTACAAGTGCAAAGTGTCAAA CAAGGGCCTCCCTTCATCCATCGAA AAGACCATCAGCAAGGCCAAGGGT CAACCTAGGGAGCCCCAGGTCTACA CTTTGCCGCCTAGCCAAGAAGAAAT GACTAAGAACCAAGTGTCCCTGACT TGCCTTGTCAAGGGCTTTTATCCGTC CGACATCGCCGTGGAGTGGGAGTCC AACGGACAACCGGAGAACAACTAC AAGACCACCCCACCGGTGCTCGATT CCGATGGCTCCTTCTTCCTGTACTCC CGGCTGACTGTGGACAAGTCAAGAT GGCAGGAGGGAAACGTGTTCTCCTG CTCCGTGATGCACGAAGCGCTGCAC AACCATTACACCCAGAAATCACTGT CACTTTCGCTGGGAAAA
SEQ ID 2017	EVQLVQSGGGVVQPGRSLRLSCAASG FTFSSYGMHWVRQAPGKGLEWVAVI WYDGSNKYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARDLNRG YCSGGSCFGYWGQGTLVTVSSASTKG PSVFPLAPCSRSTSESTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTKTYTCNVDH KPSNTKVDKRVESKYGPPCPPCPAPEF LGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSQEDPEVQFNWYVDGVEVHNA KTKPREEQFNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKGLPSSIEKTISKAK GQPREPQVYTLPPSQEEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSRLTVDKSRWQEG NVFSCSVMHEALHNHYTQKSLSLSLG K	SEQ ID 2125	GAGGTGCAGCTGGTGCAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCGTCT GGATTCACCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTT ATATGGTATGATGGAAGTAATAAAT ACTATGCAGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCCGAGGACACGG CTGTGTATTACTGTGCGAGAGATCT GAATCGAGGATATTGTAGTGGTGGT AGCTGCTTTGGCTACTGGGGCCAGG GAACCCTGGTCACCGTCTCCTCAGC ATCCACCAAGGGGCCTTCCGTGTTC CCCCTGGCCCCTTGCTCCCGCTCGA CCTCTGAATCCACCGCCGCACTCGG TTGCCTGGTCAAAGACTACTTCCCC GAGCCCGTGACTGTCTCGTGGAACT CGGGCGCCCTCACATCCGGAGTGCA TACCTTTCCCGCCGTGTTGCAGTCCA GCGGCCTGTACAGCCTGAGCTCCGT CGTGACAGTGCCGTCCTCCTCCCTT GGAACCAAGACCTATACCTGCAACG TCGACCACAAGCCCTCCAACACCAA AGTGGACAAGCGCGTCGAATCCAA GTACGGCCCCCCTTGTCCGCCTTGTC CAGCCCCTGAGTTCCTGGGTGGTCC GTCCGTGTTCCTCTTCCCGCCCAAGC CGAAGGACACTCTGATGATTTCACG CACCCCGGAAGTCACTTGCGTGGTC GTGGACGTGTCGCAGGAAGATCCCG AAGTGCAGTTCAATTGGTACGTGGA TGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTT CAACTCTACGTACCGGGTGGTGTCC GTGCTGACCGTGCTGCACCAGGACT

			GGCTGAACGGAAAGGAGTACAAGT GCAAAGTGTCAAACAAGGGCCTCCC TTCATCCATCGAAAAGACCATCAGC AAGGCCAAGGGTCAACCTAGGGAG CCCCAGGTCTACACTTTGCCGCCTA GCCAAGAAGAAATGACTAAGAACC AAGTGTCCCTGACTTGCCTTGTCAA GGGCTTTTATCCGTCCGACATCGCC GTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACC CCACCGGTGCTCGATTCCGATGGCT CCTTCTTCCTGTACTCCCGGCTGACT GTGGACAAGTCAAGATGGCAGGAG GGAAACGTGTTCTCCTGCTCCGTGA TGCACGAAGCGCTGCACAACCATTA CACCCAGAAATCACTGTCACTTTCG CTGGGAAAA
SEQ ID 2018	QVQLQESGGGLVQPGGSLRLSCAASG FTFSSYAMSWVRQAPGKGLEWVSYIS SSGTTIYYADSVKGRFTVSRDNAKNSL YLQMNSLRAEDTAVYYCARDYSSSGE CFDYWGQGTLVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTKTYTCNVDHKPSNTKV DKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQE DPEVQFNWYVDGVEVHNAKTKPREE QFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSLGK	SEQ ID 2126	CAGGTGCAGCTGCAGGAGTCTGGGG GAGGCTTGGTACAGCCGGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTTAGCAGCTATGCCA TGAGCTGGGTCCGCCAGGCTCCAGG GAAGGGGCTGGAGTGGGTTTCATAC ATTAGTAGTAGTGGTACTACCATAT ACTACGCAGACTCTGTGAAGGGCCG ATTCACCGTCTCCAGAGACAATGCC AAGAACTCACTGTATCTGCAAATGA ACAGCCTGAGAGCCGAGGACACGG CCGTGTATTACTGTGCGAGGGATTA TAGCAGCTCGGGGGAGTGCTTTGAC TACTGGGGCCAGGGAACCCTGGTCA CCGTCTCCTCAGCATCCACCAAGGG GCCTTCCGTGTTCCCCCTGGCCCCTT GCTCCCGCTCGACCTCTGAATCCAC CGCCGCACTCGGTTGCCTGGTCAAA GACTACTTCCCCGAGCCCGTGACTG TCTCGTGGAACTCGGGCGCCCTCAC ATCCGGAGTGCATACCTTTCCCGCC GTGTTGCAGTCCAGCGGCCTGTACA GCCTGAGCTCCGTCGTGACAGTGCC GTCCTCCTCCCTTGGAACCAAGACC TATACCTGCAACGTCGACCACAAGC CCTCCAACACCAAAGTGGACAAGCG CGTCGAATCCAAGTACGGCCCCCCT TGTCCGCCTTGTCCAGCCCCTGAGTT CCTGGGTGGTCCGTCCGTGTTCCTCT TCCCGCCCAAGCCGAAGGACACTCT GATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGC AGGAAGATCCCGAAGTGCAGTTCAA TTGGTACGTGGATGGGGTCGAAGTG CACAACGCCAAGACCAAGCCTAGG GAAGAACAGTTCAACTCTACGTACC GGGTGGTGTCCGTGCTGACCGTGCT GCACCAGGACTGGCTGAACGGAAA

			GGAGTACAAGTGCAAAGTGTCAAA CAAGGGCCTCCCTTCATCCATCGAA AAGACCATCAGCAAGGCCAAGGGT CAACCTAGGGAGCCCCAGGTCTACA CTTTGCCGCCTAGCCAAGAAGAAAT GACTAAGAACCAAGTGTCCCTGACT TGCCTTGTCAAGGGCTTTTATCCGTC CGACATCGCCGTGGAGTGGGAGTCC AACGGACAACCGGAGAACAACTAC AAGACCACCCCACCGGTGCTCGATT CCGATGGCTCCTTCTTCCTGTACTCC CGGCTGACTGTGGACAAGTCAAGAT GGCAGGAGGGAAACGTGTTCTCCTG CTCCGTGATGCACGAAGCGCTGCAC AACCATTACACCCAGAAATCACTGT CACTTTCGCTGGGAAAA
SEQ ID 2019	EVQLVQSGGGVVQPGRSLRLSCAASG FTFSSYGMHWVRQAPGKGLEWVAVI WYDGSNKYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARDQAA MVGYFDYWGQGTLVTVSSASTKGPSV FPLAPCSRSTSESTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTKTYTCNVDHKP SNTKVDKRVESKYGPPCPPCPAPEFLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKT KPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKGQ PREPQVYTLPPSQEEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSRLTVDKSRWQEGNV FSCSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2127	GAGGTGCAGCTGGTGCAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCGTCT GGATTCACCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTT ATATGGTATGATGGAAGTAATAAAT ACTATGCAGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCCGAGGACACGG CTGTGTATTACTGTGCGAGAGATCA GGCAGCTATGGTAGGCTACTTTGAC TACTGGGGCCAGGGAACCCTGGTCA CCGTCTCCTCAGCATCCACCAAGGG GCCTTCCGTGTTCCCCCTGGCCCCTT GCTCCCGCTCGACCTCTGAATCCAC CGCCGCACTCGGTTGCCTGGTCAAA GACTACTTCCCCGAGCCCGTGACTG TCTCGTGGAACTCGGGCGCCCTCAC ATCCGGAGTGCATACCTTTCCCGCC GTGTTGCAGTCCAGCGGCCTGTACA GCCTGAGCTCCGTCGTGACAGTGCC GTCCTCCTCCCTTGGAACCAAGACC TATACCTGCAACGTCGACCACAAGC CCTCCAACACCAAAGTGGACAAGCG CGTCGAATCCAAGTACGGCCCCCCT TGTCCGCCTTGTCCAGCCCCTGAGTT CCTGGGTGGTCCGTCCGTGTTCCTCT TCCCGCCCAAGCCGAAGGACACTCT GATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGC AGGAAGATCCCGAAGTGCAGTTCAA TTGGTACGTGGATGGGGTCGAAGTG CACAACGCCAAGACCAAGCCTAGG GAAGAACAGTTCAACTCTACGTACC GGGTGGTGTCCGTGCTGACCGTGCT GCACCAGGACTGGCTGAACGGAAA GGAGTACAAGTGCAAAGTGTCAAA

			CAAGGGCCTCCCTTCATCCATCGAA AAGACCATCAGCAAGGCCAAGGGT CAACCTAGGGAGCCCCAGGTCTACA CTTTGCCGCCTAGCCAAGAAGAAAT GACTAAGAACCAAGTGTCCCTGACT TGCCTTGTCAAGGGCTTTTATCCGTC CGACATCGCCGTGGAGTGGGAGTCC AACGGACAACCGGAGAACAACTAC AAGACCACCCCACCGGTGCTCGATT CCGATGGCTCCTTCTTCCTGTACTCC CGGCTGACTGTGGACAAGTCAAGAT GGCAGGAGGGAAACGTGTTCTCCTG CTCCGTGATGCACGAAGCGCTGCAC AACCATTACACCCAGAAATCACTGT CACTTTCGCTGGGAAAA
SEQ ID 2020	QVTLKESGGGVVQPGRSLRLSCAASGF IFSNYAIHWVRQAPGKGLEWVAVISY DGSNKYYADSVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCARTFAGYSS KLGYFDLWGRGTLVTVSSASTKGPSV FPLAPCSRSTSESTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTKTYTCNVDHKP SNTKVDKRVESKYGPPCPPCPAPEFLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKT KPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKGQ PREPQVYTLPPSQEEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSRLTVDKSRWQEGNV FSCSVMHEALHNHYTQKSLSLSLGK	SEQ ID 2128	CAGGTCACCTTGAAGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCATCTTCAGTAACTATGCTA TACACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTT ATATCATATGATGGAAGTAATAAAT ACTACGCAGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCTGAGGACACGG CTGTGTATTACTGTGCGAGGACTTTT GCGGGGTATAGCAGCAAACTGGGG TACTTCGATCTCTGGGGCCGTGGCA CCCTGGTCACCGTCTCCTCAGCATC CACCAAGGGGCCTTCCGTGTTCCCC CTGGCCCCTTGCTCCCGCTCGACCTC TGAATCCACCGCCGCACTCGGTTGC CTGGTCAAAGACTACTTCCCCGAGC CCGTGACTGTCTCGTGGAACTCGGG CGCCCTCACATCCGGAGTGCATACC TTTCCCGCCGTGTTGCAGTCCAGCG GCCTGTACAGCCTGAGCTCCGTCGT GACAGTGCCGTCCTCCTCCCTTGGA ACCAAGACCTATACCTGCAACGTCG ACCACAAGCCCTCCAACACCAAAGT GGACAAGCGCGTCGAATCCAAGTAC GGCCCCCCTTGTCCGCCTTGTCCAG CCCCTGAGTTCCTGGGTGGTCCGTC CGTGTTCCTCTTCCCGCCCAAGCCG AAGGACACTCTGATGATTTCACGCA CCCCGGAAGTCACTTGCGTGGTCGT GGACGTGTCGCAGGAAGATCCCGA AGTGCAGTTCAATTGGTACGTGGAT GGGGTCGAAGTGCACAACGCCAAG ACCAAGCCTAGGGAAGAACAGTTC AACTCTACGTACCGGGTGGTGTCCG TGCTGACCGTGCTGCACCAGGACTG GCTGAACGGAAAGGAGTACAAGTG

			CAAAGTGTCAAACAAGGGCCTCCCT TCATCCATCGAAAAGACCATCAGCA AGGCCAAGGGTCAACCTAGGGAGC CCCAGGTCTACACTTTGCCGCCTAG CCAAGAAGAAATGACTAAGAACCA AGTGTCCCTGACTTGCCTTGTCAAG GGCTTTTATCCGTCCGACATCGCCG TGGAGTGGGAGTCCAACGGACAAC CGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTC CTTCTTCCTGTACTCCCGGCTGACTG TGGACAAGTCAAGATGGCAGGAGG GAAACGTGTTCTCCTGCTCCGTGAT GCACGAAGCGCTGCACAACCATTAC ACCCAGAAATCACTGTCACTTTCGC TGGGAAAA

Table 40. Anti-CLEC2D antibody IgG1 N to A Heavy chain amino acid and DNA sequence

SEQ ID	**VH+CH+AA_IgG1 N to A**	**SEQ ID**	**VH+CH+DNA_IgG1 N to A**
SEQ ID 2129	EVQLVQSGAEVKKPGASVKVSCKASG YTFTSYAMHWVRQAPGQRLEWMGWI NAGNGNTKYSQKFQGRVTITRDTSAST AYMELSSLRSEDTAVYYCARGSLSRSG WYAGLFDYWGQGTLVTVSSASTKGPS VFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSG LYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCDKTHTCPPCPAPE LLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHN AKTKPREEQYASTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSP GK	SEQ ID 2237	GAAGTGCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTTTCCTGCAAGGCTTCT GGATACACCTTCACTAGCTATGCTA TGCATTGGGTGCGCCAGGCCCCCGG ACAAAGGCTTGAGTGGATGGGATG GATCAACGCTGGCAATGGTAACACA AAATATTCACAGAAGTTCCAGGGCA GAGTCACCATTACCAGGGACACATC CGCGAGCACAGCCTACATGGAGCTG AGCAGCCTGAGATCTGAAGACACG GCTGTGTATTACTGTGCGAGAGGCT CCTTGTCCCGAAGTGGCTGGTACGC CGGACTCTTTGACTACTGGGGCCAG GGAACCCTGGTCACCGTCTCCTCAG CATCCACCAAGGGGCCTTCCGTGTT CCCCCTGGCCCCTTCATCCAAGTCG ACCTCTGGTGGAACCGCCGCACTCG GTTGCCTGGTCAAAGACTACTTCCC CGAGCCCGTGACTGTCTCGTGGAAC TCGGGCGCCCTCACATCCGGAGTGC ATACCTTTCCCGCCGTGTTGCAGTCC AGCGGCCTGTACAGCCTGAGCTCCG TCGTGACAGTGCCGTCCTCCTCCCTT GGAACCCAGACCTATATCTGCAACG TCAATCACAAGCCCTCCAACACCAA AGTGGACAAGAAGGTCGAACCCAA GTCCTGCGACAAGACTCACACCTGT CCGCCTTGTCCAGCCCCTGAGCTGC TGGGTGGTCCGTCCGTGTTCCTCTTC CCGCCCAAGCCGAAGGACACTCTGA TGATTTCACGCACCCCGGAAGTCAC TTGCGTGGTCGTGGACGTGTCGCAC GAAGATCCCGAAGTGAAATTCAATT

			GGTACGTGGATGGGGTCGAAGTGCA CAACGCCAAGACCAAGCCTAGGGA AGAACAGTACgccTCTACGTACCGGG TGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGA GTACAAGTGCAAAGTGTCAAACAA GGCTCTCCCTGCCCCTATCGAAAAG ACCATCAGCAAGGCCAAGGGTCAA CCTAGGGAGCCCCAGGTCTACACTT TGCCGCCTAGCCGGGAAGAAATGAC TAAGAACCAAGTGTCCCTGACTTGC CTTGTCAAGGGCTTTTATCCGTCCG ACATCGCCGTGGAGTGGGAGTCCAA CGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCC GATGGCTCCTTCTTCCTGTACTCCAA GCTGACTGTGGACAAGTCAAGATGG CAGCAGGGAAACGTGTTCTCCTGCT CCGTGATGCACGAAGCGCTGCACAA CCATTACACCCAGAAATCACTGTCA CTTTCGCCGGGAAAA
SEQ ID 2130	QITLKESGGGVVQPGRSLRLSCAASGF TFSSYSMNWVRQAPGKGLQWVAIISD DGSKSYYADSVQGRFTISRDNSRNTVF LQMNSLRAEDTAMYYCARDRGTKWN QLNDVFDMWGQGTMVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYASTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSL SPGK	SEQ ID 2238	CAGATCACCTTGAAGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTCAGTAGTTATAGCA TGAACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGCAGTGGGTGGCAATT ATATCAGATGATGGAAGTAAGAGTT ACTACGCAGACTCCGTGCAGGGCCG ATTCACCATCTCCAGAGACAATTCG AGGAACACAGTATTTCTGCAAATGA ACAGCCTGAGAGCTGAGGACACGG CTATGTATTACTGTGCGAGAGACAG GGGAACTAAATGGAACCAATTGAAT GATGTTTTTGATATGTGGGGCCAAG GGACAATGGTCACCGTCTCTTCAGC ATCCACCAAGGGGCCTTCCGTGTTC CCCCTGGCCCCTTCATCCAAGTCGA CCTCTGGTGGAACCGCCGCACTCGG TTGCCTGGTCAAAGACTACTTCCCC GAGCCCGTGACTGTCTCGTGGAACT CGGGCGCCCTCACATCCGGAGTGCA TACCTTTCCCGCCGTGTTGCAGTCCA GCGGCCTGTACAGCCTGAGCTCCGT CGTGACAGTGCCGTCCTCCTCCCTT GGAACCCAGACCTATATCTGCAACG TCAATCACAAGCCCTCCAACACCAA AGTGGACAAGAAGGTCGAACCCAA GTCCTGCGACAAGACTCACACCTGT CCGCCTTGTCCAGCCCCTGAGCTGC TGGGTGGTCCGTCCGTGTTCCTCTTC CCGCCCAAGCCGAAGGACACTCTGA TGATTTCACGCACCCCGGAAGTCAC TTGCGTGGTCGTGGACGTGTCGCAC GAAGATCCCGAAGTGAAATTCAATT GGTACGTGGATGGGGTCGAAGTGCA

			CAACGCCAAGACCAAGCCTAGGGA AGAACAGTACgccTCTACGTACCGGG TGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGA GTACAAGTGCAAAGTGTCAAACAA GGCTCTCCCTGCCCCTATCGAAAAG ACCATCAGCAAGGCCAAGGGTCAA CCTAGGGAGCCCCAGGTCTACACTT TGCCGCCTAGCCGGGAAGAAATGAC TAAGAACCAAGTGTCCCTGACTTGC CTTGTCAAGGGCTTTTATCCGTCCG ACATCGCCGTGGAGTGGGAGTCCAA CGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCC GATGGCTCCTTCTTCCTGTACTCCAA GCTGACTGTGGACAAGTCAAGATGG CAGCAGGGAAACGTGTTCTCCTGCT CCGTGATGCACGAAGCGCTGCACAA CCATTACACCCAGAAATCACTGTCA CTTTCGCCGGGAAAA
SEQ ID 2131	EVQLVQSGAEVKKPGASVKVSCKASG YTFTSYYMHWVRQAPGQGLEWMGIIN PSGGSTSYAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARGRGYSSS RLYYFDYWGQGTLVTVSSASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYASTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG K	SEQ ID 2239	GAAGTGCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTTTCCTGCAAGGCATCT GGATACACCTTCACCAGCTACTATA TGCACTGGGTGCGACAGGCCCCTGG ACAAGGGCTTGAGTGGATGGGAAT AATCAACCCTAGTGGTGGTAGCACA AGCTACGCACAGAAGTTCCAGGGCA GAGTCACCATGACCAGGGACACGTC CACGAGCACAGTCTACATGGAGCTG AGCAGCCTGAGATCTGAGGACACG GCCGTGTATTACTGTGCGAGAGGCC GAGGGTATAGCAGCAGTCGGCTCTA CTACTTTGACTACTGGGGCCAGGGA ACCCTGGTCACCGTCTCCTCAGCAT CCACCAAGGGGCCTTCCGTGTTCCC CCTGGCCCCTTCATCCAAGTCGACC TCTGGTGGAACCGCCGCACTCGGTT GCCTGGTCAAAGACTACTTCCCCGA GCCCGTGACTGTCTCGTGGAACTCG GGCGCCCTCACATCCGGAGTGCATA CCTTTCCCGCCGTGTTGCAGTCCAG CGGCCTGTACAGCCTGAGCTCCGTC GTGACAGTGCCGTCCTCCTCCCTTG GAACCCAGACCTATATCTGCAACGT CAATCACAAGCCCTCCAACACCAAA GTGGACAAGAAGGTCGAACCCAAG TCCTGCGACAAGACTCACACCTGTC CGCCTTGTCCAGCCCCTGAGCTGCT GGGTGGTCCGTCCGTGTTCCTCTTCC CGCCCAAGCCGAAGGACACTCTGAT GATTTCACGCACCCCGGAAGTCACT TGCGTGGTCGTGGACGTGTCGCACG AAGATCCCGAAGTGAAATTCAATTG GTACGTGGATGGGGTCGAAGTGCAC AACGCCAAGACCAAGCCTAGGGAA

			GAACAGTACgccTCTACGTACCGGGT GGTGTCCGTGCTGACCGTGCTGCAC CAGGACTGGCTGAACGGAAAGGAG TACAAGTGCAAAGTGTCAAACAAG GCTCTCCCTGCCCCTATCGAAAAGA CCATCAGCAAGGCCAAGGGTCAACC TAGGGAGCCCCAGGTCTACACTTTG CCGCCTAGCCGGGAAGAAATGACTA AGAACCAAGTGTCCCTGACTTGCCT TGTCAAGGGCTTTTATCCGTCCGAC ATCGCCGTGGAGTGGGAGTCCAACG GACAACCGGAGAACAACTACAAGA CCACCCCACCGGTGCTCGATTCCGA TGGCTCCTTCTTCCTGTACTCCAAGC TGACTGTGGACAAGTCAAGATGGCA GCAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACT TTCGCCGGGAAAA
SEQ ID 2132	QVTLKESGGGLVRPGGSLRLSCEASGF TFSDPYMDWVRQAPGKGLEWVGRITN KRTGYATTYAASVKDRFTISRDDSRKS VYLQMNSLKTEDTAVYYCATDVSGSF AAYGGQGTLVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTK PREEQYASTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2240	CAGGTCACCTTGAAGGAGTCTGGGG GAGGCTTGGTCCGGCCTGGAGGGTC CCTGAGACTCTCCTGTGAAGCCTCT GGATTCACCTTCAGTGACCCCTACA TGGACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTTGGCCG AATTACAAATAAGCGTACCGGTTAC GCCACAACATATGCCGCGTCTGTGA AGGACAGATTCACCATCTCAAGAGA TGATTCAAGGAAGTCAGTATATCTG CAAATGAACAGCCTGAAGACCGAG GACACGGCCGTATATTATTGTGCAA CAGATGTCAGTGGGTCCTTCGCGGC CTACGGGGGCCAGGGCACCCTGGTC ACCGTCTCCTCAGCATCCACCAAGG GGCCTTCCGTGTTCCCCCTGGCCCCT TCATCCAAGTCGACCTCTGGTGGAA CCGCCGCACTCGGTTGCCTGGTCAA AGACTACTTCCCCGAGCCCGTGACT GTCTCGTGGAACTCGGGCGCCCTCA CATCCGGAGTGCATACCTTTCCCGC CGTGTTGCAGTCCAGCGGCCTGTAC AGCCTGAGCTCCGTCGTGACAGTGC CGTCCTCCTCCCTTGGAACCCAGAC CTATATCTGCAACGTCAATCACAAG CCCTCCAACACCAAAGTGGACAAGA AGGTCGAACCCAAGTCCTGCGACAA GACTCACACCTGTCCGCCTTGTCCA GCCCCTGAGCTGCTGGGTGGTCCGT CCGTGTTCCTCTTCCCGCCCAAGCC GAAGGACACTCTGATGATTTCACGC ACCCCGGAAGTCACTTGCGTGGTCG TGGACGTGTCGCACGAAGATCCCGA AGTGAAATTCAATTGGTACGTGGAT GGGGTCGAAGTGCACAACGCCAAG ACCAAGCCTAGGGAAGAACAGTACg ccTCTACGTACCGGGTGGTGTCCGTG

			CTGACCGTGCTGCACCAGGACTGGC TGAACGGAAAGGAGTACAAGTGCA AAGTGTCAAACAAGGCTCTCCCTGC CCCTATCGAAAAGACCATCAGCAAG GCCAAGGGTCAACCTAGGGAGCCCC AGGTCTACACTTTGCCGCCTAGCCG GGAAGAAATGACTAAGAACCAAGT GTCCCTGACTTGCCTTGTCAAGGGC TTTTATCCGTCCGACATCGCCGTGG AGTGGGAGTCCAACGGACAACCGG AGAACAACTACAAGACCACCCCACC GGTGCTCGATTCCGATGGCTCCTTCT TCCTGTACTCCAAGCTGACTGTGGA CAAGTCAAGATGGCAGCAGGGAAA CGTGTTCTCCTGCTCCGTGATGCAC GAAGCGCTGCACAACCATTACACCC AGAAATCACTGTCACTTTCGCCGGG AAAA
SEQ ID 2133	EVQLVQSGGGVVQPGRSLRLSCAASG FTFSSYAMHWVRQAPGQRLEWMGWI NAGNGNTKYSQKFQGRVTITRDTSAST AYMELSSLRSEDTAVYYCAGEGGAVA GTVYWGQGTLVTVSSASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2241	GAGGTCCAGCTGGTACAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCGTCT GGATTCACCTTCAGTAGCTATGCTA TGCATTGGGTGCGCCAGGCCCCCGG ACAAAGGCTTGAGTGGATGGGATG GATCAACGCTGGCAATGGTAACACA AAATATTCACAGAAGTTCCAGGGCA GAGTCACCATTACCAGGGACACATC CGCGAGCACAGCCTACATGGAGCTG AGCAGCCTGAGATCTGAAGACACG GCTGTGTATTACTGTGCGGGAGAGG GCGGAGCAGTGGCTGGTACTGTCTA CTGGGGCCAGGGAACCCTGGTCACC GTCTCCTCAGCATCCACCAAGGGGC CTTCCGTGTTCCCCCTGGCCCCTTCA TCCAAGTCGACCTCTGGTGGAACCG CCGCACTCGGTTGCCTGGTCAAAGA CTACTTCCCCGAGCCCGTGACTGTC TCGTGGAACTCGGGCGCCCTCACAT CCGGAGTGCATACCTTTCCCGCCGT GTTGCAGTCCAGCGGCCTGTACAGC CTGAGCTCCGTCGTGACAGTGCCGT CCTCCTCCCTTGGAACCCAGACCTA TATCTGCAACGTCAATCACAAGCCC TCCAACACCAAAGTGGACAAGAAG GTCGAACCCAAGTCCTGCGACAAGA CTCACACCTGTCCGCCTTGTCCAGC CCCTGAGCTGCTGGGTGGTCCGTCC GTGTTCCTCTTCCCGCCCAAGCCGA AGGACACTCTGATGATTTCACGCAC CCCGGAAGTCACTTGCGTGGTCGTG GACGTGTCGCACGAAGATCCCGAAG TGAAATTCAATTGGTACGTGGATGG GGTCGAAGTGCACAACGCCAAGAC CAAGCCTAGGGAAGAACAGTACgcc TCTACGTACCGGGTGGTGTCCGTGC TGACCGTGCTGCACCAGGACTGGCT

			GAACGGAAAGGAGTACAAGTGCAA AGTGTCAAACAAGGCTCTCCCTGCC CCTATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTACACTTTGCCGCCTAGCCGG GAAGAAATGACTAAGAACCAAGTG TCCCTGACTTGCCTTGTCAAGGGCTT TTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCAAGCTGACTGTGGACA AGTCAAGATGGCAGCAGGGAAACG TGTTCTCCTGCTCCGTGATGCACGA AGCGCTGCACAACCATTACACCCAG AAATCACTGTCACTTTCGCCGGGAA AA
SEQ ID 2134	QVQLVQSGGGLVKPGGSLRLSCAASG FTFSNAWMSWVRQAPGKGLEWVGRI KSKTDGGTTDYAAPVKGRFTISRDDSK NTLYLQMNSLKTEDTAVYYCTTDEYF YWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVD KKVEPKSCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKP REEQYASTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2242	CAGGTCCAGCTGGTGCAGTCTGGGG GAGGCTTGGTAAAGCCTGGGGGGTC CCTTAGACTCTCCTGTGCAGCCTCTG GATTCACTTTCAGTAACGCCTGGAT GAGCTGGGTCCGCCAGGCTCCAGGG AAGGGGCTGGAGTGGGTTGGCCGTA TTAAAAGCAAAACTGATGGTGGGAC AACAGACTACGCTGCACCCGTGAAA GGCAGATTCACCATCTCAAGAGATG ATTCAAAAAACACGCTGTATCTGCA AATGAACAGCCTGAAAACCGAGGA CACAGCCGTGTATTACTGTACCACA GACGAGTATTTCTACTGGGGCCAGG GAACCCTGGTCACCGTCTCCTCAGC ATCCACCAAGGGGCCTTCCGTGTTC CCCCTGGCCCCTTCATCCAAGTCGA CCTCTGGTGGAACCGCCGCACTCGG TTGCCTGGTCAAAGACTACTTCCCC GAGCCCGTGACTGTCTCGTGGAACT CGGGCGCCCTCACATCCGGAGTGCA TACCTTTCCCGCCGTGTTGCAGTCCA GCGGCCTGTACAGCCTGAGCTCCGT CGTGACAGTGCCGTCCTCCTCCCTT GGAACCCAGACCTATATCTGCAACG TCAATCACAAGCCCTCCAACACCAA AGTGGACAAGAAGGTCGAACCCAA GTCCTGCGACAAGACTCACACCTGT CCGCCTTGTCCAGCCCCTGAGCTGC TGGGTGGTCCGTCCGTGTTCCTCTTC CCGCCCAAGCCGAAGGACACTCTGA TGATTTCACGCACCCCGGAAGTCAC TTGCGTGGTCGTGGACGTGTCGCAC GAAGATCCCGAAGTGAAATTCAATT GGTACGTGGATGGGGTCGAAGTGCA CAACGCCAAGACCAAGCCTAGGGA AGAACAGTACgccTCTACGTACCGGG TGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGA GTACAAGTGCAAAGTGTCAAACAA

			GGCTCTCCCTGCCCCTATCGAAAAG ACCATCAGCAAGGCCAAGGGTCAA CCTAGGGAGCCCCAGGTCTACACTT TGCCGCCTAGCCGGGAAGAAATGAC TAAGAACCAAGTGTCCCTGACTTGC CTTGTCAAGGGCTTTTATCCGTCCG ACATCGCCGTGGAGTGGGAGTCCAA CGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCC GATGGCTCCTTCTTCCTGTACTCCAA GCTGACTGTGGACAAGTCAAGATGG CAGCAGGGAAACGTGTTCTCCTGCT CCGTGATGCACGAAGCGCTGCACAA CCATTACACCCAGAAATCACTGTCA CTTTCGCCGGGAAAA
SEQ ID 2135	QVQLQQWGAGLLKPSETLSLTCAVYG GSFSGYYWSWIRQPPGKGLEWIGEINH SGSTNYNPSLKSRVTISVDTSKNQFSLK LSSVTAADTAVYYCARVNPGSYTREV SNFDYWGQGTLVTVSSASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2243	CAGGTGCAGCTACAGCAGTGGGGC GCAGGACTGTTGAAGCCTTCGGAGA CCCTGTCCCTCACCTGCGCTGTCTAT GGTGGGTCCTTCAGTGGTTACTACT GGAGCTGGATCCGCCAGCCCCCAGG GAAGGGGCTGGAGTGGATTGGGGA AATCAATCATAGTGGAAGCACCAAC TACAACCCGTCCCTCAAGAGTCGAG TCACCATATCAGTAGACACGTCCAA GAACCAGTTCTCCCTGAAGCTGAGC TCTGTGACCGCCGCGGACACGGCTG TGTATTACTGTGCGAGAGTAAATCC GGGGAGTTATACGAGGGAGGTGAG CAACTTTGACTACTGGGGCCAGGGA ACCCTGGTGACCGTCTCCTCAGCAT CCACCAAGGGGCCTTCCGTGTTCCC CCTGGCCCCTTCATCCAAGTCGACC TCTGGTGGAACCGCCGCACTCGGTT GCCTGGTCAAAGACTACTTCCCCGA GCCCGTGACTGTCTCGTGGAACTCG GGCGCCCTCACATCCGGAGTGCATA CCTTTCCCGCCGTGTTGCAGTCCAG CGGCCTGTACAGCCTGAGCTCCGTC GTGACAGTGCCGTCCTCCTCCCTTG GAACCCAGACCTATATCTGCAACGT CAATCACAAGCCCTCCAACACCAAA GTGGACAAGAAGGTCGAACCCAAG TCCTGCGACAAGACTCACACCTGTC CGCCTTGTCCAGCCCCTGAGCTGCT GGGTGGTCCGTCCGTGTTCCTCTTCC CGCCCAAGCCGAAGGACACTCTGAT GATTTCACGCACCCCGGAAGTCACT TGCGTGGTCGTGGACGTGTCGCACG AAGATCCCGAAGTGAAATTCAATTG GTACGTGGATGGGGTCGAAGTGCAC AACGCCAAGACCAAGCCTAGGGAA GAACAGTACgccTCTACGTACCGGGT GGTGTCCGTGCTGACCGTGCTGCAC CAGGACTGGCTGAACGGAAAGGAG TACAAGTGCAAAGTGTCAAACAAG GCTCTCCCTGCCCCTATCGAAAAGA

			CCATCAGCAAGGCCAAGGGTCAACC TAGGGAGCCCCAGGTCTACACTTTG CCGCCTAGCCGGGAAGAAATGACTA AGAACCAAGTGTCCCTGACTTGCCT TGTCAAGGGCTTTTATCCGTCCGAC ATCGCCGTGGAGTGGGAGTCCAACG GACAACCGGAGAACAACTACAAGA CCACCCCACCGGTGCTCGATTCCGA TGGCTCCTTCTTCCTGTACTCCAAGC TGACTGTGGACAAGTCAAGATGGCA GCAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACT TTCGCCGGGAAAA
SEQ ID 2136	QVQLQQSGPELVKPSQTLTLTCGISGD SVSSNSVTWNWVRQSPSRGLEWLGRT YYRSQWYYNYAVSVKSRITISPDTSKN QFSLQLNSVTPEDTAVYYCATRGHNY GVDYWGPGTTVTVSSASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2244	CAGGTACAGCTGCAGCAGTCAGGTC CAGAATTGGTGAAGCCCTCGCAGAC CCTCACACTCACCTGTGGCATCTCC GGGGACAGTGTCTCTAGCAACAGTG TTACTTGGAACTGGGTCAGGCAGTC CCCATCGAGAGGCCTTGAGTGGCTG GGAAGGACTTACTACCGGTCCCAGT GGTATTATAATTATGCGGTGTCTGT GAAAAGTCGAATAACCATCAGCCCA GACACATCCAAGAACCAGTTCTCCC TGCAGTTGAATTCTGTGACTCCCGA GGACACGGCTGTCTATTACTGTGCA ACCAGGGGACATAACTACGGTGTAG ATTACTGGGGCCCGGGGACCACGGT CACCGTCTCCTCAGCATCCACCAAG GGGCCTTCCGTGTTCCCCCTGGCCC CTTCATCCAAGTCGACCTCTGGTGG AACCGCCGCACTCGGTTGCCTGGTC AAAGACTACTTCCCCGAGCCCGTGA CTGTCTCGTGGAACTCGGGCGCCCT CACATCCGGAGTGCATACCTTTCCC GCCGTGTTGCAGTCCAGCGGCCTGT ACAGCCTGAGCTCCGTCGTGACAGT GCCGTCCTCCTCCCTTGGAACCCAG ACCTATATCTGCAACGTCAATCACA AGCCCTCCAACACCAAAGTGGACAA GAAGGTCGAACCCAAGTCCTGCGAC AAGACTCACACCTGTCCGCCTTGTC CAGCCCCTGAGCTGCTGGGTGGTCC GTCCGTGTTCCTCTTCCCGCCCAAGC CGAAGGACACTCTGATGATTTCACG CACCCCGGAAGTCACTTGCGTGGTC GTGGACGTGTCGCACGAAGATCCCG AAGTGAAATTCAATTGGTACGTGGA TGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTA CgccTCTACGTACCGGGTGGTGTCCG TGCTGACCGTGCTGCACCAGGACTG GCTGAACGGAAAGGAGTACAAGTG CAAAGTGTCAAACAAGGCTCTCCCT GCCCCTATCGAAAAGACCATCAGCA AGGCCAAGGGTCAACCTAGGGAGC

			CCCAGGTCTACACTTTGCCGCCTAG CCGGGAAGAAATGACTAAGAACCA AGTGTCCCTGACTTGCCTTGTCAAG GGCTTTTATCCGTCCGACATCGCCG TGGAGTGGGAGTCCAACGGACAAC CGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTC CTTCTTCCTGTACTCCAAGCTGACTG TGGACAAGTCAAGATGGCAGCAGG GAAACGTGTTCTCCTGCTCCGTGAT GCACGAAGCGCTGCACAACCATTAC ACCCAGAAATCACTGTCACTTTCGC CGGGAAAA
SEQ ID 2137	QVQLVQSGGGLVKPGGSLRLSCAASG FTFSNAWMSWVRQAPGKGLEWVCRI KSKTDGETTDYAAPVKGRFTISRDDSK NTLYLQMNSLKTEDTAVYHCTTGVG WSPFQYWGQGTLVTVSSASTKGPSVF PLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYASTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG K	SEQ ID 2245	CAGGTGCAGCTGGTGCAGTCTGGGG GAGGCTTGGTAAAGCCTGGGGGGTC CCTTAGACTCTCCTGTGCAGCCTCTG GATTCACTTTCAGTAACGCCTGGAT GAGCTGGGTCCGCCAGGCTCCAGGG AAGGGGCTGGAGTGGGTTTGCCGTA TTAAAAGCAAAACTGATGGTGAGAC AACAGACTACGCTGCACCCGTGAAA GGCAGATTCACCATCTCAAGAGATG ATTCAAAAAACACGCTGTATCTGCA AATGAACAGCCTGAAAACTGAGGA CACAGCCGTGTATCACTGTACCACA GGGGTGGGATGGTCGCCCTTCCAAT ACTGGGGCCAGGGCACCCTGGTCAC CGTCTCCTCAGCATCCACCAAGGGG CCTTCCGTGTTCCCCCTGGCCCCTTC ATCCAAGTCGACCTCTGGTGGAACC GCCGCACTCGGTTGCCTGGTCAAAG ACTACTTCCCCGAGCCCGTGACTGT CTCGTGGAACTCGGGCGCCCTCACA TCCGGAGTGCATACCTTTCCCGCCG TGTTGCAGTCCAGCGGCCTGTACAG CCTGAGCTCCGTCGTGACAGTGCCG TCCTCCTCCCTTGGAACCCAGACCT ATATCTGCAACGTCAATCACAAGCC CTCCAACACCAAAGTGGACAAGAA GGTCGAACCCAAGTCCTGCGACAAG ACTCACACCTGTCCGCCTTGTCCAG CCCCTGAGCTGCTGGGTGGTCCGTC CGTGTTCCTCTTCCCGCCCAAGCCG AAGGACACTCTGATGATTTCACGCA CCCCGGAAGTCACTTGCGTGGTCGT GGACGTGTCGCACGAAGATCCCGAA GTGAAATTCAATTGGTACGTGGATG GGGTCGAAGTGCACAACGCCAAGA CCAAGCCTAGGGAAGAACAGTACgc cTCTACGTACCGGGTGGTGTCCGTGC TGACCGTGCTGCACCAGGACTGGCT GAACGGAAAGGAGTACAAGTGCAA AGTGTCAAACAAGGCTCTCCCTGCC CCTATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTACACTTTGCCGCCTAGCCGG

			GAAGAAATGACTAAGAACCAAGTG TCCCTGACTTGCCTTGTCAAGGGCTT TTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCAAGCTGACTGTGGACA AGTCAAGATGGCAGCAGGGAAACG TGTTCTCCTGCTCCGTGATGCACGA AGCGCTGCACAACCATTACACCCAG AAATCACTGTCACTTTCGCCGGGAA AA
SEQ ID 2138	EVQLVQSGGGLVQPGRSLRLSCTASGF TFGDYAMSWFRQAPGKGLEWVGFIRS KAYGGTTEYAASVKGRFTISRDDSKSI AYLQMNSLKTEDTAVYYCTRDDKIAA AGFTYWYFDLWGRGTLVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYASTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSL SPGK	SEQ ID 2246	GAGGTCCAGCTGGTACAGTCTGGGG GAGGCTTGGTACAGCCAGGGCGGTC CCTGAGACTCTCCTGTACAGCTTCT GGATTCACCTTTGGTGATTATGCTAT GAGCTGGTTCCGCCAGGCTCCAGGG AAGGGGCTGGAGTGGGTAGGTTTCA TTAGAAGCAAAGCTTATGGTGGGAC AACAGAATACGCCGCGTCTGTGAAA GGCAGATTCACCATCTCAAGAGATG ATTCCAAAAGCATCGCCTATCTGCA AATGAACAGCCTGAAAACCGAGGA CACAGCCGTGTATTACTGTACTAGA GACGACAAAATAGCAGCAGCTGGA TTCACATACTGGTACTTCGATCTCTG GGGCCGTGGCACCCTGGTCACCGTC TCCTCAGCATCCACCAAGGGGCCTT CCGTGTTCCCCCTGGCCCCTTCATCC AAGTCGACCTCTGGTGGAACCGCCG CACTCGGTTGCCTGGTCAAAGACTA CTTCCCCGAGCCCGTGACTGTCTCG TGGAACTCGGGCGCCCTCACATCCG GAGTGCATACCTTTCCCGCCGTGTT GCAGTCCAGCGGCCTGTACAGCCTG AGCTCCGTCGTGACAGTGCCGTCCT CCTCCCTTGGAACCCAGACCTATAT CTGCAACGTCAATCACAAGCCCTCC AACACCAAAGTGGACAAGAAGGTC GAACCCAAGTCCTGCGACAAGACTC ACACCTGTCCGCCTTGTCCAGCCCC TGAGCTGCTGGGTGGTCCGTCCGTG TTCCTCTTCCCGCCCAAGCCGAAGG ACACTCTGATGATTTCACGCACCCC GGAAGTCACTTGCGTGGTCGTGGAC GTGTCGCACGAAGATCCCGAAGTGA AATTCAATTGGTACGTGGATGGGGT CGAAGTGCACAACGCCAAGACCAA GCCTAGGGAAGAACAGTACgccTCTA CGTACCGGGTGGTGTCCGTGCTGAC CGTGCTGCACCAGGACTGGCTGAAC GGAAAGGAGTACAAGTGCAAAGTG TCAAACAAGGCTCTCCCTGCCCCTA TCGAAAAGACCATCAGCAAGGCCA AGGGTCAACCTAGGGAGCCCCAGGT CTACACTTTGCCGCCTAGCCGGGAA

			GAAATGACTAAGAACCAAGTGTCCC TGACTTGCCTTGTCAAGGGCTTTTAT CCGTCCGACATCGCCGTGGAGTGGG AGTCCAACGGACAACCGGAGAACA ACTACAAGACCACCCCACCGGTGCT CGATTCCGATGGCTCCTTCTTCCTGT ACTCCAAGCTGACTGTGGACAAGTC AAGATGGCAGCAGGGAAACGTGTT CTCCTGCTCCGTGATGCACGAAGCG CTGCACAACCATTACACCCAGAAAT CACTGTCACTTTCGCCGGGAAAA
SEQ ID 2139	QVQLVQSGAEVKKPGASVKVSCKASG YTFAAYYLHWVRQAPGQGLEWMGRI SPGNGVTSYAQKFQGRVTMTGDTSIN TVYMQLNNLISGDTAVYYCAREAADD PFDHWGQGALVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTK PREEQYASTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2247	CAGGTGCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTCTCCTGCAAGGCTTCT GGATACACCTTCGCCGCCTATTATTT ACACTGGGTGCGACAGGCCCCTGGA CAAGGCCTTGAGTGGATGGGGCGG ATCAGCCCTGGTAACGGTGTCACAA GTTATGCACAGAAATTTCAGGGCAG AGTCACCATGACCGGGGACACGTCC ATTAACACAGTCTACATGCAACTGA ACAATTTGATTTCTGGCGACACGGC CGTATATTACTGTGCGAGAGAGGCT GCCGACGACCCGTTTGACCATTGGG GCCAGGGAGCCCTGGTCACCGTCTC CTCAGCATCCACCAAGGGGCCTTCC GTGTTCCCCCTGGCCCCTTCATCCAA GTCGACCTCTGGTGGAACCGCCGCA CTCGGTTGCCTGGTCAAAGACTACT TCCCCGAGCCCGTGACTGTCTCGTG GAACTCGGGCGCCCTCACATCCGGA GTGCATACCTTTCCCGCCGTGTTGC AGTCCAGCGGCCTGTACAGCCTGAG CTCCGTCGTGACAGTGCCGTCCTCC TCCCTTGGAACCCAGACCTATATCT GCAACGTCAATCACAAGCCCTCCAA CACCAAAGTGGACAAGAAGGTCGA ACCCAAGTCCTGCGACAAGACTCAC ACCTGTCCGCCTTGTCCAGCCCCTG AGCTGCTGGGTGGTCCGTCCGTGTT CCTCTTCCCGCCCAAGCCGAAGGAC ACTCTGATGATTTCACGCACCCCGG AAGTCACTTGCGTGGTCGTGGACGT GTCGCACGAAGATCCCGAAGTGAA ATTCAATTGGTACGTGGATGGGGTC GAAGTGCACAACGCCAAGACCAAG CCTAGGGAAGAACAGTACgccTCTAC GTACCGGGTGGTGTCCGTGCTGACC GTGCTGCACCAGGACTGGCTGAACG GAAAGGAGTACAAGTGCAAAGTGT CAAACAAGGCTCTCCCTGCCCCTAT CGAAAAGACCATCAGCAAGGCCAA GGGTCAACCTAGGGAGCCCCAGGTC TACACTTTGCCGCCTAGCCGGGAAG AAATGACTAAGAACCAAGTGTCCCT

			GACTTGCCTTGTCAAGGGCTTTTATC CGTCCGACATCGCCGTGGAGTGGGA GTCCAACGGACAACCGGAGAACAA CTACAAGACCACCCCACCGGTGCTC GATTCCGATGGCTCCTTCTTCCTGTA CTCCAAGCTGACTGTGGACAAGTCA AGATGGCAGCAGGGAAACGTGTTCT CCTGCTCCGTGATGCACGAAGCGCT GCACAACCATTACACCCAGAAATCA CTGTCACTTTCGCCGGGAAAA
SEQ ID 2140	EVQLVQSGGGVVQPGRSLTLSCAASG FTFSSHLMHWVRQAPGKGLEWVAVIS YDGTSKYYGDSVKGRFTISRDNSKNTL YLQMNSLRAEDTAIYYCAKADYKYD WGQGTLVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPR EEQYASTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK	SEQ ID 2248	GAAGTGCAGCTGGTGCAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGACACTCTCCTGTGCAGCCTCT GGATTCACCTTCAGTTCCCATCTTAT GCACTGGGTCCGCCAGGCTCCAGGC AAGGGGCTGGAGTGGGTGGCAGTT ATATCATATGATGGAACTAGTAAAT ATTACGGAGACTCCGTGAAGGGCCG CTTCACCATCTCCAGAGACAATTCC AAGAACACGTTGTATCTGCAAATGA ACAGCCTGCGAGCTGAAGACACGG CTATATATTACTGTGCGAAAGCAGA TTATAAATATGACTGGGGCCAGGGA ACCCTGGTCACCGTCTCCTCAGCAT CCACCAAGGGGCCTTCCGTGTTCCC CCTGGCCCCTTCATCCAAGTCGACC TCTGGTGGAACCGCCGCACTCGGTT GCCTGGTCAAAGACTACTTCCCCGA GCCCGTGACTGTCTCGTGGAACTCG GGCGCCCTCACATCCGGAGTGCATA CCTTTCCCGCCGTGTTGCAGTCCAG CGGCCTGTACAGCCTGAGCTCCGTC GTGACAGTGCCGTCCTCCTCCCTTG GAACCCAGACCTATATCTGCAACGT CAATCACAAGCCCTCCAACACCAAA GTGGACAAGAAGGTCGAACCCAAG TCCTGCGACAAGACTCACACCTGTC CGCCTTGTCCAGCCCCTGAGCTGCT GGGTGGTCCGTCCGTGTTCCTCTTCC CGCCCAAGCCGAAGGACACTCTGAT GATTTCACGCACCCCGGAAGTCACT TGCGTGGTCGTGGACGTGTCGCACG AAGATCCCGAAGTGAAATTCAATTG GTACGTGGATGGGGTCGAAGTGCAC AACGCCAAGACCAAGCCTAGGGAA GAACAGTACgccTCTACGTACCGGGT GGTGTCCGTGCTGACCGTGCTGCAC CAGGACTGGCTGAACGGAAAGGAG TACAAGTGCAAAGTGTCAAACAAG GCTCTCCCTGCCCCTATCGAAAAGA CCATCAGCAAGGCCAAGGGTCAACC TAGGGAGCCCCAGGTCTACACTTTG CCGCCTAGCCGGGAAGAAATGACTA AGAACCAAGTGTCCCTGACTTGCCT

			TGTCAAGGGCTTTTATCCGTCCGAC ATCGCCGTGGAGTGGGAGTCCAACG GACAACCGGAGAACAACTACAAGA CCACCCCACCGGTGCTCGATTCCGA TGGCTCCTTCTTCCTGTACTCCAAGC TGACTGTGGACAAGTCAAGATGGCA GCAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACT TTCGCCGGGAAAA
SEQ ID 2141	EVQLVQSGGGLVKPGGSLRLSCTASGF TFGDYAMSWVRQAPGKGLEWVGFIRS KAYGGTTEYAASVKGRFTISRDDSKSI AYLQMNSLKTEDTAVYYCTTHRRPIY DILTGFDYWGQGTLVTVSSASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYASTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG K	SEQ ID 2249	GAGGTGCAGCTGGTGCAGTCTGGGG GAGGCTTGGTCAAGCCTGGAGGGTC CCTGAGACTCTCCTGTACAGCTTCT GGATTCACCTTTGGTGATTATGCTAT GAGCTGGGTCCGCCAGGCTCCAGGG AAGGGGCTGGAGTGGGTAGGTTTCA TTAGAAGCAAAGCTTATGGTGGGAC AACAGAATACGCCGCGTCTGTGAAA GGCAGATTCACCATCTCAAGAGATG ATTCCAAAAGCATCGCCTATCTGCA AATGAACAGCCTGAAAACCGAGGA CACAGCCGTGTATTACTGTACTACT CATAGACGCCCAATTTACGATATTT TGACTGGTTTTGACTACTGGGGCCA GGGAACCCTGGTCACCGTCTCCTCA GCATCCACCAAGGGGCCTTCCGTGT TCCCCCTGGCCCCTTCATCCAAGTC GACCTCTGGTGGAACCGCCGCACTC GGTTGCCTGGTCAAAGACTACTTCC CCGAGCCCGTGACTGTCTCGTGGAA CTCGGGCGCCCTCACATCCGGAGTG CATACCTTTCCCGCCGTGTTGCAGTC CAGCGGCCTGTACAGCCTGAGCTCC GTCGTGACAGTGCCGTCCTCCTCCC TTGGAACCCAGACCTATATCTGCAA CGTCAATCACAAGCCCTCCAACACC AAAGTGGACAAGAAGGTCGAACCC AAGTCCTGCGACAAGACTCACACCT GTCCGCCTTGTCCAGCCCCTGAGCT GCTGGGTGGTCCGTCCGTGTTCCTCT TCCCGCCCAAGCCGAAGGACACTCT GATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGC ACGAAGATCCCGAAGTGAAATTCAA TTGGTACGTGGATGGGGTCGAAGTG CACAACGCCAAGACCAAGCCTAGG GAAGAACAGTACgccTCTACGTACCG GGTGGTGTCCGTGCTGACCGTGCTG CACCAGGACTGGCTGAACGGAAAG GAGTACAAGTGCAAAGTGTCAAAC AAGGCTCTCCCTGCCCCTATCGAAA AGACCATCAGCAAGGCCAAGGGTC AACCTAGGGAGCCCCAGGTCTACAC TTTGCCGCCTAGCCGGGAAGAAATG

			ACTAAGAACCAAGTGTCCCTGACTT GCCTTGTCAAGGGCTTTTATCCGTCC GACATCGCCGTGGAGTGGGAGTCCA ACGGACAACCGGAGAACAACTACA AGACCACCCCACCGGTGCTCGATTC CGATGGCTCCTTCTTCCTGTACTCCA AGCTGACTGTGGACAAGTCAAGATG GCAGCAGGGAAACGTGTTCTCCTGC TCCGTGATGCACGAAGCGCTGCACA ACCATTACACCCAGAAATCACTGTC ACTTTCGCCGGGAAAA
SEQ ID 2142	QLQLQESGGGLVQPGRSLRLSCTASGF TFGDYAMSWVRQAPGKGLEWVGFIRS KAYGGTTEYAASVKGRFTISRDDSKSI AYLQMNSLKTEDTAVYYCTREDTMV RGVIPWGQGTLVTVSSASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2250	CAGCTGCAGCTGCAGGAGTCCGGGG GAGGCTTGGTACAGCCAGGGCGGTC CCTGAGACTCTCCTGTACAGCTTCT GGATTCACCTTTGGTGATTATGCTAT GAGCTGGGTCCGCCAGGCTCCAGGG AAGGGGCTGGAGTGGGTAGGTTTCA TTAGAAGCAAAGCTTATGGTGGGAC AACAGAATACGCCGCGTCTGTGAAA GGCAGATTCACCATCTCAAGAGATG ATTCCAAAAGCATCGCCTATCTGCA AATGAACAGCCTGAAAACCGAGGA CACAGCCGTGTATTACTGTACTAGA GAGGATACTATGGTTCGGGGAGTTA TTCCCTGGGGCCAGGGAACCCTGGT CACCGTCTCCTCAGCATCCACCAAG GGGCCTTCCGTGTTCCCCCTGGCCC CTTCATCCAAGTCGACCTCTGGTGG AACCGCCGCACTCGGTTGCCTGGTC AAAGACTACTTCCCCGAGCCCGTGA CTGTCTCGTGGAACTCGGGCGCCCT CACATCCGGAGTGCATACCTTTCCC GCCGTGTTGCAGTCCAGCGGCCTGT ACAGCCTGAGCTCCGTCGTGACAGT GCCGTCCTCCTCCCTTGGAACCCAG ACCTATATCTGCAACGTCAATCACA AGCCCTCCAACACCAAAGTGGACAA GAAGGTCGAACCCAAGTCCTGCGAC AAGACTCACACCTGTCCGCCTTGTC CAGCCCCTGAGCTGCTGGGTGGTCC GTCCGTGTTCCTCTTCCCGCCCAAGC CGAAGGACACTCTGATGATTTCACG CACCCCGGAAGTCACTTGCGTGGTC GTGGACGTGTCGCACGAAGATCCCG AAGTGAAATTCAATTGGTACGTGGA TGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTA CgccTCTACGTACCGGGTGGTGTCCG TGCTGACCGTGCTGCACCAGGACTG GCTGAACGGAAAGGAGTACAAGTG CAAAGTGTCAAACAAGGCTCTCCCT GCCCCTATCGAAAAGACCATCAGCA AGGCCAAGGGTCAACCTAGGGAGC CCCAGGTCTACACTTTGCCGCCTAG CCGGGAAGAAATGACTAAGAACCA

			AGTGTCCCTGACTTGCCTTGTCAAG GGCTTTTATCCGTCCGACATCGCCG TGGAGTGGGAGTCCAACGGACAAC CGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTC CTTCTTCCTGTACTCCAAGCTGACTG TGGACAAGTCAAGATGGCAGCAGG GAAACGTGTTCTCCTGCTCCGTGAT GCACGAAGCGCTGCACAACCATTAC ACCCAGAAATCACTGTCACTTTCGC CGGGAAAA
SEQ ID 2143	QLQLQESGSGLVKPSQTLSLTCAVSGG SISSGGYSWSWIRQPPGKGLEWIGYIY HSGSTYYNPSLKSRVTISVDRSKNQFSL KLSSVTAADTAVYYCARDRRYYDSSG YYPAYYFDYWGQGTLVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYASTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSL SPGK	SEQ ID 2251	CAGCTGCAGCTGCAGGAGTCCGGCT CAGGACTGGTGAAGCCTTCACAGAC CCTGTCCCTCACCTGCGCTGTCTCTG GTGGCTCCATCAGCAGTGGTGGTTA CTCCTGGAGCTGGATCCGGCAGCCA CCAGGGAAGGGCCTGGAGTGGATT GGGTACATCTATCATAGTGGGAGCA CCTACTACAACCCGTCCCTCAAGAG TCGAGTCACCATATCAGTAGACAGG TCCAAGAACCAGTTCTCCCTGAAGC TGAGCTCTGTGACCGCCGCGGACAC GGCTGTGTATTACTGTGCGAGAGAT CGGCGTTACTATGATAGTAGTGGTT ATTATCCCGCCTACTACTTTGACTAC TGGGGCCAGGGAACCCTGGTCACCG TCTCCTCAGCATCCACCAAGGGGCC TTCCGTGTTCCCCCTGGCCCCTTCAT CCAAGTCGACCTCTGGTGGAACCGC CGCACTCGGTTGCCTGGTCAAAGAC TACTTCCCCGAGCCCGTGACTGTCT CGTGGAACTCGGGCGCCCTCACATC CGGAGTGCATACCTTTCCCGCCGTG TTGCAGTCCAGCGGCCTGTACAGCC TGAGCTCCGTCGTGACAGTGCCGTC CTCCTCCCTTGGAACCCAGACCTAT ATCTGCAACGTCAATCACAAGCCCT CCAACACCAAAGTGGACAAGAAGG TCGAACCCAAGTCCTGCGACAAGAC TCACACCTGTCCGCCTTGTCCAGCC CCTGAGCTGCTGGGTGGTCCGTCCG TGTTCCTCTTCCCGCCCAAGCCGAA GGACACTCTGATGATTTCACGCACC CCGGAAGTCACTTGCGTGGTCGTGG ACGTGTCGCACGAAGATCCCGAAGT GAAATTCAATTGGTACGTGGATGGG GTCGAAGTGCACAACGCCAAGACC AAGCCTAGGGAAGAACAGTACgccT CTACGTACCGGGTGGTGTCCGTGCT GACCGTGCTGCACCAGGACTGGCTG AACGGAAAGGAGTACAAGTGCAAA GTGTCAAACAAGGCTCTCCCTGCCC CTATCGAAAAGACCATCAGCAAGGC CAAGGGTCAACCTAGGGAGCCCCA GGTCTACACTTTGCCGCCTAGCCGG

			GAAGAAATGACTAAGAACCAAGTG TCCCTGACTTGCCTTGTCAAGGGCTT TTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCAAGCTGACTGTGGACA AGTCAAGATGGCAGCAGGGAAACG TGTTCTCCTGCTCCGTGATGCACGA AGCGCTGCACAACCATTACACCCAG AAATCACTGTCACTTTCGCCGGGAA AA
SEQ ID 2144	EVQLVQSGGGLVKPGGSLRLSCAASG FTFSSYSMNWVRQAPGKGLEWVSYIS SSGSYTNYADSVKGRFTISRDNAKNSL YLQINSLRAEDTAIYYCARDGGYDSSG FHFDYWGQGTLVTVSSASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2252	GAAGTGCAGCTGGTGCAGTCTGGGG GAGGCCTGGTCAAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTCAGTAGCTATAGCA TGAACTGGGTCCGCCAGGCTCCAGG GAAGGGGCTGGAGTGGGTTTCATAC ATTAGTAGTAGTGGTAGTTACACAA ACTACGCAGACTCTGTGAAGGGCCG ATTCACCATCTCCAGAGACAACGCC AAGAACTCACTGTATCTGCAAATAA ACAGCCTGAGAGCCGAGGACACGG CCATTTATTACTGTGCGAGAGACGG GGGCTATGATAGTAGTGGTTTTCAC TTTGACTACTGGGGCCAGGGAACCC TGGTCACCGTCTCCTCAGCATCCAC CAAGGGGCCTTCCGTGTTCCCCCTG GCCCCTTCATCCAAGTCGACCTCTG GTGGAACCGCCGCACTCGGTTGCCT GGTCAAAGACTACTTCCCCGAGCCC GTGACTGTCTCGTGGAACTCGGGCG CCCTCACATCCGGAGTGCATACCTT TCCCGCCGTGTTGCAGTCCAGCGGC CTGTACAGCCTGAGCTCCGTCGTGA CAGTGCCGTCCTCCTCCCTTGGAAC CCAGACCTATATCTGCAACGTCAAT CACAAGCCCTCCAACACCAAAGTGG ACAAGAAGGTCGAACCCAAGTCCTG CGACAAGACTCACACCTGTCCGCCT TGTCCAGCCCCTGAGCTGCTGGGTG GTCCGTCCGTGTTCCTCTTCCCGCCC AAGCCGAAGGACACTCTGATGATTT CACGCACCCCGGAAGTCACTTGCGT GGTCGTGGACGTGTCGCACGAAGAT CCCGAAGTGAAATTCAATTGGTACG TGGATGGGGTCGAAGTGCACAACGC CAAGACCAAGCCTAGGGAAGAACA GTACgccTCTACGTACCGGGTGGTGT CCGTGCTGACCGTGCTGCACCAGGA CTGGCTGAACGGAAAGGAGTACAA GTGCAAAGTGTCAAACAAGGCTCTC CCTGCCCCTATCGAAAAGACCATCA GCAAGGCCAAGGGTCAACCTAGGG AGCCCCAGGTCTACACTTTGCCGCC TAGCCGGGAAGAAATGACTAAGAA

			CCAAGTGTCCCTGACTTGCCTTGTC AAGGGCTTTTATCCGTCCGACATCG CCGTGGAGTGGGAGTCCAACGGAC AACCGGAGAACAACTACAAGACCA CCCCACCGGTGCTCGATTCCGATGG CTCCTTCTTCCTGTACTCCAAGCTGA CTGTGGACAAGTCAAGATGGCAGCA GGGAAACGTGTTCTCCTGCTCCGTG ATGCACGAAGCGCTGCACAACCATT ACACCCAGAAATCACTGTCACTTTC GCCGGGAAAA
SEQ ID 2145	QVQLQQSGPGLVKPSQTLSLTCAISGD SVSNNRAAWNWIRQSPSRGLEWLGRT YYRSKWYNEYAVSVKSRITINPDTSKN QFSLQLNSMTPEDSAVYYCAILPSSGY LQDHHYYGMDVWGQGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPP CPAPELLGGPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYASTYRVVSVLT VLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK	SEQ ID 2253	CAGGTACAGCTGCAGCAGTCAGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAACAACAGGGC TGCTTGGAACTGGATCAGGCAGTCG CCATCGAGAGGCCTTGAGTGGCTGG GAAGGACATACTACAGGTCCAAGTG GTATAATGAATATGCAGTCTCTGTG AAAAGTCGAATAACCATCAACCCAG ACACATCCAAGAACCAGTTCTCCCT GCAGCTGAACTCTATGACTCCCGAG GACTCGGCTGTGTATTACTGTGCAA TTTTGCCTAGTAGTGGTTATCTACAG GACCACCACTACTACGGTATGGACG TCTGGGGCCAAGGGACCACGGTCAC CGTCTCCTCAGCATCCACCAAGGGG CCTTCCGTGTTCCCCCTGGCCCCTTC ATCCAAGTCGACCTCTGGTGGAACC GCCGCACTCGGTTGCCTGGTCAAAG ACTACTTCCCCGAGCCCGTGACTGT CTCGTGGAACTCGGGCGCCCTCACA TCCGGAGTGCATACCTTTCCCGCCG TGTTGCAGTCCAGCGGCCTGTACAG CCTGAGCTCCGTCGTGACAGTGCCG TCCTCCTCCCTTGGAACCCAGACCT ATATCTGCAACGTCAATCACAAGCC CTCCAACACCAAAGTGGACAAGAA GGTCGAACCCAAGTCCTGCGACAAG ACTCACACCTGTCCGCCTTGTCCAG CCCCTGAGCTGCTGGGTGGTCCGTC CGTGTTCCTCTTCCCGCCCAAGCCG AAGGACACTCTGATGATTTCACGCA CCCCGGAAGTCACTTGCGTGGTCGT GGACGTGTCGCACGAAGATCCCGAA GTGAAATTCAATTGGTACGTGGATG GGGTCGAAGTGCACAACGCCAAGA CCAAGCCTAGGGAAGAACAGTACgc cTCTACGTACCGGGTGGTGTCCGTGC TGACCGTGCTGCACCAGGACTGGCT GAACGGAAAGGAGTACAAGTGCAA AGTGTCAAACAAGGCTCTCCCTGCC CCTATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTACACTTTGCCGCCTAGCCGG

			GAAGAAATGACTAAGAACCAAGTG TCCCTGACTTGCCTTGTCAAGGGCTT TTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCAAGCTGACTGTGGACA AGTCAAGATGGCAGCAGGGAAACG TGTTCTCCTGCTCCGTGATGCACGA AGCGCTGCACAACCATTACACCCAG AAATCACTGTCACTTTCGCCGGGAA AA
SEQ ID 2146	EVQLVQSGAEVKKPGASVKVSCKASG YTFTSYGISWVRQAPGQGLEWMGWIS AYNGNTNYAQKLQGRVTMTTDTSTST AYMELSSLRSEDTAVYYCARAAVGDG YSYGRLDWGQGTLVTVSSASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYASTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG K	SEQ ID 2254	GAGGTGCAGCTGGTGCAGTCTGGAG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTCTCCTGCAAGGCTTCT GGTTACACCTTTACCAGCTACGGTA TCAGCTGGGTGCGACAGGCCCCTGG ACAAGGGCTTGAGTGGATGGGATG GATCAGCGCTTACAATGGTAACACA AACTATGCACAGAAGCTCCAGGGCA GAGTCACCATGACCACAGACACATC CACGAGCACAGCCTACATGGAGCTG AGCAGCCTGAGATCTGAGGACACG GCCGTGTATTACTGTGCGAGAGCCG CGGTGGGGGATGGATACAGCTATGG TCGGCTCGATTGGGGCCAGGGAACC CTGGTCACCGTCTCCTCAGCATCCA CCAAGGGGCCTTCCGTGTTCCCCCT GGCCCCTTCATCCAAGTCGACCTCT GGTGGAACCGCCGCACTCGGTTGCC TGGTCAAAGACTACTTCCCCGAGCC CGTGACTGTCTCGTGGAACTCGGGC GCCCTCACATCCGGAGTGCATACCT TTCCCGCCGTGTTGCAGTCCAGCGG CCTGTACAGCCTGAGCTCCGTCGTG ACAGTGCCGTCCTCCTCCCTTGGAA CCCAGACCTATATCTGCAACGTCAA TCACAAGCCCTCCAACACCAAAGTG GACAAGAAGGTCGAACCCAAGTCCT GCGACAAGACTCACACCTGTCCGCC TTGTCCAGCCCCTGAGCTGCTGGGT GGTCCGTCCGTGTTCCTCTTCCCGCC CAAGCCGAAGGACACTCTGATGATT TCACGCACCCCGGAAGTCACTTGCG TGGTCGTGGACGTGTCGCACGAAGA TCCCGAAGTGAAATTCAATTGGTAC GTGGATGGGGTCGAAGTGCACAAC GCCAAGACCAAGCCTAGGGAAGAA CAGTACgccTCTACGTACCGGGTGGT GTCCGTGCTGACCGTGCTGCACCAG GACTGGCTGAACGGAAAGGAGTAC AAGTGCAAAGTGTCAAACAAGGCTC TCCCTGCCCCTATCGAAAAGACCAT CAGCAAGGCCAAGGGTCAACCTAG GGAGCCCCAGGTCTACACTTTGCCG CCTAGCCGGGAAGAAATGACTAAG

			AACCAAGTGTCCCTGACTTGCCTTG TCAAGGGCTTTTATCCGTCCGACAT CGCCGTGGAGTGGGAGTCCAACGG ACAACCGGAGAACAACTACAAGAC CACCCCACCGGTGCTCGATTCCGAT GGCTCCTTCTTCCTGTACTCCAAGCT GACTGTGGACAAGTCAAGATGGCA GCAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACT TTCGCCGGGAAAA
SEQ ID 2147	EVQLVQSGAEVKKPGESLKISCKGSGY SFTSYWIGWVRQMPGKGLEWMGIIYP GDSDTRYSPSFQGQVTISADKSISTAYL QWSSLKASDTAMYYCARLPSYYYDSS GYFTWYFDLWGRGTLVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYASTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSL SPGK	SEQ ID 2255	GAGGTCCAGCTGGTACAGTCTGGAG CAGAGGTGAAAAAGCCCGGGGAGT CTCTGAAGATCTCCTGTAAGGGTTC TGGATACAGCTTTACCAGCTACTGG ATCGGCTGGGTGCGCCAGATGCCCG GGAAAGGCCTGGAGTGGATGGGGA TCATCTATCCTGGTGACTCTGATACC AGATACAGCCCGTCCTTCCAAGGCC AGGTCACCATCTCAGCCGACAAGTC CATCAGCACCGCCTACCTGCAGTGG AGCAGCCTGAAGGCCTCGGACACCG CCATGTATTACTGTGCGAGACTCCC CTCGTATTACTATGATAGTAGTGGT TACTTTACCTGGTACTTCGATCTCTG GGGCCGTGGCACCCTGGTGACCGTC TCTTCAGCATCCACCAAGGGGCCTT CCGTGTTCCCCCTGGCCCCTTCATCC AAGTCGACCTCTGGTGGAACCGCCG CACTCGGTTGCCTGGTCAAAGACTA CTTCCCCGAGCCCGTGACTGTCTCG TGGAACTCGGGCGCCCTCACATCCG GAGTGCATACCTTTCCCGCCGTGTT GCAGTCCAGCGGCCTGTACAGCCTG AGCTCCGTCGTGACAGTGCCGTCCT CCTCCCTTGGAACCCAGACCTATAT CTGCAACGTCAATCACAAGCCCTCC AACACCAAAGTGGACAAGAAGGTC GAACCCAAGTCCTGCGACAAGACTC ACACCTGTCCGCCTTGTCCAGCCCC TGAGCTGCTGGGTGGTCCGTCCGTG TTCCTCTTCCCGCCCAAGCCGAAGG ACACTCTGATGATTTCACGCACCCC GGAAGTCACTTGCGTGGTCGTGGAC GTGTCGCACGAAGATCCCGAAGTGA AATTCAATTGGTACGTGGATGGGGT CGAAGTGCACAACGCCAAGACCAA GCCTAGGGAAGAACAGTACgccTCTA CGTACCGGGTGGTGTCCGTGCTGAC CGTGCTGCACCAGGACTGGCTGAAC GGAAAGGAGTACAAGTGCAAAGTG TCAAACAAGGCTCTCCCTGCCCCTA TCGAAAAGACCATCAGCAAGGCCA AGGGTCAACCTAGGGAGCCCCAGGT CTACACTTTGCCGCCTAGCCGGGAA

			GAAATGACTAAGAACCAAGTGTCCC TGACTTGCCTTGTCAAGGGCTTTTAT CCGTCCGACATCGCCGTGGAGTGGG AGTCCAACGGACAACCGGAGAACA ACTACAAGACCACCCCACCGGTGCT CGATTCCGATGGCTCCTTCTTCCTGT ACTCCAAGCTGACTGTGGACAAGTC AAGATGGCAGCAGGGAAACGTGTT CTCCTGCTCCGTGATGCACGAAGCG CTGCACAACCATTACACCCAGAAAT CACTGTCACTTTCGCCGGGAAAA
SEQ ID 2148	EVQLVQSGAEVKKPGASVKVSCKASG YTFTSYGISWVRQAPGQGLEWMGWII PIFGIANYAQKFQGRVTITADKSTSTAY MELSSLRSEDTAVYYCARELYNYGSK DYFDYWGQGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2256	GAGGTCCAGCTGGTACAGTCTGGAG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTCTCCTGCAAGGCTTCT GGTTACACCTTTACCAGCTATGGTA TCAGCTGGGTGCGACAGGCCCCTGG ACAAGGGCTTGAGTGGATGGGATG GATCATCCCTATCTTTGGTATAGCA AACTACGCACAGAAGTTCCAGGGCA GAGTCACGATTACCGCGGACAAATC CACGAGCACAGCCTACATGGAGCTG AGCAGCCTGAGATCTGAGGACACG GCCGTGTATTACTGTGCGAGAGAAC TATACAACTATGGTTCAAAGGACTA CTTTGACTACTGGGGCCAGGGAACC CTGGTCACCGTCTCCTCAGCATCCA CCAAGGGGCCTTCCGTGTTCCCCCT GGCCCCTTCATCCAAGTCGACCTCT GGTGGAACCGCCGCACTCGGTTGCC TGGTCAAAGACTACTTCCCCGAGCC CGTGACTGTCTCGTGGAACTCGGGC GCCCTCACATCCGGAGTGCATACCT TTCCCGCCGTGTTGCAGTCCAGCGG CCTGTACAGCCTGAGCTCCGTCGTG ACAGTGCCGTCCTCCTCCCTTGGAA CCCAGACCTATATCTGCAACGTCAA TCACAAGCCCTCCAACACCAAAGTG GACAAGAAGGTCGAACCCAAGTCCT GCGACAAGACTCACACCTGTCCGCC TTGTCCAGCCCCTGAGCTGCTGGGT GGTCCGTCCGTGTTCCTCTTCCCGCC CAAGCCGAAGGACACTCTGATGATT TCACGCACCCCGGAAGTCACTTGCG TGGTCGTGGACGTGTCGCACGAAGA TCCCGAAGTGAAATTCAATTGGTAC GTGGATGGGGTCGAAGTGCACAAC GCCAAGACCAAGCCTAGGGAAGAA CAGTACgccTCTACGTACCGGGTGGT GTCCGTGCTGACCGTGCTGCACCAG GACTGGCTGAACGGAAAGGAGTAC AAGTGCAAAGTGTCAAACAAGGCTC TCCCTGCCCCTATCGAAAAGACCAT CAGCAAGGCCAAGGGTCAACCTAG GGAGCCCCAGGTCTACACTTTGCCG CCTAGCCGGGAAGAAATGACTAAG

			AACCAAGTGTCCCTGACTTGCCTTG TCAAGGGCTTTTATCCGTCCGACAT CGCCGTGGAGTGGGAGTCCAACGG ACAACCGGAGAACAACTACAAGAC CACCCCACCGGTGCTCGATTCCGAT GGCTCCTTCTTCCTGTACTCCAAGCT GACTGTGGACAAGTCAAGATGGCA GCAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACT TTCGCCGGGAAAA
SEQ ID 2149	EVQLVQSGAEVKKPGESLKISCKGSGY SFTSYWIGWVRQMPGKGLEWMGIIYP GDSDTRYSPSFQGQVTISADKSISTAYL QWSSLKASDTAMYYCARGGTWDTAM VTGFDYWGQGTLVTVSSASTKGPSVF PLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYASTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG K	SEQ ID 2257	GAAGTGCAGCTGGTGCAGTCTGGAG CAGAGGTGAAAAAGCCCGGGGAGT CTCTGAAGATCTCCTGTAAGGGTTC TGGATACAGCTTTACCAGCTACTGG ATCGGCTGGGTGCGCCAGATGCCCG GGAAAGGCCTGGAGTGGATGGGGA TCATCTATCCTGGTGACTCTGATACC AGATACAGCCCGTCCTTCCAAGGCC AGGTCACCATCTCAGCCGACAAGTC CATCAGCACCGCCTACCTGCAGTGG AGCAGCCTGAAGGCCTCGGACACCG CCATGTATTACTGTGCGAGGGGCGG TACTTGGGATACAGCTATGGTTACG GGCTTTGACTACTGGGGCCAGGGAA CCCTGGTCACCGTCTCCTCAGCATC CACCAAGGGGCCTTCCGTGTTCCCC CTGGCCCCTTCATCCAAGTCGACCT CTGGTGGAACCGCCGCACTCGGTTG CCTGGTCAAAGACTACTTCCCCGAG CCCGTGACTGTCTCGTGGAACTCGG GCGCCCTCACATCCGGAGTGCATAC CTTTCCCGCCGTGTTGCAGTCCAGC GGCCTGTACAGCCTGAGCTCCGTCG TGACAGTGCCGTCCTCCTCCCTTGG AACCCAGACCTATATCTGCAACGTC AATCACAAGCCCTCCAACACCAAAG TGGACAAGAAGGTCGAACCCAAGT CCTGCGACAAGACTCACACCTGTCC GCCTTGTCCAGCCCCTGAGCTGCTG GGTGGTCCGTCCGTGTTCCTCTTCCC GCCCAAGCCGAAGGACACTCTGATG ATTTCACGCACCCCGGAAGTCACTT GCGTGGTCGTGGACGTGTCGCACGA AGATCCCGAAGTGAAATTCAATTGG TACGTGGATGGGGTCGAAGTGCACA ACGCCAAGACCAAGCCTAGGGAAG AACAGTACgccTCTACGTACCGGGTG GTGTCCGTGCTGACCGTGCTGCACC AGGACTGGCTGAACGGAAAGGAGT ACAAGTGCAAAGTGTCAAACAAGG CTCTCCCTGCCCCTATCGAAAAGAC CATCAGCAAGGCCAAGGGTCAACCT AGGGAGCCCCAGGTCTACACTTTGC CGCCTAGCCGGGAAGAAATGACTA

			AGAACCAAGTGTCCCTGACTTGCCT TGTCAAGGGCTTTTATCCGTCCGAC ATCGCCGTGGAGTGGGAGTCCAACG GACAACCGGAGAACAACTACAAGA CCACCCCACCGGTGCTCGATTCCGA TGGCTCCTTCTTCCTGTACTCCAAGC TGACTGTGGACAAGTCAAGATGGCA GCAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACT TTCGCCGGGAAAA
SEQ ID 2150	EVQLVQSGAEVKKPGESLKISCKGSGY SFTSYWIAWVRQMPGKGLEWMGVIYP GDSDTRYSPSFQGQVTISADKSINTAYL QWSSLKASDTAMYYCARPHYDILTGS RAPFDYWGQGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2258	GAAGTGCAGCTGGTGCAGTCTGGAG CAGAGGTGAAAAAGCCCGGGGAGT CTCTGAAGATCTCCTGTAAGGGTTC TGGATACAGCTTTACCAGCTACTGG ATCGCCTGGGTGCGCCAGATGCCCG GGAAAGGCCTGGAGTGGATGGGGG TCATCTATCCTGGTGACTCTGATACC AGATACAGCCCGTCCTTCCAAGGCC AGGTCACCATCTCAGCCGACAAGTC CATCAATACCGCCTACCTGCAGTGG AGCAGCCTGAAGGCCTCGGACACCG CCATGTATTACTGTGCGAGACCCCA TTACGATATTTTGACTGGTTCCCGG GCGCCCTTTGACTACTGGGGCCAGG GAACCCTGGTCACCGTCTCCTCAGC ATCCACCAAGGGGCCTTCCGTGTTC CCCCTGGCCCCTTCATCCAAGTCGA CCTCTGGTGGAACCGCCGCACTCGG TTGCCTGGTCAAAGACTACTTCCCC GAGCCCGTGACTGTCTCGTGGAACT CGGGCGCCCTCACATCCGGAGTGCA TACCTTTCCCGCCGTGTTGCAGTCCA GCGGCCTGTACAGCCTGAGCTCCGT CGTGACAGTGCCGTCCTCCTCCCTT GGAACCCAGACCTATATCTGCAACG TCAATCACAAGCCCTCCAACACCAA AGTGGACAAGAAGGTCGAACCCAA GTCCTGCGACAAGACTCACACCTGT CCGCCTTGTCCAGCCCCTGAGCTGC TGGGTGGTCCGTCCGTGTTCCTCTTC CCGCCCAAGCCGAAGGACACTCTGA TGATTTCACGCACCCCGGAAGTCAC TTGCGTGGTCGTGGACGTGTCGCAC GAAGATCCCGAAGTGAAATTCAATT GGTACGTGGATGGGGTCGAAGTGCA CAACGCCAAGACCAAGCCTAGGGA AGAACAGTACgccTCTACGTACCGGG TGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGA GTACAAGTGCAAAGTGTCAAACAA GGCTCTCCCTGCCCCTATCGAAAAG ACCATCAGCAAGGCCAAGGGTCAA CCTAGGGAGCCCCAGGTCTACACTT TGCCGCCTAGCCGGGAAGAAATGAC

			TAAGAACCAAGTGTCCCTGACTTGC CTTGTCAAGGGCTTTTATCCGTCCG ACATCGCCGTGGAGTGGGAGTCCAA CGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCC GATGGCTCCTTCTTCCTGTACTCCAA GCTGACTGTGGACAAGTCAAGATGG CAGCAGGGAAACGTGTTCTCCTGCT CCGTGATGCACGAAGCGCTGCACAA CCATTACACCCAGAAATCACTGTCA CTTTCGCCGGGAAAA
SEQ ID 2151	QVQLQQWGAGLLKPSETLSLTCAVYG GSFSGYYWSWIRQPPGKGLEWIGEINH SGSTNYNPSLKSRVTISVDTSKNQFSLK LSSVTAADTAVYYCARARVESKDGYF DYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTK PREEQYASTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2259	CAGGTGCAGCTACAGCAGTGGGGC GCAGGACTGTTGAAGCCTTCGGAGA CCCTGTCCCTCACCTGCGCTGTCTAT GGTGGGTCCTTCAGTGGTTACTACT GGAGCTGGATCCGCCAGCCCCCAGG GAAGGGGCTGGAGTGGATTGGGGA AATCAATCATAGTGGAAGCACCAAC TACAACCCGTCCCTCAAGAGTCGAG TCACCATATCAGTAGACACGTCCAA GAACCAGTTCTCCCTGAAGCTGAGC TCTGTGACCGCCGCGGACACGGCTG TGTATTACTGTGCGAGAGCCCGAGT GGAATCCAAGGATGGGTACTTTGAC TACTGGGGCCAGGGAACCCTGGTCA CCGTCTCCTCAGCATCCACCAAGGG GCCTTCCGTGTTCCCCCTGGCCCCTT CATCCAAGTCGACCTCTGGTGGAAC CGCCGCACTCGGTTGCCTGGTCAAA GACTACTTCCCCGAGCCCGTGACTG TCTCGTGGAACTCGGGCGCCCTCAC ATCCGGAGTGCATACCTTTCCCGCC GTGTTGCAGTCCAGCGGCCTGTACA GCCTGAGCTCCGTCGTGACAGTGCC GTCCTCCTCCCTTGGAACCCAGACC TATATCTGCAACGTCAATCACAAGC CCTCCAACACCAAAGTGGACAAGA AGGTCGAACCCAAGTCCTGCGACAA GACTCACACCTGTCCGCCTTGTCCA GCCCCTGAGCTGCTGGGTGGTCCGT CCGTGTTCCTCTTCCCGCCCAAGCC GAAGGACACTCTGATGATTTCACGC ACCCCGGAAGTCACTTGCGTGGTCG TGGACGTGTCGCACGAAGATCCCGA AGTGAAATTCAATTGGTACGTGGAT GGGGTCGAAGTGCACAACGCCAAG ACCAAGCCTAGGGAAGAACAGTACg ccTCTACGTACCGGGTGGTGTCCGTG CTGACCGTGCTGCACCAGGACTGGC TGAACGGAAAGGAGTACAAGTGCA AAGTGTCAAACAAGGCTCTCCCTGC CCCTATCGAAAAGACCATCAGCAAG GCCAAGGGTCAACCTAGGGAGCCCC AGGTCTACACTTTGCCGCCTAGCCG GGAAGAAATGACTAAGAACCAAGT

			GTCCCTGACTTGCCTTGTCAAGGGC TTTTATCCGTCCGACATCGCCGTGG AGTGGGAGTCCAACGGACAACCGG AGAACAACTACAAGACCACCCCACC GGTGCTCGATTCCGATGGCTCCTTCT TCCTGTACTCCAAGCTGACTGTGGA CAAGTCAAGATGGCAGCAGGGAAA CGTGTTCTCCTGCTCCGTGATGCAC GAAGCGCTGCACAACCATTACACCC AGAAATCACTGTCACTTTCGCCGGG AAAA
SEQ ID 2152	EVQLVESGGGVVQPGRSLRLSCAASGF TFTDAWMNWVRQAPGKGLEWIGRVK NKADGETTDYAAPVKGRITISRDDAK NTLYVQMNSLKTEDTAVYYCTADLRL STWDAYDFWGQGTMVTVSSASTKGPS VFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSG LYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCDKTHTCPPCPAPE LLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHN AKTKPREEQYASTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSP GK	SEQ ID 2260	GAGGTGCAGCTGGTGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACTTTCACTGATGCCTGGA TGAACTGGGTCCGCCAGGCTCCAGG GAAGGGGCTGGAGTGGATTGGCCGT GTTAAAAACAAAGCTGATGGTGAG ACAACGGACTACGCTGCACCCGTCA AAGGCAGAATCACCATCTCAAGAG ATGATGCAAAGAACACTCTGTATGT GCAAATGAACAGCCTGAAAACCGA GGACACAGCCGTGTATTATTGTACC GCTGACCTGCGACTTTCTACGTGGG ATGCTTATGATTTCTGGGGCCAAGG GACAATGGTCACCGTCTCTTCAGCA TCCACCAAGGGGCCTTCCGTGTTCC CCCTGGCCCCTTCATCCAAGTCGAC CTCTGGTGGAACCGCCGCACTCGGT TGCCTGGTCAAAGACTACTTCCCCG AGCCCGTGACTGTCTCGTGGAACTC GGGCGCCCTCACATCCGGAGTGCAT ACCTTTCCCGCCGTGTTGCAGTCCA GCGGCCTGTACAGCCTGAGCTCCGT CGTGACAGTGCCGTCCTCCTCCCTT GGAACCCAGACCTATATCTGCAACG TCAATCACAAGCCCTCCAACACCAA AGTGGACAAGAAGGTCGAACCCAA GTCCTGCGACAAGACTCACACCTGT CCGCCTTGTCCAGCCCCTGAGCTGC TGGGTGGTCCGTCCGTGTTCCTCTTC CCGCCCAAGCCGAAGGACACTCTGA TGATTTCACGCACCCCGGAAGTCAC TTGCGTGGTCGTGGACGTGTCGCAC GAAGATCCCGAAGTGAAATTCAATT GGTACGTGGATGGGGTCGAAGTGCA CAACGCCAAGACCAAGCCTAGGGA AGAACAGTACgccTCTACGTACCGGG TGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGA GTACAAGTGCAAAGTGTCAAACAA GGCTCTCCCTGCCCCTATCGAAAAG ACCATCAGCAAGGCCAAGGGTCAA CCTAGGGAGCCCCAGGTCTACACTT TGCCGCCTAGCCGGGAAGAAATGAC

			TAAGAACCAAGTGTCCCTGACTTGC CTTGTCAAGGGCTTTTATCCGTCCG ACATCGCCGTGGAGTGGGAGTCCAA CGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCC GATGGCTCCTTCTTCCTGTACTCCAA GCTGACTGTGGACAAGTCAAGATGG CAGCAGGGAAACGTGTTCTCCTGCT CCGTGATGCACGAAGCGCTGCACAA CCATTACACCCAGAAATCACTGTCA CTTTCGCCGGGAAAA
SEQ ID 2153	QITLKESGGGLVQPGGSLRLSCTVSGF TFSNNWMTWVRQTPGKGLEWVANIK QDGTEKHYVDSVKGRFTISRDNAENSL YLQMNSLRGEDTAVYYCARNSQRSFD YWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVD KKVEPKSCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKP REEQYASTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2261	CAGATCACCTTGAAGGAGTCTGGGG GAGGCTTGGTCCAGCCTGGGGGGTC CCTAAGACTCTCTTGTACAGTCTCA GGATTCACCTTTAGTAACAATTGGA TGACCTGGGTCCGCCAGACTCCAGG GAAGGGGCTGGAGTGGGTGGCCAA CATAAAGCAAGATGGAACTGAGAA ACACTATGTGGACTCTGTGAAGGGC CGATTCACCATCTCCAGAGACAACG CCGAGAACTCACTGTATCTGCAGAT GAACAGCCTGAGAGGTGAGGACAC GGCCGTGTATTATTGTGCGAGAAAC AGTCAACGTTCGTTTGACTACTGGG GCCAGGGCACCCTGGTGACCGTCTC CTCAGCATCCACCAAGGGGCCTTCC GTGTTCCCCCTGGCCCCTTCATCCAA GTCGACCTCTGGTGGAACCGCCGCA CTCGGTTGCCTGGTCAAAGACTACT TCCCCGAGCCCGTGACTGTCTCGTG GAACTCGGGCGCCCTCACATCCGGA GTGCATACCTTTCCCGCCGTGTTGC AGTCCAGCGGCCTGTACAGCCTGAG CTCCGTCGTGACAGTGCCGTCCTCC TCCCTTGGAACCCAGACCTATATCT GCAACGTCAATCACAAGCCCTCCAA CACCAAAGTGGACAAGAAGGTCGA ACCCAAGTCCTGCGACAAGACTCAC ACCTGTCCGCCTTGTCCAGCCCCTG AGCTGCTGGGTGGTCCGTCCGTGTT CCTCTTCCCGCCCAAGCCGAAGGAC ACTCTGATGATTTCACGCACCCCGG AAGTCACTTGCGTGGTCGTGGACGT GTCGCACGAAGATCCCGAAGTGAA ATTCAATTGGTACGTGGATGGGGTC GAAGTGCACAACGCCAAGACCAAG CCTAGGGAAGAACAGTACgccTCTAC GTACCGGGTGGTGTCCGTGCTGACC GTGCTGCACCAGGACTGGCTGAACG GAAAGGAGTACAAGTGCAAAGTGT CAAACAAGGCTCTCCCTGCCCCTAT CGAAAAGACCATCAGCAAGGCCAA GGGTCAACCTAGGGAGCCCCAGGTC TACACTTTGCCGCCTAGCCGGGAAG AAATGACTAAGAACCAAGTGTCCCT

			GACTTGCCTTGTCAAGGGCTTTTATC CGTCCGACATCGCCGTGGAGTGGGA GTCCAACGGACAACCGGAGAACAA CTACAAGACCACCCCACCGGTGCTC GATTCCGATGGCTCCTTCTTCCTGTA CTCCAAGCTGACTGTGGACAAGTCA AGATGGCAGCAGGGAAACGTGTTCT CCTGCTCCGTGATGCACGAAGCGCT GCACAACCATTACACCCAGAAATCA CTGTCACTTTCGCCGGGAAAA
SEQ ID 2154	QVTLKESGGGVVQPGRSLRLSCAASGF TFSSYGMHWVRQAPGKGLEWVAVISY DGSNKYYADSVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCAKDLGDPR GGILNYWGQGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2262	CAGGTCACCTTGAAGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTT ATATCATATGATGGAAGTAATAAAT ACTATGCAGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCTGAGGACACGG CTGTGTATTACTGTGCGAAAGATTT AGGGGATCCCCGGGGTGGTATTTTG AACTACTGGGGCCAGGGCACCCTGG TCACCGTCTCCTCAGCATCCACCAA GGGGCCTTCCGTGTTCCCCCTGGCC CCTTCATCCAAGTCGACCTCTGGTG GAACCGCCGCACTCGGTTGCCTGGT CAAAGACTACTTCCCCGAGCCCGTG ACTGTCTCGTGGAACTCGGGCGCCC TCACATCCGGAGTGCATACCTTTCC CGCCGTGTTGCAGTCCAGCGGCCTG TACAGCCTGAGCTCCGTCGTGACAG TGCCGTCCTCCTCCCTTGGAACCCA GACCTATATCTGCAACGTCAATCAC AAGCCCTCCAACACCAAAGTGGACA AGAAGGTCGAACCCAAGTCCTGCGA CAAGACTCACACCTGTCCGCCTTGT CCAGCCCCTGAGCTGCTGGGTGGTC CGTCCGTGTTCCTCTTCCCGCCCAAG CCGAAGGACACTCTGATGATTTCAC GCACCCCGGAAGTCACTTGCGTGGT CGTGGACGTGTCGCACGAAGATCCC GAAGTGAAATTCAATTGGTACGTGG ATGGGGTCGAAGTGCACAACGCCA AGACCAAGCCTAGGGAAGAACAGT ACgccTCTACGTACCGGGTGGTGTCC GTGCTGACCGTGCTGCACCAGGACT GGCTGAACGGAAAGGAGTACAAGT GCAAAGTGTCAAACAAGGCTCTCCC TGCCCCTATCGAAAAGACCATCAGC AAGGCCAAGGGTCAACCTAGGGAG CCCCAGGTCTACACTTTGCCGCCTA GCCGGGAAGAAATGACTAAGAACC

			AAGTGTCCCTGACTTGCCTTGTCAA GGGCTTTTATCCGTCCGACATCGCC GTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACC CCACCGGTGCTCGATTCCGATGGCT CCTTCTTCCTGTACTCCAAGCTGACT GTGGACAAGTCAAGATGGCAGCAG GGAAACGTGTTCTCCTGCTCCGTGA TGCACGAAGCGCTGCACAACCATTA CACCCAGAAATCACTGTCACTTTCG CCGGGAAAA
SEQ ID 2155	EVQLVESGGGVVQPGRSLRLSCAASGF TFSSYAMHWVRQAPGKGLEWVAVISY DGSNKYYADSVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCARSSPWGEL SLYQGAFDIWGQGTMVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYASTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSL SPGK	SEQ ID 2263	GAGGTGCAGCTGGTGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTCAGTAGCTATGCTA TGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTT ATATCATATGATGGAAGTAATAAAT ACTACGCAGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCTGAGGACACGG CTGTGTATTACTGTGCCCGGTCGAG CCCCTGGGGGGAGTTATCGTTATAC CAGGGGGCTTTTGATATCTGGGGCC AAGGGACAATGGTCACCGTCTCTTC AGCATCCACCAAGGGGCCTTCCGTG TTCCCCCTGGCCCCTTCATCCAAGTC GACCTCTGGTGGAACCGCCGCACTC GGTTGCCTGGTCAAAGACTACTTCC CCGAGCCCGTGACTGTCTCGTGGAA CTCGGGCGCCCTCACATCCGGAGTG CATACCTTTCCCGCCGTGTTGCAGTC CAGCGGCCTGTACAGCCTGAGCTCC GTCGTGACAGTGCCGTCCTCCTCCC TTGGAACCCAGACCTATATCTGCAA CGTCAATCACAAGCCCTCCAACACC AAAGTGGACAAGAAGGTCGAACCC AAGTCCTGCGACAAGACTCACACCT GTCCGCCTTGTCCAGCCCCTGAGCT GCTGGGTGGTCCGTCCGTGTTCCTCT TCCCGCCCAAGCCGAAGGACACTCT GATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGC ACGAAGATCCCGAAGTGAAATTCAA TTGGTACGTGGATGGGGTCGAAGTG CACAACGCCAAGACCAAGCCTAGG GAAGAACAGTACgccTCTACGTACCG GGTGGTGTCCGTGCTGACCGTGCTG CACCAGGACTGGCTGAACGGAAAG GAGTACAAGTGCAAAGTGTCAAAC AAGGCTCTCCCTGCCCCTATCGAAA AGACCATCAGCAAGGCCAAGGGTC AACCTAGGGAGCCCCAGGTCTACAC TTTGCCGCCTAGCCGGGAAGAAATG

			ACTAAGAACCAAGTGTCCCTGACTT GCCTTGTCAAGGGCTTTTATCCGTCC GACATCGCCGTGGAGTGGGAGTCCA ACGGACAACCGGAGAACAACTACA AGACCACCCCACCGGTGCTCGATTC CGATGGCTCCTTCTTCCTGTACTCCA AGCTGACTGTGGACAAGTCAAGATG GCAGCAGGGAAACGTGTTCTCCTGC TCCGTGATGCACGAAGCGCTGCACA ACCATTACACCCAGAAATCACTGTC ACTTTCGCCGGGAAAA
SEQ ID 2156	QITLKESGGGLVQPGRSLRLSCAASGF TFDDYAMHWVRQAPGKGLEWVSAIS GSGGSTYYADSVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCAKDNDFWS GKVFDYWGQGTLVTVSSASTKGPSVF PLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYASTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG K	SEQ ID 2264	CAGATCACCTTGAAGGAGTCTGGGG GAGGCTTGGTACAGCCTGGCAGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTTGATGATTATGCCA TGCACTGGGTCCGGCAAGCTCCAGG GAAGGGGCTGGAGTGGGTCTCAGCT ATTAGTGGTAGTGGTGGTAGCACAT ACTACGCAGACTCCGTGAAGGGCCG GTTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCCGAGGACACGG CCGTATATTACTGTGCGAAAGATAA CGATTTTTGGAGTGGGAAAGTCTTT GACTACTGGGGCCAGGGCACCCTGG TCACCGTCTCCTCAGCATCCACCAA GGGGCCTTCCGTGTTCCCCCTGGCC CCTTCATCCAAGTCGACCTCTGGTG GAACCGCCGCACTCGGTTGCCTGGT CAAAGACTACTTCCCCGAGCCCGTG ACTGTCTCGTGGAACTCGGGCGCCC TCACATCCGGAGTGCATACCTTTCC CGCCGTGTTGCAGTCCAGCGGCCTG TACAGCCTGAGCTCCGTCGTGACAG TGCCGTCCTCCTCCCTTGGAACCCA GACCTATATCTGCAACGTCAATCAC AAGCCCTCCAACACCAAAGTGGACA AGAAGGTCGAACCCAAGTCCTGCGA CAAGACTCACACCTGTCCGCCTTGT CCAGCCCCTGAGCTGCTGGGTGGTC CGTCCGTGTTCCTCTTCCCGCCCAAG CCGAAGGACACTCTGATGATTTCAC GCACCCCGGAAGTCACTTGCGTGGT CGTGGACGTGTCGCACGAAGATCCC GAAGTGAAATTCAATTGGTACGTGG ATGGGGTCGAAGTGCACAACGCCA AGACCAAGCCTAGGGAAGAACAGT ACgccTCTACGTACCGGGTGGTGTCC GTGCTGACCGTGCTGCACCAGGACT GGCTGAACGGAAAGGAGTACAAGT GCAAAGTGTCAAACAAGGCTCTCCC TGCCCCTATCGAAAAGACCATCAGC AAGGCCAAGGGTCAACCTAGGGAG CCCCAGGTCTACACTTTGCCGCCTA GCCGGGAAGAAATGACTAAGAACC

			AAGTGTCCCTGACTTGCCTTGTCAA GGGCTTTTATCCGTCCGACATCGCC GTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACC CCACCGGTGCTCGATTCCGATGGCT CCTTCTTCCTGTACTCCAAGCTGACT GTGGACAAGTCAAGATGGCAGCAG GGAAACGTGTTCTCCTGCTCCGTGA TGCACGAAGCGCTGCACAACCATTA CACCCAGAAATCACTGTCACTTTCG CCGGGAAAA
SEQ ID 2157	EVQLVQSGGGLVQPGGSLRLSCAASG FTFSSYSMNWVRQAPGKGLEWVSYIS STSSTIYYADSVKGRFTISRDNSKNMLF LQMNSLRAEDTAVYYCAKEGGSGWR HYFDYWGQGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2265	GAAGTGCAGCTGGTGCAGTCTGGGG GAGGCTTGGTACAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTCAGTAGTTATAGCA TGAACTGGGTCCGCCAGGCTCCAGG GAAGGGGCTGGAGTGGGTTTCATAC ATCAGTAGTACTAGTAGTACCATAT ACTACGCAGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCC AAGAATATGCTGTTTCTACAAATGA ACAGCCTGAGAGCTGAGGACACGG CTGTGTATTACTGTGCGAAAGAAGG GGGCAGTGGCTGGCGCCACTACTTT GACTACTGGGGCCAGGGAACCCTGG TCACCGTCTCCTCAGCATCCACCAA GGGGCCTTCCGTGTTCCCCCTGGCC CCTTCATCCAAGTCGACCTCTGGTG GAACCGCCGCACTCGGTTGCCTGGT CAAAGACTACTTCCCCGAGCCCGTG ACTGTCTCGTGGAACTCGGGCGCCC TCACATCCGGAGTGCATACCTTTCC CGCCGTGTTGCAGTCCAGCGGCCTG TACAGCCTGAGCTCCGTCGTGACAG TGCCGTCCTCCTCCCTTGGAACCCA GACCTATATCTGCAACGTCAATCAC AAGCCCTCCAACACCAAAGTGGACA AGAAGGTCGAACCCAAGTCCTGCGA CAAGACTCACACCTGTCCGCCTTGT CCAGCCCCTGAGCTGCTGGGTGGTC CGTCCGTGTTCCTCTTCCCGCCCAAG CCGAAGGACACTCTGATGATTTCAC GCACCCCGGAAGTCACTTGCGTGGT CGTGGACGTGTCGCACGAAGATCCC GAAGTGAAATTCAATTGGTACGTGG ATGGGGTCGAAGTGCACAACGCCA AGACCAAGCCTAGGGAAGAACAGT ACgccTCTACGTACCGGGTGGTGTCC GTGCTGACCGTGCTGCACCAGGACT GGCTGAACGGAAAGGAGTACAAGT GCAAAGTGTCAAACAAGGCTCTCCC TGCCCCTATCGAAAAGACCATCAGC AAGGCCAAGGGTCAACCTAGGGAG CCCCAGGTCTACACTTTGCCGCCTA GCCGGGAAGAAATGACTAAGAACC

			AAGTGTCCCTGACTTGCCTTGTCAA GGGCTTTTATCCGTCCGACATCGCC GTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACC CCACCGGTGCTCGATTCCGATGGCT CCTTCTTCCTGTACTCCAAGCTGACT GTGGACAAGTCAAGATGGCAGCAG GGAAACGTGTTCTCCTGCTCCGTGA TGCACGAAGCGCTGCACAACCATTA CACCCAGAAATCACTGTCACTTTCG CCGGGAAAA
SEQ ID 2158	QVTLKESGGGVVQPGRSLRLSCAASGF TFSSYAMHWVRQAPGKGLEWVAVISY DGSNKYYADSVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCARDYCSSTS CQNWFDPWGQGTLVTVSSASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYASTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG K	SEQ ID 2266	CAGGTCACCTTGAAGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTGTCCTGTGCAGCCTCT GGATTCACCTTCAGCAGCTATGCTA TGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTT ATATCATATGATGGAAGTAATAAAT ACTACGCAGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCTGAGGACACGG CTGTGTATTACTGTGCGAGAGATTA TTGTAGTAGTACCAGCTGCCAGAAC TGGTTCGACCCCTGGGGCCAGGGCA CCCTGGTCACCGTCTCCTCAGCATC CACCAAGGGGCCTTCCGTGTTCCCC CTGGCCCCTTCATCCAAGTCGACCT CTGGTGGAACCGCCGCACTCGGTTG CCTGGTCAAAGACTACTTCCCCGAG CCCGTGACTGTCTCGTGGAACTCGG GCGCCCTCACATCCGGAGTGCATAC CTTTCCCGCCGTGTTGCAGTCCAGC GGCCTGTACAGCCTGAGCTCCGTCG TGACAGTGCCGTCCTCCTCCCTTGG AACCCAGACCTATATCTGCAACGTC AATCACAAGCCCTCCAACACCAAAG TGGACAAGAAGGTCGAACCCAAGT CCTGCGACAAGACTCACACCTGTCC GCCTTGTCCAGCCCCTGAGCTGCTG GGTGGTCCGTCCGTGTTCCTCTTCCC GCCCAAGCCGAAGGACACTCTGATG ATTTCACGCACCCCGGAAGTCACTT GCGTGGTCGTGGACGTGTCGCACGA AGATCCCGAAGTGAAATTCAATTGG TACGTGGATGGGGTCGAAGTGCACA ACGCCAAGACCAAGCCTAGGGAAG AACAGTACgccTCTACGTACCGGGTG GTGTCCGTGCTGACCGTGCTGCACC AGGACTGGCTGAACGGAAAGGAGT ACAAGTGCAAAGTGTCAAACAAGG CTCTCCCTGCCCCTATCGAAAAGAC CATCAGCAAGGCCAAGGGTCAACCT AGGGAGCCCCAGGTCTACACTTTGC CGCCTAGCCGGGAAGAAATGACTA

			AGAACCAAGTGTCCCTGACTTGCCT TGTCAAGGGCTTTTATCCGTCCGAC ATCGCCGTGGAGTGGGAGTCCAACG GACAACCGGAGAACAACTACAAGA CCACCCCACCGGTGCTCGATTCCGA TGGCTCCTTCTTCCTGTACTCCAAGC TGACTGTGGACAAGTCAAGATGGCA GCAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACT TTCGCCGGGAAAA
SEQ ID 2159	QVQLVQSGGGLVQPGGSLRLSCAASG FTFSNYVMSWVRQAPGKGLEWVSAIS GIGDTTYYADSVKGRFTISRDNAKNTL YLQMNSLRAEDTAVYYCARGRVAGD AFDIWGQGTMVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTK PREEQYASTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2267	CAGGTCCAGCTGGTGCAGTCTGGGG GAGGCTTGGTACAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTTAGCAACTATGTCA TGAGCTGGGTCCGCCAGGCTCCAGG GAAGGGGCTGGAGTGGGTCTCAGCT ATTAGTGGTATTGGTGATACTACAT ACTACGCGGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAACGCC AAGAACACGCTGTATCTGCAAATGA ACAGTCTGAGAGCCGAGGACACGG CTGTGTATTACTGTGCAAGAGGGCG CGTGGCGGGGGATGCTTTTGATATC TGGGGCCAAGGGACAATGGTGACC GTCTCTTCAGCATCCACCAAGGGGC CTTCCGTGTTCCCCCTGGCCCCTTCA TCCAAGTCGACCTCTGGTGGAACCG CCGCACTCGGTTGCCTGGTCAAAGA CTACTTCCCCGAGCCCGTGACTGTC TCGTGGAACTCGGGCGCCCTCACAT CCGGAGTGCATACCTTTCCCGCCGT GTTGCAGTCCAGCGGCCTGTACAGC CTGAGCTCCGTCGTGACAGTGCCGT CCTCCTCCCTTGGAACCCAGACCTA TATCTGCAACGTCAATCACAAGCCC TCCAACACCAAAGTGGACAAGAAG GTCGAACCCAAGTCCTGCGACAAGA CTCACACCTGTCCGCCTTGTCCAGC CCCTGAGCTGCTGGGTGGTCCGTCC GTGTTCCTCTTCCCGCCCAAGCCGA AGGACACTCTGATGATTTCACGCAC CCCGGAAGTCACTTGCGTGGTCGTG GACGTGTCGCACGAAGATCCCGAAG TGAAATTCAATTGGTACGTGGATGG GGTCGAAGTGCACAACGCCAAGAC CAAGCCTAGGGAAGAACAGTACgcc TCTACGTACCGGGTGGTGTCCGTGC TGACCGTGCTGCACCAGGACTGGCT GAACGGAAAGGAGTACAAGTGCAA AGTGTCAAACAAGGCTCTCCCTGCC CCTATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTACACTTTGCCGCCTAGCCGG GAAGAAATGACTAAGAACCAAGTG

			TCCCTGACTTGCCTTGTCAAGGGCTT TTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCAAGCTGACTGTGGACA AGTCAAGATGGCAGCAGGGAAACG TGTTCTCCTGCTCCGTGATGCACGA AGCGCTGCACAACCATTACACCCAG AAATCACTGTCACTTTCGCCGGGAA AA
SEQ ID 2160	QLQLQESGGGLVQPGGSLRLSCAASGF TFSSYAMSWVRQAPGKGLEWVSAISG SGGSTYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKDQGAAAG TLGYFDYWGQGTLVTVSSASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYASTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG K	SEQ ID 2268	CAGCTGCAGCTGCAGGAGTCGGGG GGAGGCTTGGTACAGCCTGGGGGGT CCCTGAGACTCTCCTGTGCAGCCTC TGGATTCACCTTTAGCAGCTATGCC ATGAGCTGGGTCCGCCAGGCTCCAG GGAAGGGGCTGGAGTGGGTCTCAG CTATTAGTGGTAGTGGTGGTAGCAC ATACTACGCAGACTCCGTGAAGGGC CGGTTCACCATCTCCAGAGACAATT CCAAGAACACGCTGTATCTGCAAAT GAACAGCCTGAGAGCCGAGGACAC GGCCGTATATTACTGTGCGAAAGAT CAAGGGGCAGCAGCTGGTACCCTGG GGTACTTTGACTACTGGGGCCAGGG AACCCTGGTGACCGTCTCCTCAGCA TCCACCAAGGGGCCTTCCGTGTTCC CCCTGGCCCCTTCATCCAAGTCGAC CTCTGGTGGAACCGCCGCACTCGGT TGCCTGGTCAAAGACTACTTCCCCG AGCCCGTGACTGTCTCGTGGAACTC GGGCGCCCTCACATCCGGAGTGCAT ACCTTTCCCGCCGTGTTGCAGTCCA GCGGCCTGTACAGCCTGAGCTCCGT CGTGACAGTGCCGTCCTCCTCCCTT GGAACCCAGACCTATATCTGCAACG TCAATCACAAGCCCTCCAACACCAA AGTGGACAAGAAGGTCGAACCCAA GTCCTGCGACAAGACTCACACCTGT CCGCCTTGTCCAGCCCCTGAGCTGC TGGGTGGTCCGTCCGTGTTCCTCTTC CCGCCCAAGCCGAAGGACACTCTGA TGATTTCACGCACCCCGGAAGTCAC TTGCGTGGTCGTGGACGTGTCGCAC GAAGATCCCGAAGTGAAATTCAATT GGTACGTGGATGGGGTCGAAGTGCA CAACGCCAAGACCAAGCCTAGGGA AGAACAGTACgccTCTACGTACCGGG TGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGA GTACAAGTGCAAAGTGTCAAACAA GGCTCTCCCTGCCCCTATCGAAAAG ACCATCAGCAAGGCCAAGGGTCAA CCTAGGGAGCCCCAGGTCTACACTT TGCCGCCTAGCCGGGAAGAAATGAC

			TAAGAACCAAGTGTCCCTGACTTGC CTTGTCAAGGGCTTTTATCCGTCCG ACATCGCCGTGGAGTGGGAGTCCAA CGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCC GATGGCTCCTTCTTCCTGTACTCCAA GCTGACTGTGGACAAGTCAAGATGG CAGCAGGGAAACGTGTTCTCCTGCT CCGTGATGCACGAAGCGCTGCACAA CCATTACACCCAGAAATCACTGTCA CTTTCGCCGGGAAAA
SEQ ID 2161	QVQLVQSGAEVKKPGASVKVSCKASG YTFTSYDINWVRQATGQGLEWMGWM NPNSGNTGYAQKFQGRVTMTRNTSIST AYMELSSLRSEDTAVYYCTRGIYDSSG SSNPFDSWGQGTLVTVSSASTKGPSVF PLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYASTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG K	SEQ ID 2269	CAGGTGCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTCTCCTGCAAGGCTTCT GGATACACCTTCACCAGTTATGATA TCAACTGGGTGCGACAGGCCACTGG ACAAGGGCTTGAGTGGATGGGATG GATGAACCCTAACAGTGGTAACACA GGCTATGCACAGAAGTTCCAGGGCA GAGTCACCATGACCAGGAACACCTC CATAAGCACAGCCTACATGGAGCTG AGCAGCCTGAGATCTGAGGACACG GCCGTGTATTACTGTACGAGAGGAA TCTATGATAGTAGTGGTTCTTCCAAT CCCTTTGACTCCTGGGGCCAGGGAA CCCTGGTGACCGTCTCCTCAGCATC CACCAAGGGGCCTTCCGTGTTCCCC CTGGCCCCTTCATCCAAGTCGACCT CTGGTGGAACCGCCGCACTCGGTTG CCTGGTCAAAGACTACTTCCCCGAG CCCGTGACTGTCTCGTGGAACTCGG GCGCCCTCACATCCGGAGTGCATAC CTTTCCCGCCGTGTTGCAGTCCAGC GGCCTGTACAGCCTGAGCTCCGTCG TGACAGTGCCGTCCTCCTCCCTTGG AACCCAGACCTATATCTGCAACGTC AATCACAAGCCCTCCAACACCAAAG TGGACAAGAAGGTCGAACCCAAGT CCTGCGACAAGACTCACACCTGTCC GCCTTGTCCAGCCCCTGAGCTGCTG GGTGGTCCGTCCGTGTTCCTCTTCCC GCCCAAGCCGAAGGACACTCTGATG ATTTCACGCACCCCGGAAGTCACTT GCGTGGTCGTGGACGTGTCGCACGA AGATCCCGAAGTGAAATTCAATTGG TACGTGGATGGGGTCGAAGTGCACA ACGCCAAGACCAAGCCTAGGGAAG AACAGTACgccTCTACGTACCGGGTG GTGTCCGTGCTGACCGTGCTGCACC AGGACTGGCTGAACGGAAAGGAGT ACAAGTGCAAAGTGTCAAACAAGG CTCTCCCTGCCCCTATCGAAAAGAC CATCAGCAAGGCCAAGGGTCAACCT AGGGAGCCCCAGGTCTACACTTTGC CGCCTAGCCGGGAAGAAATGACTA

			AGAACCAAGTGTCCCTGACTTGCCT TGTCAAGGGCTTTTATCCGTCCGAC ATCGCCGTGGAGTGGGAGTCCAACG GACAACCGGAGAACAACTACAAGA CCACCCCACCGGTGCTCGATTCCGA TGGCTCCTTCTTCCTGTACTCCAAGC TGACTGTGGACAAGTCAAGATGGCA GCAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACT TTCGCCGGGAAAA
SEQ ID 2162	EVQLVQSGAEVKKPGASVKISCEASGY TFTDYAIHWVRQAPGQRLEWMGWIN AGDGGTKSSREFQGRVTITRDTSATTA YMEVSSLRSEDTAVYYCARGYCSGGS CPGTDFDYWGQGTLVTVSSASTKGPS VFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSG LYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCDKTHTCPPCPAPE LLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHN AKTKPREEQYASTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSP GK	SEQ ID 2270	GAGGTGCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGATTTCCTGCGAGGCTTCT GGATACACCTTCACTGATTATGCTA TACATTGGGTGCGCCAGGCCCCCGG ACAAAGACTTGAGTGGATGGGATG GATCAACGCTGGCGATGGTGGCACA AAAAGTTCACGGGAGTTCCAGGGCA GAGTCACCATTACCAGGGACACATC CGCGACCACAGCCTACATGGAGGTG AGCAGTCTGAGATCTGAAGACACGG CTGTCTATTACTGTGCGAGAGGATA TTGTAGTGGTGGTAGCTGCCCAGGA ACGGATTTTGACTACTGGGGCCAGG GAACCCTGGTCACCGTCTCCTCAGC ATCCACCAAGGGGCCTTCCGTGTTC CCCCTGGCCCCTTCATCCAAGTCGA CCTCTGGTGGAACCGCCGCACTCGG TTGCCTGGTCAAAGACTACTTCCCC GAGCCCGTGACTGTCTCGTGGAACT CGGGCGCCCTCACATCCGGAGTGCA TACCTTTCCCGCCGTGTTGCAGTCCA GCGGCCTGTACAGCCTGAGCTCCGT CGTGACAGTGCCGTCCTCCTCCCTT GGAACCCAGACCTATATCTGCAACG TCAATCACAAGCCCTCCAACACCAA AGTGGACAAGAAGGTCGAACCCAA GTCCTGCGACAAGACTCACACCTGT CCGCCTTGTCCAGCCCCTGAGCTGC TGGGTGGTCCGTCCGTGTTCCTCTTC CCGCCCAAGCCGAAGGACACTCTGA TGATTTCACGCACCCCGGAAGTCAC TTGCGTGGTCGTGGACGTGTCGCAC GAAGATCCCGAAGTGAAATTCAATT GGTACGTGGATGGGGTCGAAGTGCA CAACGCCAAGACCAAGCCTAGGGA AGAACAGTACgccTCTACGTACCGGG TGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGA GTACAAGTGCAAAGTGTCAAACAA GGCTCTCCCTGCCCCTATCGAAAAG ACCATCAGCAAGGCCAAGGGTCAA CCTAGGGAGCCCCAGGTCTACACTT TGCCGCCTAGCCGGGAAGAAATGAC

			TAAGAACCAAGTGTCCCTGACTTGC CTTGTCAAGGGCTTTTATCCGTCCG ACATCGCCGTGGAGTGGGAGTCCAA CGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCC GATGGCTCCTTCTTCCTGTACTCCAA GCTGACTGTGGACAAGTCAAGATGG CAGCAGGGAAACGTGTTCTCCTGCT CCGTGATGCACGAAGCGCTGCACAA CCATTACACCCAGAAATCACTGTCA CTTTCGCCGGGAAAA
SEQ ID 2163	QVQLVQSGAEVKKPGASVKVSCKASG YTFTSYYMHWVRQAPGQGLEWMGIIN PSGGSTSYAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARDGVGGRD GYNFDYWGQGTLVTVSSASTKGPSVF PLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYASTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG K	SEQ ID 2271	CAGGTGCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTTTCCTGCAAGGCATCT GGATACACCTTCACCAGCTACTATA TGCACTGGGTGCGACAGGCCCCTGG ACAAGGGCTTGAGTGGATGGGAAT AATCAACCCTAGTGGTGGTAGCACA AGCTACGCACAGAAGTTCCAGGGCA GAGTCACCATGACCAGGGACACGTC CACGAGCACAGTCTACATGGAGCTG AGCAGCCTGAGATCTGAGGACACG GCCGTGTATTACTGTGCGAGAGATG GTGTAGGAGGGAGAGATGGCTACA ATTTTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTCTCCTCAGCATCC ACCAAGGGGCCTTCCGTGTTCCCCC TGGCCCCTTCATCCAAGTCGACCTC TGGTGGAACCGCCGCACTCGGTTGC CTGGTCAAAGACTACTTCCCCGAGC CCGTGACTGTCTCGTGGAACTCGGG CGCCCTCACATCCGGAGTGCATACC TTTCCCGCCGTGTTGCAGTCCAGCG GCCTGTACAGCCTGAGCTCCGTCGT GACAGTGCCGTCCTCCTCCCTTGGA ACCCAGACCTATATCTGCAACGTCA ATCACAAGCCCTCCAACACCAAAGT GGACAAGAAGGTCGAACCCAAGTC CTGCGACAAGACTCACACCTGTCCG CCTTGTCCAGCCCCTGAGCTGCTGG GTGGTCCGTCCGTGTTCCTCTTCCCG CCCAAGCCGAAGGACACTCTGATGA TTTCACGCACCCCGGAAGTCACTTG CGTGGTCGTGGACGTGTCGCACGAA GATCCCGAAGTGAAATTCAATTGGT ACGTGGATGGGGTCGAAGTGCACA ACGCCAAGACCAAGCCTAGGGAAG AACAGTACgccTCTACGTACCGGGTG GTGTCCGTGCTGACCGTGCTGCACC AGGACTGGCTGAACGGAAAGGAGT ACAAGTGCAAAGTGTCAAACAAGG CTCTCCCTGCCCCTATCGAAAAGAC CATCAGCAAGGCCAAGGGTCAACCT AGGGAGCCCCAGGTCTACACTTTGC CGCCTAGCCGGGAAGAAATGACTA

			AGAACCAAGTGTCCCTGACTTGCCT TGTCAAGGGCTTTTATCCGTCCGAC ATCGCCGTGGAGTGGGAGTCCAACG GACAACCGGAGAACAACTACAAGA CCACCCCACCGGTGCTCGATTCCGA TGGCTCCTTCTTCCTGTACTCCAAGC TGACTGTGGACAAGTCAAGATGGCA GCAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACT TTCGCCGGGAAAA
SEQ ID 2164	EVQLVQSGGGLVQPGGSLRLSCAASG FTVSSNYMSWVRQAPGKGLEWVSVIY SGGSTYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARAPLAADG YFDYWGQGTLVTVSSASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2272	GAAGTGCAGCTGGTGCAGTCTGGGG GAGGCTTGGTCCAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCGTCAGTAGCAACTACA TGAGCTGGGTCCGCCAGGCTCCAGG GAAGGGGCTGGAGTGGGTCTCAGTT ATTTATAGCGGTGGTAGCACATACT ACGCAGACTCCGTGAAGGGCCGATT CACCATCTCCAGAGACAATTCCAAG AACACGCTGTATCTTCAAATGAACA GCCTGAGAGCTGAGGACACGGCTGT GTATTACTGTGCGAGAGCCCCCCTA GCAGCAGATGGCTACTTTGACTACT GGGGCCAGGGAACCCTGGTCACCGT CTCCTCAGCATCCACCAAGGGGCCT TCCGTGTTCCCCCTGGCCCCTTCATC CAAGTCGACCTCTGGTGGAACCGCC GCACTCGGTTGCCTGGTCAAAGACT ACTTCCCCGAGCCCGTGACTGTCTC GTGGAACTCGGGCGCCCTCACATCC GGAGTGCATACCTTTCCCGCCGTGT TGCAGTCCAGCGGCCTGTACAGCCT GAGCTCCGTCGTGACAGTGCCGTCC TCCTCCCTTGGAACCCAGACCTATA TCTGCAACGTCAATCACAAGCCCTC CAACACCAAAGTGGACAAGAAGGT CGAACCCAAGTCCTGCGACAAGACT CACACCTGTCCGCCTTGTCCAGCCC CTGAGCTGCTGGGTGGTCCGTCCGT GTTCCTCTTCCCGCCCAAGCCGAAG GACACTCTGATGATTTCACGCACCC CGGAAGTCACTTGCGTGGTCGTGGA CGTGTCGCACGAAGATCCCGAAGTG AAATTCAATTGGTACGTGGATGGGG TCGAAGTGCACAACGCCAAGACCA AGCCTAGGGAAGAACAGTACgccTCT ACGTACCGGGTGGTGTCCGTGCTGA CCGTGCTGCACCAGGACTGGCTGAA CGGAAAGGAGTACAAGTGCAAAGT GTCAAACAAGGCTCTCCCTGCCCCT ATCGAAAAGACCATCAGCAAGGCC AAGGGTCAACCTAGGGAGCCCCAG GTCTACACTTTGCCGCCTAGCCGGG AAGAAATGACTAAGAACCAAGTGT

			CCCTGACTTGCCTTGTCAAGGGCTTT TATCCGTCCGACATCGCCGTGGAGT GGGAGTCCAACGGACAACCGGAGA ACAACTACAAGACCACCCCACCGGT GCTCGATTCCGATGGCTCCTTCTTCC TGTACTCCAAGCTGACTGTGGACAA GTCAAGATGGCAGCAGGGAAACGT GTTCTCCTGCTCCGTGATGCACGAA GCGCTGCACAACCATTACACCCAGA AATCACTGTCACTTTCGCCGGGAAA A
SEQ ID 2165	EVQLVQSGAEVKKPGSSVKVSCKASG GTFSSYAISWVRQAPGQGLEWMGGIIP IFGTANYAQKFQGRVTITADESTSTAY MELSSLRSEDTAVYYCARARGLQYLI WYFDLWGRGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2273	GAGGTCCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGTCCTC GGTGAAGGTCTCCTGCAAGGCTTCT GGAGGCACCTTCAGCAGCTATGCTA TCAGCTGGGTGCGACAGGCCCCTGG ACAAGGGCTTGAGTGGATGGGAGG GATCATCCCTATCTTTGGTACAGCA AACTACGCACAGAAGTTCCAGGGCA GAGTCACGATTACCGCGGACGAATC CACGAGCACAGCCTACATGGAGCTG AGCAGCCTGAGATCTGAGGACACG GCCGTGTATTACTGTGCGAGAGCCC GGGGGCTACAGTACCTAATCTGGTA CTTCGATCTCTGGGGCCGTGGCACC CTGGTGACCGTCTCCTCAGCATCCA CCAAGGGGCCTTCCGTGTTCCCCCT GGCCCCTTCATCCAAGTCGACCTCT GGTGGAACCGCCGCACTCGGTTGCC TGGTCAAAGACTACTTCCCCGAGCC CGTGACTGTCTCGTGGAACTCGGGC GCCCTCACATCCGGAGTGCATACCT TTCCCGCCGTGTTGCAGTCCAGCGG CCTGTACAGCCTGAGCTCCGTCGTG ACAGTGCCGTCCTCCTCCCTTGGAA CCCAGACCTATATCTGCAACGTCAA TCACAAGCCCTCCAACACCAAAGTG GACAAGAAGGTCGAACCCAAGTCCT GCGACAAGACTCACACCTGTCCGCC TTGTCCAGCCCCTGAGCTGCTGGGT GGTCCGTCCGTGTTCCTCTTCCCGCC CAAGCCGAAGGACACTCTGATGATT TCACGCACCCCGGAAGTCACTTGCG TGGTCGTGGACGTGTCGCACGAAGA TCCCGAAGTGAAATTCAATTGGTAC GTGGATGGGGTCGAAGTGCACAAC GCCAAGACCAAGCCTAGGGAAGAA CAGTACgccTCTACGTACCGGGTGGT GTCCGTGCTGACCGTGCTGCACCAG GACTGGCTGAACGGAAAGGAGTAC AAGTGCAAAGTGTCAAACAAGGCTC TCCCTGCCCCTATCGAAAAGACCAT CAGCAAGGCCAAGGGTCAACCTAG GGAGCCCCAGGTCTACACTTTGCCG CCTAGCCGGGAAGAAATGACTAAG

			AACCAAGTGTCCCTGACTTGCCTTG TCAAGGGCTTTTATCCGTCCGACAT CGCCGTGGAGTGGGAGTCCAACGG ACAACCGGAGAACAACTACAAGAC CACCCCACCGGTGCTCGATTCCGAT GGCTCCTTCTTCCTGTACTCCAAGCT GACTGTGGACAAGTCAAGATGGCA GCAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACT TTCGCCGGGAAAA
SEQ ID 2166	QVQLVQSGAEVKKPGASVKVSCKASG YTFTSYYMHWVRQAPGQGLEWMGIIN PSGGSTSYAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCASPGMVRGV ITAPLDYWGQGTLVTVSSASTKGPSVF PLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYASTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG K	SEQ ID 2274	CAGGTCCAGCTGGTACAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTTTCCTGCAAGGCATCT GGATACACCTTCACCAGCTACTATA TGCACTGGGTGCGACAGGCCCCTGG ACAAGGGCTTGAGTGGATGGGAAT AATCAACCCTAGTGGTGGTAGCACA AGCTACGCACAGAAGTTCCAGGGCA GAGTCACCATGACCAGGGACACGTC CACGAGCACAGTCTACATGGAGCTG AGCAGCCTGAGATCTGAGGACACG GCCGTGTATTACTGTGCGAGCCCGG GTATGGTTCGGGGAGTTATTACTGC CCCGCTTGACTACTGGGGCCAGGGC ACCCTGGTCACCGTCTCCTCAGCAT CCACCAAGGGGCCTTCCGTGTTCCC CCTGGCCCCTTCATCCAAGTCGACC TCTGGTGGAACCGCCGCACTCGGTT GCCTGGTCAAAGACTACTTCCCCGA GCCCGTGACTGTCTCGTGGAACTCG GGCGCCCTCACATCCGGAGTGCATA CCTTTCCCGCCGTGTTGCAGTCCAG CGGCCTGTACAGCCTGAGCTCCGTC GTGACAGTGCCGTCCTCCTCCCTTG GAACCCAGACCTATATCTGCAACGT CAATCACAAGCCCTCCAACACCAAA GTGGACAAGAAGGTCGAACCCAAG TCCTGCGACAAGACTCACACCTGTC CGCCTTGTCCAGCCCCTGAGCTGCT GGGTGGTCCGTCCGTGTTCCTCTTCC CGCCCAAGCCGAAGGACACTCTGAT GATTTCACGCACCCCGGAAGTCACT TGCGTGGTCGTGGACGTGTCGCACG AAGATCCCGAAGTGAAATTCAATTG GTACGTGGATGGGGTCGAAGTGCAC AACGCCAAGACCAAGCCTAGGGAA GAACAGTACgccTCTACGTACCGGGT GGTGTCCGTGCTGACCGTGCTGCAC CAGGACTGGCTGAACGGAAAGGAG TACAAGTGCAAAGTGTCAAACAAG GCTCTCCCTGCCCCTATCGAAAAGA CCATCAGCAAGGCCAAGGGTCAACC TAGGGAGCCCCAGGTCTACACTTTG CCGCCTAGCCGGGAAGAAATGACTA

			AGAACCAAGTGTCCCTGACTTGCCT TGTCAAGGGCTTTTATCCGTCCGAC ATCGCCGTGGAGTGGGAGTCCAACG GACAACCGGAGAACAACTACAAGA CCACCCCACCGGTGCTCGATTCCGA TGGCTCCTTCTTCCTGTACTCCAAGC TGACTGTGGACAAGTCAAGATGGCA GCAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACT TTCGCCGGGAAAA
SEQ ID 2167	EVQLVQSGGGLVKPGGSLRLSCAASG FTFSSYAISWVRQAPGQGLEWMGGIIP MYGTANYAQKFQGRVTITADESTSTA YMELSSLRSEDTALYYCAREAKWGM YYFDYWGQGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2275	GAGGTCCAGCTGGTACAGTCTGGGG GAGGCCTGGTCAAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTCAGCAGCTATGCTA TCAGCTGGGTGCGACAGGCCCCTGG ACAAGGGCTTGAGTGGATGGGAGG GATCATCCCTATGTATGGTACAGCA AACTACGCACAGAAGTTCCAGGGCA GAGTCACGATTACCGCGGACGAATC CACGAGCACAGCCTACATGGAACTG AGCAGCCTGAGATCTGAGGACACG GCCCTCTATTACTGTGCGAGAGAAG CTAAGTGGGGAATGTACTACTTTGA CTACTGGGGCCAGGGCACCCTGGTC ACCGTCTCCTCAGCATCCACCAAGG GGCCTTCCGTGTTCCCCCTGGCCCCT TCATCCAAGTCGACCTCTGGTGGAA CCGCCGCACTCGGTTGCCTGGTCAA AGACTACTTCCCCGAGCCCGTGACT GTCTCGTGGAACTCGGGCGCCCTCA CATCCGGAGTGCATACCTTTCCCGC CGTGTTGCAGTCCAGCGGCCTGTAC AGCCTGAGCTCCGTCGTGACAGTGC CGTCCTCCTCCCTTGGAACCCAGAC CTATATCTGCAACGTCAATCACAAG CCCTCCAACACCAAAGTGGACAAGA AGGTCGAACCCAAGTCCTGCGACAA GACTCACACCTGTCCGCCTTGTCCA GCCCCTGAGCTGCTGGGTGGTCCGT CCGTGTTCCTCTTCCCGCCCAAGCC GAAGGACACTCTGATGATTTCACGC ACCCCGGAAGTCACTTGCGTGGTCG TGGACGTGTCGCACGAAGATCCCGA AGTGAAATTCAATTGGTACGTGGAT GGGGTCGAAGTGCACAACGCCAAG ACCAAGCCTAGGGAAGAACAGTACg ccTCTACGTACCGGGTGGTGTCCGTG CTGACCGTGCTGCACCAGGACTGGC TGAACGGAAAGGAGTACAAGTGCA AAGTGTCAAACAAGGCTCTCCCTGC CCCTATCGAAAAGACCATCAGCAAG GCCAAGGGTCAACCTAGGGAGCCCC AGGTCTACACTTTGCCGCCTAGCCG GGAAGAAATGACTAAGAACCAAGT

			GTCCCTGACTTGCCTTGTCAAGGGC TTTTATCCGTCCGACATCGCCGTGG AGTGGGAGTCCAACGGACAACCGG AGAACAACTACAAGACCACCCCACC GGTGCTCGATTCCGATGGCTCCTTCT TCCTGTACTCCAAGCTGACTGTGGA CAAGTCAAGATGGCAGCAGGGAAA CGTGTTCTCCTGCTCCGTGATGCAC GAAGCGCTGCACAACCATTACACCC AGAAATCACTGTCACTTTCGCCGGG AAAA
SEQ ID 2168	EVQLVESGGGVVQPGRSLRLSCAASGF TFSSYAIHWVRQAPGKGLEWVAIISDD GSKSYYADSVQGRFTISRDNSRNTVYL QMNSLRAEDTAMYYCARDRGTKWNQ LNDVFDMWGQGTMVTVSSASTKGPS VFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSG LYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCDKTHTCPPCPAPE LLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHN AKTKPREEQYASTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSP GK	SEQ ID 2276	GAGGTGCAGCTGGTGGAGTCCGGG GGAGGCGTGGTCCAGCCTGGGAGGT CCCTGAGACTCTCCTGTGCAGCCTC TGGATTCACCTTCAGTAGCTATGCT ATACACTGGGTCCGCCAGGCTCCAG GCAAGGGGCTGGAGTGGGTGGCAA TTATATCAGATGATGGAAGTAAGAG TTACTACGCAGACTCCGTGCAGGGC CGATTCACCATCTCCAGAGACAATT CGAGGAACACAGTATATCTGCAAAT GAACAGCCTGAGAGCTGAGGACAC GGCTATGTATTACTGTGCGAGAGAC AGGGGAACTAAATGGAACCAATTG AATGATGTTTTTGATATGTGGGGCC AAGGGACAATGGTCACCGTCTCTTC AGCATCCACCAAGGGGCCTTCCGTG TTCCCCCTGGCCCCTTCATCCAAGTC GACCTCTGGTGGAACCGCCGCACTC GGTTGCCTGGTCAAAGACTACTTCC CCGAGCCCGTGACTGTCTCGTGGAA CTCGGGCGCCCTCACATCCGGAGTG CATACCTTTCCCGCCGTGTTGCAGTC CAGCGGCCTGTACAGCCTGAGCTCC GTCGTGACAGTGCCGTCCTCCTCCC TTGGAACCCAGACCTATATCTGCAA CGTCAATCACAAGCCCTCCAACACC AAAGTGGACAAGAAGGTCGAACCC AAGTCCTGCGACAAGACTCACACCT GTCCGCCTTGTCCAGCCCCTGAGCT GCTGGGTGGTCCGTCCGTGTTCCTCT TCCCGCCCAAGCCGAAGGACACTCT GATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGC ACGAAGATCCCGAAGTGAAATTCAA TTGGTACGTGGATGGGGTCGAAGTG CACAACGCCAAGACCAAGCCTAGG GAAGAACAGTACgccTCTACGTACCG GGTGGTGTCCGTGCTGACCGTGCTG CACCAGGACTGGCTGAACGGAAAG GAGTACAAGTGCAAAGTGTCAAAC AAGGCTCTCCCTGCCCCTATCGAAA AGACCATCAGCAAGGCCAAGGGTC AACCTAGGGAGCCCCAGGTCTACAC TTTGCCGCCTAGCCGGGAAGAAATG

			ACTAAGAACCAAGTGTCCCTGACTT GCCTTGTCAAGGGCTTTTATCCGTCC GACATCGCCGTGGAGTGGGAGTCCA ACGGACAACCGGAGAACAACTACA AGACCACCCCACCGGTGCTCGATTC CGATGGCTCCTTCTTCCTGTACTCCA AGCTGACTGTGGACAAGTCAAGATG GCAGCAGGGAAACGTGTTCTCCTGC TCCGTGATGCACGAAGCGCTGCACA ACCATTACACCCAGAAATCACTGTC ACTTTCGCCGGGAAAA
SEQ ID 2169	QMQLVQSGAEVKKPGASVKVSCTASG YTFTSSDINWVRQATGQGLEWMGWM NPNSGNTGYAEKFQGRVTMTSDSSIST AYMELRSLTTEDTAVYYCARGGGASY TDSWGQGTLVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTK PREEQYASTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2277	CAGATGCAGCTGGTGCAATCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTCTCCTGCACGGCTTCT GGATACACCTTCACCAGTTCTGATA TCAACTGGGTGCGACAGGCCACTGG ACAAGGGCTTGAGTGGATGGGATG GATGAACCCTAACAGTGGTAACACC GGCTATGCAGAGAAGTTCCAGGGCA GGGTCACCATGACCAGCGACTCCTC CATAAGCACCGCCTACATGGAGTTG AGAAGCCTGACCACTGAGGACACG GCCGTATATTACTGTGCGAGAGGTG GGGGTGCGAGCTATACTGACTCCTG GGGCCAGGGCACCCTGGTCACCGTC TCCTCAGCATCCACCAAGGGGCCTT CCGTGTTCCCCCTGGCCCCTTCATCC AAGTCGACCTCTGGTGGAACCGCCG CACTCGGTTGCCTGGTCAAAGACTA CTTCCCCGAGCCCGTGACTGTCTCG TGGAACTCGGGCGCCCTCACATCCG GAGTGCATACCTTTCCCGCCGTGTT GCAGTCCAGCGGCCTGTACAGCCTG AGCTCCGTCGTGACAGTGCCGTCCT CCTCCCTTGGAACCCAGACCTATAT CTGCAACGTCAATCACAAGCCCTCC AACACCAAAGTGGACAAGAAGGTC GAACCCAAGTCCTGCGACAAGACTC ACACCTGTCCGCCTTGTCCAGCCCC TGAGCTGCTGGGTGGTCCGTCCGTG TTCCTCTTCCCGCCCAAGCCGAAGG ACACTCTGATGATTTCACGCACCCC GGAAGTCACTTGCGTGGTCGTGGAC GTGTCGCACGAAGATCCCGAAGTGA AATTCAATTGGTACGTGGATGGGGT CGAAGTGCACAACGCCAAGACCAA GCCTAGGGAAGAACAGTACgccTCTA CGTACCGGGTGGTGTCCGTGCTGAC CGTGCTGCACCAGGACTGGCTGAAC GGAAAGGAGTACAAGTGCAAAGTG TCAAACAAGGCTCTCCCTGCCCCTA TCGAAAAGACCATCAGCAAGGCCA AGGGTCAACCTAGGGAGCCCCAGGT CTACACTTTGCCGCCTAGCCGGGAA GAAATGACTAAGAACCAAGTGTCCC

			TGACTTGCCTTGTCAAGGGCTTTTAT CCGTCCGACATCGCCGTGGAGTGGG AGTCCAACGGACAACCGGAGAACA ACTACAAGACCACCCCACCGGTGCT CGATTCCGATGGCTCCTTCTTCCTGT ACTCCAAGCTGACTGTGGACAAGTC AAGATGGCAGCAGGGAAACGTGTT CTCCTGCTCCGTGATGCACGAAGCG CTGCACAACCATTACACCCAGAAAT CACTGTCACTTTCGCCGGGAAAA
SEQ ID 2170	QVQLVQSGGGLVQPGRSLRLSCTASGF TFGDYAMSWFRQAPGKGLEWVGFIRS KAYGGTTEYAASVKGRFTISRDDSKSI AYLQMNSLKTEDTAVYYCTAKGGYV GYSYGPFGGYWGQGTLVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYASTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSL SPGK	SEQ ID 2278	CAGGTCCAGCTGGTGCAGTCTGGGG GAGGCTTGGTACAGCCAGGGCGGTC CCTGAGACTCTCCTGTACAGCTTCT GGATTCACCTTTGGTGATTATGCTAT GAGCTGGTTCCGCCAGGCTCCAGGG AAGGGGCTGGAGTGGGTAGGTTTCA TTAGAAGCAAAGCTTATGGTGGGAC AACAGAATACGCCGCGTCTGTGAAA GGCAGATTCACCATCTCAAGAGATG ATTCCAAAAGCATCGCCTATCTGCA AATGAACAGCCTGAAAACCGAGGA CACAGCCGTGTATTACTGTACCGCT AAGGGGGGCTACGTCGGATACAGCT ATGGACCTTTTGGGGGCTACTGGGG CCAGGGAACCCTGGTCACCGTCTCC TCAGCATCCACCAAGGGGCCTTCCG TGTTCCCCCTGGCCCCTTCATCCAAG TCGACCTCTGGTGGAACCGCCGCAC TCGGTTGCCTGGTCAAAGACTACTT CCCCGAGCCCGTGACTGTCTCGTGG AACTCGGGCGCCCTCACATCCGGAG TGCATACCTTTCCCGCCGTGTTGCA GTCCAGCGGCCTGTACAGCCTGAGC TCCGTCGTGACAGTGCCGTCCTCCT CCCTTGGAACCCAGACCTATATCTG CAACGTCAATCACAAGCCCTCCAAC ACCAAAGTGGACAAGAAGGTCGAA CCCAAGTCCTGCGACAAGACTCACA CCTGTCCGCCTTGTCCAGCCCCTGA GCTGCTGGGTGGTCCGTCCGTGTTC CTCTTCCCGCCCAAGCCGAAGGACA CTCTGATGATTTCACGCACCCCGGA AGTCACTTGCGTGGTCGTGGACGTG TCGCACGAAGATCCCGAAGTGAAAT TCAATTGGTACGTGGATGGGGTCGA AGTGCACAACGCCAAGACCAAGCCT AGGGAAGAACAGTACgccTCTACGTA CCGGGTGGTGTCCGTGCTGACCGTG CTGCACCAGGACTGGCTGAACGGAA AGGAGTACAAGTGCAAAGTGTCAA ACAAGGCTCTCCCTGCCCCTATCGA AAAGACCATCAGCAAGGCCAAGGG TCAACCTAGGGAGCCCCAGGTCTAC ACTTTGCCGCCTAGCCGGGAAGAAA

			TGACTAAGAACCAAGTGTCCCTGAC TTGCCTTGTCAAGGGCTTTTATCCGT CCGACATCGCCGTGGAGTGGGAGTC CAACGGACAACCGGAGAACAACTA CAAGACCACCCCACCGGTGCTCGAT TCCGATGGCTCCTTCTTCCTGTACTC CAAGCTGACTGTGGACAAGTCAAGA TGGCAGCAGGGAAACGTGTTCTCCT GCTCCGTGATGCACGAAGCGCTGCA CAACCATTACACCCAGAAATCACTG TCACTTTCGCCGGGAAAA
SEQ ID 2171	QVQLVQSGGGLVQPGRSLRLSCTASGF TFGDYAMSWFRQAPGKGLEWVGFIRS KAYGGTTEYAASVKGRFTISRDDSKSI AYLQMNSLKTEDTAVYYCTRGGTMV RGFGFNYWGQGTLVTVSSASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYASTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG K	SEQ ID 2279	CAGGTGCAGCTGGTGCAGTCTGGGG GAGGCTTGGTACAGCCAGGGCGGTC CCTGAGACTCTCCTGTACAGCTTCT GGATTCACCTTTGGTGATTATGCTAT GAGCTGGTTCCGCCAGGCTCCAGGG AAGGGGCTGGAGTGGGTAGGTTTCA TTAGAAGCAAAGCTTATGGTGGGAC AACAGAATACGCCGCGTCTGTGAAA GGCAGATTCACCATCTCAAGAGATG ATTCCAAAAGCATCGCCTATCTGCA AATGAACAGCCTGAAAACCGAGGA CACAGCCGTGTATTACTGTACTAGA GGGGGGACTATGGTTCGGGGTTTCG GATTTAACTACTGGGGCCAGGGAAC CCTGGTCACCGTCTCCTCAGCATCC ACCAAGGGGCCTTCCGTGTTCCCCC TGGCCCCTTCATCCAAGTCGACCTC TGGTGGAACCGCCGCACTCGGTTGC CTGGTCAAAGACTACTTCCCCGAGC CCGTGACTGTCTCGTGGAACTCGGG CGCCCTCACATCCGGAGTGCATACC TTTCCCGCCGTGTTGCAGTCCAGCG GCCTGTACAGCCTGAGCTCCGTCGT GACAGTGCCGTCCTCCTCCCTTGGA ACCCAGACCTATATCTGCAACGTCA ATCACAAGCCCTCCAACACCAAAGT GGACAAGAAGGTCGAACCCAAGTC CTGCGACAAGACTCACACCTGTCCG CCTTGTCCAGCCCCTGAGCTGCTGG GTGGTCCGTCCGTGTTCCTCTTCCCG CCCAAGCCGAAGGACACTCTGATGA TTTCACGCACCCCGGAAGTCACTTG CGTGGTCGTGGACGTGTCGCACGAA GATCCCGAAGTGAAATTCAATTGGT ACGTGGATGGGGTCGAAGTGCACA ACGCCAAGACCAAGCCTAGGGAAG AACAGTACgccTCTACGTACCGGGTG GTGTCCGTGCTGACCGTGCTGCACC AGGACTGGCTGAACGGAAAGGAGT ACAAGTGCAAAGTGTCAAACAAGG CTCTCCCTGCCCCTATCGAAAAGAC CATCAGCAAGGCCAAGGGTCAACCT AGGGAGCCCCAGGTCTACACTTTGC CGCCTAGCCGGGAAGAAATGACTA

			AGAACCAAGTGTCCCTGACTTGCCT TGTCAAGGGCTTTTATCCGTCCGAC ATCGCCGTGGAGTGGGAGTCCAACG GACAACCGGAGAACAACTACAAGA CCACCCCACCGGTGCTCGATTCCGA TGGCTCCTTCTTCCTGTACTCCAAGC TGACTGTGGACAAGTCAAGATGGCA GCAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACT TTCGCCGGGAAAA
SEQ ID 2172	QVQLQQWGAGLLKPSETLSLTCAVYG GSFSGYYWSWIRQPPGKGLEWIGEINH SGSTNYNPSLKSRVTISVDTSKNQFSLK LSSVTAADTAVYYCARARRAMIGPLP RLVGYFDLWGRGTLVTVSSASTKGPS VFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSG LYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCDKTHTCPPCPAPE LLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHN AKTKPREEQYASTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSP GK	SEQ ID 2280	CAGGTGCAGCTACAGCAGTGGGGC GCAGGACTGTTGAAGCCTTCGGAGA CCCTGTCCCTCACCTGCGCTGTCTAT GGTGGGTCCTTCAGTGGTTACTACT GGAGCTGGATCCGCCAGCCCCCAGG GAAGGGGCTGGAGTGGATTGGGGA AATCAATCATAGTGGAAGCACCAAC TACAACCCGTCCCTCAAGAGTCGAG TCACCATATCAGTAGACACGTCCAA GAACCAGTTCTCCCTGAAGCTGAGC TCTGTGACCGCCGCGGACACGGCTG TGTATTACTGTGCGAGAGCCCGGCG GGCTATGATAGGGCCGCTTCCGCGA CTTGTCGGGTACTTCGATCTCTGGG GCCGTGGAACCCTGGTCACCGTCTC CTCAGCATCCACCAAGGGGCCTTCC GTGTTCCCCCTGGCCCCTTCATCCAA GTCGACCTCTGGTGGAACCGCCGCA CTCGGTTGCCTGGTCAAAGACTACT TCCCCGAGCCCGTGACTGTCTCGTG GAACTCGGGCGCCCTCACATCCGGA GTGCATACCTTTCCCGCCGTGTTGC AGTCCAGCGGCCTGTACAGCCTGAG CTCCGTCGTGACAGTGCCGTCCTCC TCCCTTGGAACCCAGACCTATATCT GCAACGTCAATCACAAGCCCTCCAA CACCAAAGTGGACAAGAAGGTCGA ACCCAAGTCCTGCGACAAGACTCAC ACCTGTCCGCCTTGTCCAGCCCCTG AGCTGCTGGGTGGTCCGTCCGTGTT CCTCTTCCCGCCCAAGCCGAAGGAC ACTCTGATGATTTCACGCACCCCGG AAGTCACTTGCGTGGTCGTGGACGT GTCGCACGAAGATCCCGAAGTGAA ATTCAATTGGTACGTGGATGGGGTC GAAGTGCACAACGCCAAGACCAAG CCTAGGGAAGAACAGTACgccTCTAC GTACCGGGTGGTGTCCGTGCTGACC GTGCTGCACCAGGACTGGCTGAACG GAAAGGAGTACAAGTGCAAAGTGT CAAACAAGGCTCTCCCTGCCCCTAT CGAAAAGACCATCAGCAAGGCCAA GGGTCAACCTAGGGAGCCCCAGGTC TACACTTTGCCGCCTAGCCGGGAAG

			AAATGACTAAGAACCAAGTGTCCCT GACTTGCCTTGTCAAGGGCTTTTATC CGTCCGACATCGCCGTGGAGTGGGA GTCCAACGGACAACCGGAGAACAA CTACAAGACCACCCCACCGGTGCTC GATTCCGATGGCTCCTTCTTCCTGTA CTCCAAGCTGACTGTGGACAAGTCA AGATGGCAGCAGGGAAACGTGTTCT CCTGCTCCGTGATGCACGAAGCGCT GCACAACCATTACACCCAGAAATCA CTGTCACTTTCGCCGGGAAAA
SEQ ID 2173	QVQLQQWGAGLLKPSETLSLTCAVYG GSFSGYYWSWIRQPPGKGLEWIGEINH SGSTNYNPSLKSRVTISVDTSKNQFSLK LSSVTAADTAVYYCARGRPAPSWVKT RNWFDPWGQGTLVTVSSASTKGPSVF PLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYASTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG K	SEQ ID 2281	CAGGTGCAGCTACAGCAGTGGGGC GCAGGACTGTTGAAGCCTTCGGAGA CCCTGTCCCTCACCTGCGCTGTCTAT GGTGGGTCCTTCAGTGGTTACTACT GGAGCTGGATCCGCCAGCCCCCAGG GAAGGGGCTGGAGTGGATTGGGGA AATCAATCATAGTGGAAGCACCAAC TACAACCCGTCCCTCAAGAGTCGAG TCACCATATCAGTAGACACGTCCAA GAACCAGTTCTCCCTGAAGCTGAGC TCTGTGACCGCCGCGGACACGGCTG TGTATTACTGTGCGAGAGGCCGCCC CGCCCCATCCTGGGTTAAAACCCGT AACTGGTTCGACCCCTGGGGCCAGG GAACCCTGGTCACCGTCTCCTCAGC ATCCACCAAGGGGCCTTCCGTGTTC CCCCTGGCCCCTTCATCCAAGTCGA CCTCTGGTGGAACCGCCGCACTCGG TTGCCTGGTCAAAGACTACTTCCCC GAGCCCGTGACTGTCTCGTGGAACT CGGGCGCCCTCACATCCGGAGTGCA TACCTTTCCCGCCGTGTTGCAGTCCA GCGGCCTGTACAGCCTGAGCTCCGT CGTGACAGTGCCGTCCTCCTCCCTT GGAACCCAGACCTATATCTGCAACG TCAATCACAAGCCCTCCAACACCAA AGTGGACAAGAAGGTCGAACCCAA GTCCTGCGACAAGACTCACACCTGT CCGCCTTGTCCAGCCCCTGAGCTGC TGGGTGGTCCGTCCGTGTTCCTCTTC CCGCCCAAGCCGAAGGACACTCTGA TGATTTCACGCACCCCGGAAGTCAC TTGCGTGGTCGTGGACGTGTCGCAC GAAGATCCCGAAGTGAAATTCAATT GGTACGTGGATGGGGTCGAAGTGCA CAACGCCAAGACCAAGCCTAGGGA AGAACAGTACgccTCTACGTACCGGG TGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGA GTACAAGTGCAAAGTGTCAAACAA GGCTCTCCCTGCCCCTATCGAAAAG ACCATCAGCAAGGCCAAGGGTCAA CCTAGGGAGCCCCAGGTCTACACTT TGCCGCCTAGCCGGGAAGAAATGAC

			TAAGAACCAAGTGTCCCTGACTTGC CTTGTCAAGGGCTTTTATCCGTCCG ACATCGCCGTGGAGTGGGAGTCCAA CGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCC GATGGCTCCTTCTTCCTGTACTCCAA GCTGACTGTGGACAAGTCAAGATGG CAGCAGGGAAACGTGTTCTCCTGCT CCGTGATGCACGAAGCGCTGCACAA CCATTACACCCAGAAATCACTGTCA CTTTCGCCGGGAAAA
SEQ ID 2174	QVQLQQSGPGLVKPSQTLSLTCAISGD SVSSNSAAWNWIRQSPSRGLEWLGRT YYRSKWYNDYAVSVKSRITINPDTSKN QFSLQLNSVTPEDTAVYYCAREASSG WNWGQGTLVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTK PREEQYASTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2282	CAGGTACAGCTGCAGCAGTCAGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCAACAGTGC TGCTTGGAACTGGATCAGGCAGTCC CCATCGAGAGGCCTTGAGTGGCTGG GAAGGACATACTACAGGTCCAAGTG GTATAATGATTATGCAGTATCTGTG AAAAGTCGAATAACCATCAACCCAG ACACATCCAAGAACCAGTTCTCCCT GCAGCTGAACTCTGTGACTCCCGAG GACACGGCTGTGTATTACTGTGCAA GAGAGGCTAGCAGTGGCTGGAACT GGGGCCAGGGAACCCTGGTCACCGT CTCCTCAGCATCCACCAAGGGGCCT TCCGTGTTCCCCCTGGCCCCTTCATC CAAGTCGACCTCTGGTGGAACCGCC GCACTCGGTTGCCTGGTCAAAGACT ACTTCCCCGAGCCCGTGACTGTCTC GTGGAACTCGGGCGCCCTCACATCC GGAGTGCATACCTTTCCCGCCGTGT TGCAGTCCAGCGGCCTGTACAGCCT GAGCTCCGTCGTGACAGTGCCGTCC TCCTCCCTTGGAACCCAGACCTATA TCTGCAACGTCAATCACAAGCCCTC CAACACCAAAGTGGACAAGAAGGT CGAACCCAAGTCCTGCGACAAGACT CACACCTGTCCGCCTTGTCCAGCCC CTGAGCTGCTGGGTGGTCCGTCCGT GTTCCTCTTCCCGCCCAAGCCGAAG GACACTCTGATGATTTCACGCACCC CGGAAGTCACTTGCGTGGTCGTGGA CGTGTCGCACGAAGATCCCGAAGTG AAATTCAATTGGTACGTGGATGGGG TCGAAGTGCACAACGCCAAGACCA AGCCTAGGGAAGAACAGTACgccTCT ACGTACCGGGTGGTGTCCGTGCTGA CCGTGCTGCACCAGGACTGGCTGAA CGGAAAGGAGTACAAGTGCAAAGT GTCAAACAAGGCTCTCCCTGCCCCT ATCGAAAAGACCATCAGCAAGGCC AAGGGTCAACCTAGGGAGCCCCAG GTCTACACTTTGCCGCCTAGCCGGG AAGAAATGACTAAGAACCAAGTGT

			CCCTGACTTGCCTTGTCAAGGGCTTT TATCCGTCCGACATCGCCGTGGAGT GGGAGTCCAACGGACAACCGGAGA ACAACTACAAGACCACCCCACCGGT GCTCGATTCCGATGGCTCCTTCTTCC TGTACTCCAAGCTGACTGTGGACAA GTCAAGATGGCAGCAGGGAAACGT GTTCTCCTGCTCCGTGATGCACGAA GCGCTGCACAACCATTACACCCAGA AATCACTGTCACTTTCGCCGGGAAA A
SEQ ID 2175	QVQLQESGPGLVKPSQTLSLTCAISGD SVSSNNAAWNWIRQSPSRGLEWLGRT FYRSKWYNDYAVSVKSRLTVNPDTSK NQFSLRLNSVSPEDTAVYYCARGGRY TKGGYFDDWGQGTLVTVSSASTKGPS VFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSG LYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCDKTHTCPPCPAPE LLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHN AKTKPREEQYASTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSP GK	SEQ ID 2283	CAGGTGCAGCTGCAGGAGTCCGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCAACAATGC TGCTTGGAACTGGATCAGGCAGTCC CCATCGAGAGGCCTTGAGTGGCTGG GAAGGACATTCTACAGGTCCAAGTG GTATAATGACTATGCAGTTTCTGTG AAAAGTCGACTAACCGTCAACCCAG ACACATCCAAGAACCAGTTCTCCCT GCGGTTGAACTCTGTGAGTCCCGAG GACACGGCTGTGTATTACTGTGCAA GAGGGGGAAGATATACCAAGGGAG GGTACTTTGACGACTGGGGCCAGGG AACCCTGGTGACCGTCTCCTCAGCA TCCACCAAGGGGCCTTCCGTGTTCC CCCTGGCCCCTTCATCCAAGTCGAC CTCTGGTGGAACCGCCGCACTCGGT TGCCTGGTCAAAGACTACTTCCCCG AGCCCGTGACTGTCTCGTGGAACTC GGGCGCCCTCACATCCGGAGTGCAT ACCTTTCCCGCCGTGTTGCAGTCCA GCGGCCTGTACAGCCTGAGCTCCGT CGTGACAGTGCCGTCCTCCTCCCTT GGAACCCAGACCTATATCTGCAACG TCAATCACAAGCCCTCCAACACCAA AGTGGACAAGAAGGTCGAACCCAA GTCCTGCGACAAGACTCACACCTGT CCGCCTTGTCCAGCCCCTGAGCTGC TGGGTGGTCCGTCCGTGTTCCTCTTC CCGCCCAAGCCGAAGGACACTCTGA TGATTTCACGCACCCCGGAAGTCAC TTGCGTGGTCGTGGACGTGTCGCAC GAAGATCCCGAAGTGAAATTCAATT GGTACGTGGATGGGGTCGAAGTGCA CAACGCCAAGACCAAGCCTAGGGA AGAACAGTACgccTCTACGTACCGGG TGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGA GTACAAGTGCAAAGTGTCAAACAA GGCTCTCCCTGCCCCTATCGAAAAG ACCATCAGCAAGGCCAAGGGTCAA CCTAGGGAGCCCCAGGTCTACACTT TGCCGCCTAGCCGGGAAGAAATGAC

			TAAGAACCAAGTGTCCCTGACTTGC CTTGTCAAGGGCTTTTATCCGTCCG ACATCGCCGTGGAGTGGGAGTCCAA CGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCC GATGGCTCCTTCTTCCTGTACTCCAA GCTGACTGTGGACAAGTCAAGATGG CAGCAGGGAAACGTGTTCTCCTGCT CCGTGATGCACGAAGCGCTGCACAA CCATTACACCCAGAAATCACTGTCA CTTTCGCCGGGAAAA
SEQ ID 2176	QVTLKESGPTLVKPTQTLTLTCTFSGFS LSTSGVGVGWIRQPPGKALEWLALIY WDDDKRYSPSLKSRLTITKDTSKNQV VLTMTNMDPVDTATYYCAHRLDSSGR GGYFDYWGQGTLVTVSSASTKGPSVF PLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYASTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG K	SEQ ID 2284	CAGGTCACCTTGAAGGAGTCTGGTC CTACGCTGGTGAAACCCACACAGAC CCTCACGCTGACCTGCACCTTCTCTG GGTTCTCACTCAGCACTAGTGGAGT GGGTGTGGGCTGGATCCGTCAGCCC CCAGGAAAGGCCCTGGAGTGGCTTG CACTCATTTATTGGGATGATGATAA GCGCTACAGCCCATCTCTGAAGAGC AGGCTCACCATCACCAAGGACACCT CCAAAAACCAGGTGGTCCTTACAAT GACCAACATGGACCCTGTGGACACA GCCACATATTACTGTGCACACAGAT TGGATAGCAGTGGCCGTGGTGGTTA CTTTGACTACTGGGGCCAGGGCACC CTGGTCACCGTCTCCTCAGCATCCA CCAAGGGGCCTTCCGTGTTCCCCCT GGCCCCTTCATCCAAGTCGACCTCT GGTGGAACCGCCGCACTCGGTTGCC TGGTCAAAGACTACTTCCCCGAGCC CGTGACTGTCTCGTGGAACTCGGGC GCCCTCACATCCGGAGTGCATACCT TTCCCGCCGTGTTGCAGTCCAGCGG CCTGTACAGCCTGAGCTCCGTCGTG ACAGTGCCGTCCTCCTCCCTTGGAA CCCAGACCTATATCTGCAACGTCAA TCACAAGCCCTCCAACACCAAAGTG GACAAGAAGGTCGAACCCAAGTCCT GCGACAAGACTCACACCTGTCCGCC TTGTCCAGCCCCTGAGCTGCTGGGT GGTCCGTCCGTGTTCCTCTTCCCGCC CAAGCCGAAGGACACTCTGATGATT TCACGCACCCCGGAAGTCACTTGCG TGGTCGTGGACGTGTCGCACGAAGA TCCCGAAGTGAAATTCAATTGGTAC GTGGATGGGGTCGAAGTGCACAAC GCCAAGACCAAGCCTAGGGAAGAA CAGTACgccTCTACGTACCGGGTGGT GTCCGTGCTGACCGTGCTGCACCAG GACTGGCTGAACGGAAAGGAGTAC AAGTGCAAAGTGTCAAACAAGGCTC TCCCTGCCCCTATCGAAAAGACCAT CAGCAAGGCCAAGGGTCAACCTAG GGAGCCCCAGGTCTACACTTTGCCG CCTAGCCGGGAAGAAATGACTAAG

			AACCAAGTGTCCCTGACTTGCCTTG TCAAGGGCTTTTATCCGTCCGACAT CGCCGTGGAGTGGGAGTCCAACGG ACAACCGGAGAACAACTACAAGAC CACCCCACCGGTGCTCGATTCCGAT GGCTCCTTCTTCCTGTACTCCAAGCT GACTGTGGACAAGTCAAGATGGCA GCAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACT TTCGCCGGGAAAA
SEQ ID 2177	EVQLVESGGGVVQPGRSLRLSCTASGF TFSSYGMHWVRQAPGKGLEWVAVISY DGSNKYYADSVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCAKELVGTSS PYYYYYYGMDVWGQGTMVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPP CPAPELLGGPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYASTYRVVSVLT VLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK	SEQ ID 2285	GAGGTGCAGCTGGTGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTACAGCCTCT GGATTCACCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTT ATATCATATGATGGAAGTAATAAAT ACTATGCAGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCTGAGGACACGG CTGTGTATTACTGTGCGAAAGAGTT GGTGGGTACCAGCTCTCCTTATTAC TACTACTACTACGGTATGGACGTCT GGGGCCAAGGGACAATGGTCACCG TCTCTTCAGCATCCACCAAGGGGCC TTCCGTGTTCCCCCTGGCCCCTTCAT CCAAGTCGACCTCTGGTGGAACCGC CGCACTCGGTTGCCTGGTCAAAGAC TACTTCCCCGAGCCCGTGACTGTCT CGTGGAACTCGGGCGCCCTCACATC CGGAGTGCATACCTTTCCCGCCGTG TTGCAGTCCAGCGGCCTGTACAGCC TGAGCTCCGTCGTGACAGTGCCGTC CTCCTCCCTTGGAACCCAGACCTAT ATCTGCAACGTCAATCACAAGCCCT CCAACACCAAAGTGGACAAGAAGG TCGAACCCAAGTCCTGCGACAAGAC TCACACCTGTCCGCCTTGTCCAGCC CCTGAGCTGCTGGGTGGTCCGTCCG TGTTCCTCTTCCCGCCCAAGCCGAA GGACACTCTGATGATTTCACGCACC CCGGAAGTCACTTGCGTGGTCGTGG ACGTGTCGCACGAAGATCCCGAAGT GAAATTCAATTGGTACGTGGATGGG GTCGAAGTGCACAACGCCAAGACC AAGCCTAGGGAAGAACAGTACgccT CTACGTACCGGGTGGTGTCCGTGCT GACCGTGCTGCACCAGGACTGGCTG AACGGAAAGGAGTACAAGTGCAAA GTGTCAAACAAGGCTCTCCCTGCCC CTATCGAAAAGACCATCAGCAAGGC CAAGGGTCAACCTAGGGAGCCCCA GGTCTACACTTTGCCGCCTAGCCGG

			GAAGAAATGACTAAGAACCAAGTG TCCCTGACTTGCCTTGTCAAGGGCTT TTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCAAGCTGACTGTGGACA AGTCAAGATGGCAGCAGGGAAACG TGTTCTCCTGCTCCGTGATGCACGA AGCGCTGCACAACCATTACACCCAG AAATCACTGTCACTTTCGCCGGGAA AA
SEQ ID 2178	QLQLQESGGGLVQPGGSLRLSCAASGF TVSSNYMSWVRQAPGKGLEWVSVIYS GGSTYYADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARDYYYGSGSS PWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVD KKVEPKSCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKP REEQYASTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2286	CAGCTGCAGCTGCAGGAGTCGGGG GGAGGCTTGGTCCAGCCTGGGGGGT CCCTGAGACTCTCCTGTGCAGCCTC TGGATTCACCGTCAGTAGCAACTAC ATGAGCTGGGTCCGCCAGGCTCCAG GGAAGGGGCTGGAGTGGGTCTCAGT TATTTATAGCGGTGGTAGCACATAC TACGCAGACTCCGTGAAGGGCAGAT TCACCATCTCCAGAGACAATTCCAA GAACACGCTGTATCTTCAAATGAAC AGCCTGAGAGCCGAGGACACGGCT GTGTATTACTGTGCGAGAGACTATT ACTATGGTTCGGGGAGTTCTCCCTG GGGCCAGGGAACCCTGGTCACCGTC TCCTCAGCATCCACCAAGGGGCCTT CCGTGTTCCCCCTGGCCCCTTCATCC AAGTCGACCTCTGGTGGAACCGCCG CACTCGGTTGCCTGGTCAAAGACTA CTTCCCCGAGCCCGTGACTGTCTCG TGGAACTCGGGCGCCCTCACATCCG GAGTGCATACCTTTCCCGCCGTGTT GCAGTCCAGCGGCCTGTACAGCCTG AGCTCCGTCGTGACAGTGCCGTCCT CCTCCCTTGGAACCCAGACCTATAT CTGCAACGTCAATCACAAGCCCTCC AACACCAAAGTGGACAAGAAGGTC GAACCCAAGTCCTGCGACAAGACTC ACACCTGTCCGCCTTGTCCAGCCCC TGAGCTGCTGGGTGGTCCGTCCGTG TTCCTCTTCCCGCCCAAGCCGAAGG ACACTCTGATGATTTCACGCACCCC GGAAGTCACTTGCGTGGTCGTGGAC GTGTCGCACGAAGATCCCGAAGTGA AATTCAATTGGTACGTGGATGGGGT CGAAGTGCACAACGCCAAGACCAA GCCTAGGGAAGAACAGTACgccTCTA CGTACCGGGTGGTGTCCGTGCTGAC CGTGCTGCACCAGGACTGGCTGAAC GGAAAGGAGTACAAGTGCAAAGTG TCAAACAAGGCTCTCCCTGCCCCTA TCGAAAAGACCATCAGCAAGGCCA AGGGTCAACCTAGGGAGCCCCAGGT CTACACTTTGCCGCCTAGCCGGGAA GAAATGACTAAGAACCAAGTGTCCC

			TGACTTGCCTTGTCAAGGGCTTTTAT CCGTCCGACATCGCCGTGGAGTGGG AGTCCAACGGACAACCGGAGAACA ACTACAAGACCACCCCACCGGTGCT CGATTCCGATGGCTCCTTCTTCCTGT ACTCCAAGCTGACTGTGGACAAGTC AAGATGGCAGCAGGGAAACGTGTT CTCCTGCTCCGTGATGCACGAAGCG CTGCACAACCATTACACCCAGAAAT CACTGTCACTTTCGCCGGGAAAA
SEQ ID 2179	QVQLQQWGAGLLKPSETLSLTCAVYG GSFSGYYWSWIRQPPGKGLEWIGEINH SGSTNYNPSLKSRVTISVDTSKNQFSLK LSSVTAADTAVYYCARGRPYCSSTSCY PEWFDPWGQGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2287	CAGGTGCAGCTACAGCAGTGGGGC GCAGGACTGTTGAAGCCTTCGGAGA CCCTGTCCCTCACCTGCGCTGTCTAT GGTGGGTCCTTCAGTGGTTACTACT GGAGCTGGATCCGCCAGCCCCCAGG GAAGGGGCTGGAGTGGATTGGGGA AATCAATCATAGTGGAAGCACCAAC TACAACCCGTCCCTCAAGAGTCGAG TCACCATATCAGTAGACACGTCCAA GAACCAGTTCTCCCTGAAGCTGAGC TCTGTGACCGCCGCGGACACGGCTG TGTATTACTGTGCGAGAGGCCGGCC ATATTGTAGTAGTACCAGCTGCTAC CCAGAGTGGTTCGACCCCTGGGGCC AGGGAACCCTGGTCACCGTCTCCTC AGCATCCACCAAGGGGCCTTCCGTG TTCCCCCTGGCCCCTTCATCCAAGTC GACCTCTGGTGGAACCGCCGCACTC GGTTGCCTGGTCAAAGACTACTTCC CCGAGCCCGTGACTGTCTCGTGGAA CTCGGGCGCCCTCACATCCGGAGTG CATACCTTTCCCGCCGTGTTGCAGTC CAGCGGCCTGTACAGCCTGAGCTCC GTCGTGACAGTGCCGTCCTCCTCCC TTGGAACCCAGACCTATATCTGCAA CGTCAATCACAAGCCCTCCAACACC AAAGTGGACAAGAAGGTCGAACCC AAGTCCTGCGACAAGACTCACACCT GTCCGCCTTGTCCAGCCCCTGAGCT GCTGGGTGGTCCGTCCGTGTTCCTCT TCCCGCCCAAGCCGAAGGACACTCT GATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGC ACGAAGATCCCGAAGTGAAATTCAA TTGGTACGTGGATGGGGTCGAAGTG CACAACGCCAAGACCAAGCCTAGG GAAGAACAGTACgccTCTACGTACCG GGTGGTGTCCGTGCTGACCGTGCTG CACCAGGACTGGCTGAACGGAAAG GAGTACAAGTGCAAAGTGTCAAAC AAGGCTCTCCCTGCCCCTATCGAAA AGACCATCAGCAAGGCCAAGGGTC AACCTAGGGAGCCCCAGGTCTACAC TTTGCCGCCTAGCCGGGAAGAAATG

			ACTAAGAACCAAGTGTCCCTGACTT GCCTTGTCAAGGGCTTTTATCCGTCC GACATCGCCGTGGAGTGGGAGTCCA ACGGACAACCGGAGAACAACTACA AGACCACCCCACCGGTGCTCGATTC CGATGGCTCCTTCTTCCTGTACTCCA AGCTGACTGTGGACAAGTCAAGATG GCAGCAGGGAAACGTGTTCTCCTGC TCCGTGATGCACGAAGCGCTGCACA ACCATTACACCCAGAAATCACTGTC ACTTTCGCCGGGAAAA
SEQ ID 2180	QVTLKESGGGVVQPGRSLRLSCAASGF TFSSYGMHWVRQAPGKGLEWVAVISY DGSNKYYADSVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCAKLRGIDYY DSSGYQRGFDYWGQGTLVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCP APELLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYASTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSL SLSPGK	SEQ ID 2288	CAGGTCACCTTGAAGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTT ATATCATATGATGGAAGTAATAAAT ACTATGCAGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCTGAGGACACGG CTGTGTATTACTGTGCGAAATTAAG GGGTATAGATTACTATGATAGTAGT GGTTACCAACGGGGGTTTGACTACT GGGGCCAGGGAACCCTGGTCACCGT CTCCTCAGCATCCACCAAGGGGCCT TCCGTGTTCCCCCTGGCCCCTTCATC CAAGTCGACCTCTGGTGGAACCGCC GCACTCGGTTGCCTGGTCAAAGACT ACTTCCCCGAGCCCGTGACTGTCTC GTGGAACTCGGGCGCCCTCACATCC GGAGTGCATACCTTTCCCGCCGTGT TGCAGTCCAGCGGCCTGTACAGCCT GAGCTCCGTCGTGACAGTGCCGTCC TCCTCCCTTGGAACCCAGACCTATA TCTGCAACGTCAATCACAAGCCCTC CAACACCAAAGTGGACAAGAAGGT CGAACCCAAGTCCTGCGACAAGACT CACACCTGTCCGCCTTGTCCAGCCC CTGAGCTGCTGGGTGGTCCGTCCGT GTTCCTCTTCCCGCCCAAGCCGAAG GACACTCTGATGATTTCACGCACCC CGGAAGTCACTTGCGTGGTCGTGGA CGTGTCGCACGAAGATCCCGAAGTG AAATTCAATTGGTACGTGGATGGGG TCGAAGTGCACAACGCCAAGACCA AGCCTAGGGAAGAACAGTACgccTCT ACGTACCGGGTGGTGTCCGTGCTGA CCGTGCTGCACCAGGACTGGCTGAA CGGAAAGGAGTACAAGTGCAAAGT GTCAAACAAGGCTCTCCCTGCCCCT ATCGAAAAGACCATCAGCAAGGCC AAGGGTCAACCTAGGGAGCCCCAG GTCTACACTTTGCCGCCTAGCCGGG

			AAGAAATGACTAAGAACCAAGTGT CCCTGACTTGCCTTGTCAAGGGCTTT TATCCGTCCGACATCGCCGTGGAGT GGGAGTCCAACGGACAACCGGAGA ACAACTACAAGACCACCCCACCGGT GCTCGATTCCGATGGCTCCTTCTTCC TGTACTCCAAGCTGACTGTGGACAA GTCAAGATGGCAGCAGGGAAACGT GTTCTCCTGCTCCGTGATGCACGAA GCGCTGCACAACCATTACACCCAGA AATCACTGTCACTTTCGCCGGGAAA A
SEQ ID 2181	QVQLQESGPGLVKPSETLSLTCTVSGG SISSYYWSWIRQPPGKGLEWIGYIYYT GSTNYNPSLKSRVTISVDTSKNQFSLKL SSVTTADTAVYYCARGGRGDGAAFDI WGQGTMVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPR EEQYASTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK	SEQ ID 2289	CAGGTGCAGCTGCAGGAGTCCGGCC CAGGACTGGTGAAGCCTTCGGAGAC CCTGTCCCTCACCTGCACTGTCTCTG GTGGCTCCATCAGTAGTTACTACTG GAGCTGGATCCGGCAGCCCCCAGGG AAGGGACTGGAGTGGATTGGCTATA TCTATTACACTGGGAGCACCAACTA CAACCCCTCCCTCAAGAGCCGAGTC ACCATATCAGTAGACACGTCCAAGA ACCAGTTCTCCCTGAAGCTGAGCTC TGTGACCACTGCGGACACGGCCGTG TATTACTGTGCGAGAGGTGGGAGGG GGGATGGGGCCGCTTTTGACATCTG GGGCCAAGGGACAATGGTCACCGTC TCTTCAGCATCCACCAAGGGGCCTT CCGTGTTCCCCCTGGCCCCTTCATCC AAGTCGACCTCTGGTGGAACCGCCG CACTCGGTTGCCTGGTCAAAGACTA CTTCCCCGAGCCCGTGACTGTCTCG TGGAACTCGGGCGCCCTCACATCCG GAGTGCATACCTTTCCCGCCGTGTT GCAGTCCAGCGGCCTGTACAGCCTG AGCTCCGTCGTGACAGTGCCGTCCT CCTCCCTTGGAACCCAGACCTATAT CTGCAACGTCAATCACAAGCCCTCC AACACCAAAGTGGACAAGAAGGTC GAACCCAAGTCCTGCGACAAGACTC ACACCTGTCCGCCTTGTCCAGCCCC TGAGCTGCTGGGTGGTCCGTCCGTG TTCCTCTTCCCGCCCAAGCCGAAGG ACACTCTGATGATTTCACGCACCCC GGAAGTCACTTGCGTGGTCGTGGAC GTGTCGCACGAAGATCCCGAAGTGA AATTCAATTGGTACGTGGATGGGGT CGAAGTGCACAACGCCAAGACCAA GCCTAGGGAAGAACAGTACgccTCTA CGTACCGGGTGGTGTCCGTGCTGAC CGTGCTGCACCAGGACTGGCTGAAC GGAAAGGAGTACAAGTGCAAAGTG TCAAACAAGGCTCTCCCTGCCCCTA TCGAAAAGACCATCAGCAAGGCCA AGGGTCAACCTAGGGAGCCCCAGGT CTACACTTTGCCGCCTAGCCGGGAA GAAATGACTAAGAACCAAGTGTCCC

			TGACTTGCCTTGTCAAGGGCTTTTAT CCGTCCGACATCGCCGTGGAGTGGG AGTCCAACGGACAACCGGAGAACA ACTACAAGACCACCCCACCGGTGCT CGATTCCGATGGCTCCTTCTTCCTGT ACTCCAAGCTGACTGTGGACAAGTC AAGATGGCAGCAGGGAAACGTGTT CTCCTGCTCCGTGATGCACGAAGCG CTGCACAACCATTACACCCAGAAAT CACTGTCACTTTCGCCGGGAAAA
SEQ ID 2182	QVQLVQSGGGVVQPGRSLRLSCAASG FTFSSSAMHWVRQAPGKGLEWVAMI WHDESKKYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARPPDGG NSGRWYFDLWGRGTLVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYASTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSL SPGK	SEQ ID 2290	CAGGTGCAGCTGGTGCAATCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCGTCT GGATTCACCTTCAGCAGCTCTGCCA TGCACTGGGTCCGCCAGGCTCCAGG CAAGGGACTGGAGTGGGTGGCAAT GATTTGGCATGATGAGAGTAAGAAA TACTATGCAGACTCCGTGAAGGGCC GATTCACTATCTCCAGAGACAATTC CAAGAACACGCTGTATCTGCAAATG AACAGCCTGAGAGCTGAGGACACG GCTGTGTATTACTGTGCGAGACCCC CCGACGGTGGTAACTCCGGTCGCTG GTACTTCGATCTCTGGGGCCGTGGC ACCCTGGTCACCGTCTCCTCAGCAT CCACCAAGGGGCCTTCCGTGTTCCC CCTGGCCCCTTCATCCAAGTCGACC TCTGGTGGAACCGCCGCACTCGGTT GCCTGGTCAAAGACTACTTCCCCGA GCCCGTGACTGTCTCGTGGAACTCG GGCGCCCTCACATCCGGAGTGCATA CCTTTCCCGCCGTGTTGCAGTCCAG CGGCCTGTACAGCCTGAGCTCCGTC GTGACAGTGCCGTCCTCCTCCCTTG GAACCCAGACCTATATCTGCAACGT CAATCACAAGCCCTCCAACACCAAA GTGGACAAGAAGGTCGAACCCAAG TCCTGCGACAAGACTCACACCTGTC CGCCTTGTCCAGCCCCTGAGCTGCT GGGTGGTCCGTCCGTGTTCCTCTTCC CGCCCAAGCCGAAGGACACTCTGAT GATTTCACGCACCCCGGAAGTCACT TGCGTGGTCGTGGACGTGTCGCACG AAGATCCCGAAGTGAAATTCAATTG GTACGTGGATGGGGTCGAAGTGCAC AACGCCAAGACCAAGCCTAGGGAA GAACAGTACgccTCTACGTACCGGGT GGTGTCCGTGCTGACCGTGCTGCAC CAGGACTGGCTGAACGGAAAGGAG TACAAGTGCAAAGTGTCAAACAAG GCTCTCCCTGCCCCTATCGAAAAGA CCATCAGCAAGGCCAAGGGTCAACC TAGGGAGCCCCAGGTCTACACTTTG CCGCCTAGCCGGGAAGAAATGACTA

			AGAACCAAGTGTCCCTGACTTGCCT TGTCAAGGGCTTTTATCCGTCCGAC ATCGCCGTGGAGTGGGAGTCCAACG GACAACCGGAGAACAACTACAAGA CCACCCCACCGGTGCTCGATTCCGA TGGCTCCTTCTTCCTGTACTCCAAGC TGACTGTGGACAAGTCAAGATGGCA GCAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACT TTCGCCGGGAAAA
SEQ ID 2183	QMQLVQSGGGLVQPGGSLRLSCAASG FTFSSYAMSWVRQAPGKGLEWVSAIS GSGGSTYYADSVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCAKDKNVRK HDYGDHPYGGYFDYWGQGTLVTVSS ASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAP IEKTISKAKGQPREPQVYTLPPSREEMT KNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	SEQ ID 2291	CAGATGCAGCTGGTGCAATCTGGGG GAGGCTTGGTACAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTTAGCAGCTATGCCA TGAGCTGGGTCCGCCAGGCTCCAGG GAAGGGGCTGGAGTGGGTCTCAGCT ATTAGTGGTAGTGGTGGTAGCACAT ACTACGCAGACTCCGTGAAGGGCCG GTTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCCGAGGACACGG CCGTATATTACTGTGCGAAAGACAA GAACGTCCGAAAACATGACTACGGT GACCACCCCTACGGGGGGTACTTTG ACTACTGGGGCCAGGGCACCCTGGT GACCGTCTCCTCAGCATCCACCAAG GGGCCTTCCGTGTTCCCCCTGGCCC CTTCATCCAAGTCGACCTCTGGTGG AACCGCCGCACTCGGTTGCCTGGTC AAAGACTACTTCCCCGAGCCCGTGA CTGTCTCGTGGAACTCGGGCGCCCT CACATCCGGAGTGCATACCTTTCCC GCCGTGTTGCAGTCCAGCGGCCTGT ACAGCCTGAGCTCCGTCGTGACAGT GCCGTCCTCCTCCCTTGGAACCCAG ACCTATATCTGCAACGTCAATCACA AGCCCTCCAACACCAAAGTGGACAA GAAGGTCGAACCCAAGTCCTGCGAC AAGACTCACACCTGTCCGCCTTGTC CAGCCCCTGAGCTGCTGGGTGGTCC GTCCGTGTTCCTCTTCCCGCCCAAGC CGAAGGACACTCTGATGATTTCACG CACCCCGGAAGTCACTTGCGTGGTC GTGGACGTGTCGCACGAAGATCCCG AAGTGAAATTCAATTGGTACGTGGA TGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTA CgccTCTACGTACCGGGTGGTGTCCG TGCTGACCGTGCTGCACCAGGACTG GCTGAACGGAAAGGAGTACAAGTG CAAAGTGTCAAACAAGGCTCTCCCT GCCCCTATCGAAAAGACCATCAGCA AGGCCAAGGGTCAACCTAGGGAGC CCCAGGTCTACACTTTGCCGCCTAG

			CCGGGAAGAAATGACTAAGAACCA AGTGTCCCTGACTTGCCTTGTCAAG GGCTTTTATCCGTCCGACATCGCCG TGGAGTGGGAGTCCAACGGACAAC CGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTC CTTCTTCCTGTACTCCAAGCTGACTG TGGACAAGTCAAGATGGCAGCAGG GAAACGTGTTCTCCTGCTCCGTGAT GCACGAAGCGCTGCACAACCATTAC ACCCAGAAATCACTGTCACTTTCGC CGGGAAAA
SEQ ID 2184	EVQLVQSGAEVKKPGASVKVSCKASG YTFTSYAMHWVRQAPGQRLEWMGWI NAGNGNTKYSQKFQGRVTITRDTSAST AYMELSSLRSEDTAVYYCARVAGATS LWYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTK PREEQYASTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2292	GAGGTCCAGCTGGTACAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTTTCCTGCAAGGCTTCT GGATACACCTTCACTAGCTATGCTA TGCATTGGGTGCGCCAGGCCCCCGG ACAAAGGCTTGAGTGGATGGGATG GATCAACGCTGGCAATGGTAACACA AAATATTCACAGAAGTTCCAGGGCA GAGTCACCATTACCAGGGACACATC CGCGAGCACAGCCTACATGGAGCTG AGCAGCCTGAGATCTGAAGACACG GCTGTGTATTACTGTGCGAGAGTGG CGGGAGCTACTTCCCTATGGTACTG GGGCCAGGGCACCCTGGTCACCGTC TCCTCAGCATCCACCAAGGGGCCTT CCGTGTTCCCCCTGGCCCCTTCATCC AAGTCGACCTCTGGTGGAACCGCCG CACTCGGTTGCCTGGTCAAAGACTA CTTCCCCGAGCCCGTGACTGTCTCG TGGAACTCGGGCGCCCTCACATCCG GAGTGCATACCTTTCCCGCCGTGTT GCAGTCCAGCGGCCTGTACAGCCTG AGCTCCGTCGTGACAGTGCCGTCCT CCTCCCTTGGAACCCAGACCTATAT CTGCAACGTCAATCACAAGCCCTCC AACACCAAAGTGGACAAGAAGGTC GAACCCAAGTCCTGCGACAAGACTC ACACCTGTCCGCCTTGTCCAGCCCC TGAGCTGCTGGGTGGTCCGTCCGTG TTCCTCTTCCCGCCCAAGCCGAAGG ACACTCTGATGATTTCACGCACCCC GGAAGTCACTTGCGTGGTCGTGGAC GTGTCGCACGAAGATCCCGAAGTGA AATTCAATTGGTACGTGGATGGGGT CGAAGTGCACAACGCCAAGACCAA GCCTAGGGAAGAACAGTACgccTCTA CGTACCGGGTGGTGTCCGTGCTGAC CGTGCTGCACCAGGACTGGCTGAAC GGAAAGGAGTACAAGTGCAAAGTG TCAAACAAGGCTCTCCCTGCCCCTA TCGAAAAGACCATCAGCAAGGCCA AGGGTCAACCTAGGGAGCCCCAGGT CTACACTTTGCCGCCTAGCCGGGAA GAAATGACTAAGAACCAAGTGTCCC

			TGACTTGCCTTGTCAAGGGCTTTTAT CCGTCCGACATCGCCGTGGAGTGGG AGTCCAACGGACAACCGGAGAACA ACTACAAGACCACCCCACCGGTGCT CGATTCCGATGGCTCCTTCTTCCTGT ACTCCAAGCTGACTGTGGACAAGTC AAGATGGCAGCAGGGAAACGTGTT CTCCTGCTCCGTGATGCACGAAGCG CTGCACAACCATTACACCCAGAAAT CACTGTCACTTTCGCCGGGAAAA
SEQ ID 2185	QVQLQQSGPGLVKPSQSLSLTCAISGD SVSSNSAAWNWIRQSPSRGLEWLGRT YYRSKWYNDYAVSVKSRITIKPDTSKN QFSLQLNSVTPEDTAVYYCTRLANSDG VDVWGQGTMVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTK PREEQYASTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2293	CAGGTACAGCTGCAGCAGTCAGGTC CAGGACTGGTGAAGCCCTCGCAGAG CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCAACAGTGC TGCTTGGAACTGGATCAGGCAGTCC CCATCGAGAGGCCTTGAGTGGCTGG GAAGGACATACTACAGGTCCAAGTG GTATAATGATTATGCAGTATCTGTG AAGAGTCGAATAACCATCAAACCA GACACATCCAAGAACCAGTTCTCCC TGCAGCTGAACTCTGTGACTCCCGA GGACACGGCTGTGTATTACTGTACA AGGCTAGCTAATTCCGACGGTGTGG ACGTCTGGGGCCAAGGGACAATGGT CACCGTCTCCTCAGCATCCACCAAG GGGCCTTCCGTGTTCCCCCTGGCCC CTTCATCCAAGTCGACCTCTGGTGG AACCGCCGCACTCGGTTGCCTGGTC AAAGACTACTTCCCCGAGCCCGTGA CTGTCTCGTGGAACTCGGGCGCCCT CACATCCGGAGTGCATACCTTTCCC GCCGTGTTGCAGTCCAGCGGCCTGT ACAGCCTGAGCTCCGTCGTGACAGT GCCGTCCTCCTCCCTTGGAACCCAG ACCTATATCTGCAACGTCAATCACA AGCCCTCCAACACCAAAGTGGACAA GAAGGTCGAACCCAAGTCCTGCGAC AAGACTCACACCTGTCCGCCTTGTC CAGCCCCTGAGCTGCTGGGTGGTCC GTCCGTGTTCCTCTTCCCGCCCAAGC CGAAGGACACTCTGATGATTTCACG CACCCCGGAAGTCACTTGCGTGGTC GTGGACGTGTCGCACGAAGATCCCG AAGTGAAATTCAATTGGTACGTGGA TGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTA CgccTCTACGTACCGGGTGGTGTCCG TGCTGACCGTGCTGCACCAGGACTG GCTGAACGGAAAGGAGTACAAGTG CAAAGTGTCAAACAAGGCTCTCCCT GCCCCTATCGAAAAGACCATCAGCA AGGCCAAGGGTCAACCTAGGGAGC CCCAGGTCTACACTTTGCCGCCTAG CCGGGAAGAAATGACTAAGAACCA

			AGTGTCCCTGACTTGCCTTGTCAAG GGCTTTTATCCGTCCGACATCGCCG TGGAGTGGGAGTCCAACGGACAAC CGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTC CTTCTTCCTGTACTCCAAGCTGACTG TGGACAAGTCAAGATGGCAGCAGG GAAACGTGTTCTCCTGCTCCGTGAT GCACGAAGCGCTGCACAACCATTAC ACCCAGAAATCACTGTCACTTTCGC CGGGAAAA
SEQ ID 2186	QVQLQQSGPGLVKPSQTLSLTCAISGD SVSSDSAVWTWIRQSPSRGLEWLGRT YYKSKWYNDYAASVKSRITINPDTSK NQFSLHLNSVTPEDTAVYYCARGVTR TFDYWGQGTTVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTK PREEQYASTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2294	CAGGTACAGCTGCAGCAGTCAGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCGACAGTGC TGTTTGGACCTGGATCAGGCAGTCC CCATCGAGAGGCCTTGAGTGGCTGG GAAGGACATACTACAAGTCGAAGT GGTATAATGATTATGCAGCATCTGT GAAAAGTCGAATAACCATCAACCCA GACACATCCAAGAACCAGTTCTCCC TGCACCTGAACTCTGTGACTCCCGA GGACACGGCTGTGTATTACTGTGCA AGAGGTGTAACCCGGACCTTTGACT ACTGGGGCCAGGGGACCACGGTCA CCGTCTCCTCAGCATCCACCAAGGG GCCTTCCGTGTTCCCCCTGGCCCCTT CATCCAAGTCGACCTCTGGTGGAAC CGCCGCACTCGGTTGCCTGGTCAAA GACTACTTCCCCGAGCCCGTGACTG TCTCGTGGAACTCGGGCGCCCTCAC ATCCGGAGTGCATACCTTTCCCGCC GTGTTGCAGTCCAGCGGCCTGTACA GCCTGAGCTCCGTCGTGACAGTGCC GTCCTCCTCCCTTGGAACCCAGACC TATATCTGCAACGTCAATCACAAGC CCTCCAACACCAAAGTGGACAAGA AGGTCGAACCCAAGTCCTGCGACAA GACTCACACCTGTCCGCCTTGTCCA GCCCCTGAGCTGCTGGGTGGTCCGT CCGTGTTCCTCTTCCCGCCCAAGCC GAAGGACACTCTGATGATTTCACGC ACCCCGGAAGTCACTTGCGTGGTCG TGGACGTGTCGCACGAAGATCCCGA AGTGAAATTCAATTGGTACGTGGAT GGGGTCGAAGTGCACAACGCCAAG ACCAAGCCTAGGGAAGAACAGTACg ccTCTACGTACCGGGTGGTGTCCGTG CTGACCGTGCTGCACCAGGACTGGC TGAACGGAAAGGAGTACAAGTGCA AAGTGTCAAACAAGGCTCTCCCTGC CCCTATCGAAAAGACCATCAGCAAG GCCAAGGGTCAACCTAGGGAGCCCC AGGTCTACACTTTGCCGCCTAGCCG GGAAGAAATGACTAAGAACCAAGT

			GTCCCTGACTTGCCTTGTCAAGGGC TTTTATCCGTCCGACATCGCCGTGG AGTGGGAGTCCAACGGACAACCGG AGAACAACTACAAGACCACCCCACC GGTGCTCGATTCCGATGGCTCCTTCT TCCTGTACTCCAAGCTGACTGTGGA CAAGTCAAGATGGCAGCAGGGAAA CGTGTTCTCCTGCTCCGTGATGCAC GAAGCGCTGCACAACCATTACACCC AGAAATCACTGTCACTTTCGCCGGG AAAA
SEQ ID 2187	QLQLQESGPGLVKPSQTLSLTCAISGDS VSSNSAAWNWIRQSPSRGLEWLGRTY YRSKWYNDYAVSVKSRITINPDTSKNQ FSLQLNSVTPEDTAVYYCAEGNGPFDP WGQGTLVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPR EEQYASTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK	SEQ ID 2295	CAGCTGCAGCTGCAGGAGTCGGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCAACAGTGC TGCTTGGAACTGGATCAGGCAGTCC CCATCGAGAGGCCTTGAGTGGCTGG GAAGGACATACTACAGGTCCAAGTG GTATAATGATTATGCAGTATCTGTG AAAAGTCGAATAACCATCAACCCAG ACACATCCAAGAACCAGTTCTCCCT GCAGCTGAACTCTGTGACTCCCGAG GACACGGCTGTGTATTACTGTGCAG AAGGCAATGGGCCGTTCGACCCCTG GGGCCAGGGAACCCTGGTGACCGTC TCCTCAGCATCCACCAAGGGGCCTT CCGTGTTCCCCCTGGCCCCTTCATCC AAGTCGACCTCTGGTGGAACCGCCG CACTCGGTTGCCTGGTCAAAGACTA CTTCCCCGAGCCCGTGACTGTCTCG TGGAACTCGGGCGCCCTCACATCCG GAGTGCATACCTTTCCCGCCGTGTT GCAGTCCAGCGGCCTGTACAGCCTG AGCTCCGTCGTGACAGTGCCGTCCT CCTCCCTTGGAACCCAGACCTATAT CTGCAACGTCAATCACAAGCCCTCC AACACCAAAGTGGACAAGAAGGTC GAACCCAAGTCCTGCGACAAGACTC ACACCTGTCCGCCTTGTCCAGCCCC TGAGCTGCTGGGTGGTCCGTCCGTG TTCCTCTTCCCGCCCAAGCCGAAGG ACACTCTGATGATTTCACGCACCCC GGAAGTCACTTGCGTGGTCGTGGAC GTGTCGCACGAAGATCCCGAAGTGA AATTCAATTGGTACGTGGATGGGGT CGAAGTGCACAACGCCAAGACCAA GCCTAGGGAAGAACAGTACgccTCTA CGTACCGGGTGGTGTCCGTGCTGAC CGTGCTGCACCAGGACTGGCTGAAC GGAAAGGAGTACAAGTGCAAAGTG TCAAACAAGGCTCTCCCTGCCCCTA TCGAAAAGACCATCAGCAAGGCCA AGGGTCAACCTAGGGAGCCCCAGGT CTACACTTTGCCGCCTAGCCGGGAA GAAATGACTAAGAACCAAGTGTCCC

			TGACTTGCCTTGTCAAGGGCTTTTAT CCGTCCGACATCGCCGTGGAGTGGG AGTCCAACGGACAACCGGAGAACA ACTACAAGACCACCCCACCGGTGCT CGATTCCGATGGCTCCTTCTTCCTGT ACTCCAAGCTGACTGTGGACAAGTC AAGATGGCAGCAGGGAAACGTGTT CTCCTGCTCCGTGATGCACGAAGCG CTGCACAACCATTACACCCAGAAAT CACTGTCACTTTCGCCGGGAAAA
SEQ ID 2188	QITLKESGGGVVQPGRSLRLSCVASGF TFSTYPMHWVRQAPGKGLEWVAVISY DGRNEYYADSVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCATRDTPLVG VSIYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTK PREEQYASTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2296	CAGATCACCTTGAAGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGTAGCCTCT GGATTCACCTTCAGTACCTATCCCA TGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTT ATATCATATGATGGACGTAATGAAT ACTACGCAGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCC AAAAACACGCTGTATCTGCAAATGA ACAGTCTGCGAGCTGAAGACACGGC TGTCTATTATTGTGCGACTCGGGAT ACACCTTTGGTTGGGGTTTCGATAT ACTGGGGCCAGGGCACCCTGGTCAC CGTCTCCTCAGCATCCACCAAGGGG CCTTCCGTGTTCCCCCTGGCCCCTTC ATCCAAGTCGACCTCTGGTGGAACC GCCGCACTCGGTTGCCTGGTCAAAG ACTACTTCCCCGAGCCCGTGACTGT CTCGTGGAACTCGGGCGCCCTCACA TCCGGAGTGCATACCTTTCCCGCCG TGTTGCAGTCCAGCGGCCTGTACAG CCTGAGCTCCGTCGTGACAGTGCCG TCCTCCTCCCTTGGAACCCAGACCT ATATCTGCAACGTCAATCACAAGCC CTCCAACACCAAAGTGGACAAGAA GGTCGAACCCAAGTCCTGCGACAAG ACTCACACCTGTCCGCCTTGTCCAG CCCCTGAGCTGCTGGGTGGTCCGTC CGTGTTCCTCTTCCCGCCCAAGCCG AAGGACACTCTGATGATTTCACGCA CCCCGGAAGTCACTTGCGTGGTCGT GGACGTGTCGCACGAAGATCCCGAA GTGAAATTCAATTGGTACGTGGATG GGGTCGAAGTGCACAACGCCAAGA CCAAGCCTAGGGAAGAACAGTACgc cTCTACGTACCGGGTGGTGTCCGTGC TGACCGTGCTGCACCAGGACTGGCT GAACGGAAAGGAGTACAAGTGCAA AGTGTCAAACAAGGCTCTCCCTGCC CCTATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTACACTTTGCCGCCTAGCCGG GAAGAAATGACTAAGAACCAAGTG

			TCCCTGACTTGCCTTGTCAAGGGCTT TTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCAAGCTGACTGTGGACA AGTCAAGATGGCAGCAGGGAAACG TGTTCTCCTGCTCCGTGATGCACGA AGCGCTGCACAACCATTACACCCAG AAATCACTGTCACTTTCGCCGGGAA AA
SEQ ID 2189	QMQLVQSGGGLVKAGGSLRLSCSASG FTFSSYAMHWVRQAPGKGLEYVSAISS NGGSTYYADSVKGRFTISRDNSKNTLY LQMSSLRAEDTAVYYCVNRAGYGDY RHFQHWGQGTLVTVSSASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2297	CAGATGCAGCTGGTGCAATCTGGGG GAGGCCTGGTCAAGGCTGGGGGGTC CCTGAGACTCTCCTGTTCAGCCTCTG GATTCACCTTCAGTAGCTATGCTAT GCACTGGGTCCGCCAGGCTCCAGGG AAGGGACTGGAATATGTTTCAGCTA TTAGTAGTAATGGGGGTAGCACATA CTACGCAGACTCAGTGAAGGGCAG ATTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTTCAAATGA GCAGTCTGAGAGCTGAGGACACGG CTGTGTATTACTGTGTGAATCGGGC GGGTTACGGTGACTACAGACACTTC CAGCACTGGGGCCAGGGCACCCTGG TCACCGTCTCCTCAGCATCCACCAA GGGGCCTTCCGTGTTCCCCCTGGCC CCTTCATCCAAGTCGACCTCTGGTG GAACCGCCGCACTCGGTTGCCTGGT CAAAGACTACTTCCCCGAGCCCGTG ACTGTCTCGTGGAACTCGGGCGCCC TCACATCCGGAGTGCATACCTTTCC CGCCGTGTTGCAGTCCAGCGGCCTG TACAGCCTGAGCTCCGTCGTGACAG TGCCGTCCTCCTCCCTTGGAACCCA GACCTATATCTGCAACGTCAATCAC AAGCCCTCCAACACCAAAGTGGACA AGAAGGTCGAACCCAAGTCCTGCGA CAAGACTCACACCTGTCCGCCTTGT CCAGCCCCTGAGCTGCTGGGTGGTC CGTCCGTGTTCCTCTTCCCGCCCAAG CCGAAGGACACTCTGATGATTTCAC GCACCCCGGAAGTCACTTGCGTGGT CGTGGACGTGTCGCACGAAGATCCC GAAGTGAAATTCAATTGGTACGTGG ATGGGGTCGAAGTGCACAACGCCA AGACCAAGCCTAGGGAAGAACAGT ACgccTCTACGTACCGGGTGGTGTCC GTGCTGACCGTGCTGCACCAGGACT GGCTGAACGGAAAGGAGTACAAGT GCAAAGTGTCAAACAAGGCTCTCCC TGCCCCTATCGAAAAGACCATCAGC AAGGCCAAGGGTCAACCTAGGGAG CCCCAGGTCTACACTTTGCCGCCTA GCCGGGAAGAAATGACTAAGAACC

			AAGTGTCCCTGACTTGCCTTGTCAA GGGCTTTTATCCGTCCGACATCGCC GTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACC CCACCGGTGCTCGATTCCGATGGCT CCTTCTTCCTGTACTCCAAGCTGACT GTGGACAAGTCAAGATGGCAGCAG GGAAACGTGTTCTCCTGCTCCGTGA TGCACGAAGCGCTGCACAACCATTA CACCCAGAAATCACTGTCACTTTCG CCGGGAAAA
SEQ ID 2190	EVQLVQSGGGVVQPGGSLRLSCAASG FTFSSYGMHWVRQAPGKGLEWVAFIS YDGSNKYYADSVKGRFTISRDNSKNT LYLQMNSLRAEDTAVYYCATTGDRFQ EFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTK PREEQYASTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2298	GAGGTGCAGCTGGTGCAGTCTGGGG GAGGCGTGGTCCAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCGTCT GGATTCACCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCATTT ATATCATATGATGGAAGTAATAAAT ACTACGCAGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCCGAGGACACGG CCGTATATTACTGTGCGACAACAGG GGACCGCTTCCAAGAGTTTGACTAC TGGGGCCAGGGAACCCTGGTCACCG TCTCCTCAGCATCCACCAAGGGGCC TTCCGTGTTCCCCCTGGCCCCTTCAT CCAAGTCGACCTCTGGTGGAACCGC CGCACTCGGTTGCCTGGTCAAAGAC TACTTCCCCGAGCCCGTGACTGTCT CGTGGAACTCGGGCGCCCTCACATC CGGAGTGCATACCTTTCCCGCCGTG TTGCAGTCCAGCGGCCTGTACAGCC TGAGCTCCGTCGTGACAGTGCCGTC CTCCTCCCTTGGAACCCAGACCTAT ATCTGCAACGTCAATCACAAGCCCT CCAACACCAAAGTGGACAAGAAGG TCGAACCCAAGTCCTGCGACAAGAC TCACACCTGTCCGCCTTGTCCAGCC CCTGAGCTGCTGGGTGGTCCGTCCG TGTTCCTCTTCCCGCCCAAGCCGAA GGACACTCTGATGATTTCACGCACC CCGGAAGTCACTTGCGTGGTCGTGG ACGTGTCGCACGAAGATCCCGAAGT GAAATTCAATTGGTACGTGGATGGG GTCGAAGTGCACAACGCCAAGACC AAGCCTAGGGAAGAACAGTACgccT CTACGTACCGGGTGGTGTCCGTGCT GACCGTGCTGCACCAGGACTGGCTG AACGGAAAGGAGTACAAGTGCAAA GTGTCAAACAAGGCTCTCCCTGCCC CTATCGAAAAGACCATCAGCAAGGC CAAGGGTCAACCTAGGGAGCCCCA GGTCTACACTTTGCCGCCTAGCCGG GAAGAAATGACTAAGAACCAAGTG

			TCCCTGACTTGCCTTGTCAAGGGCTT TTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCAAGCTGACTGTGGACA AGTCAAGATGGCAGCAGGGAAACG TGTTCTCCTGCTCCGTGATGCACGA AGCGCTGCACAACCATTACACCCAG AAATCACTGTCACTTTCGCCGGGAA AA
SEQ ID 2191	QMQLVQSGGVLLQPGRSLRLSCTASG FTFAAYNINWFRQGPGGGLEWVGFIR ANADSGTTEYAASVKGRFFISRDDSRS TAYLQMTSLKTEDTAVYYCARDDRGR GDDFDYWGQGTLVTVSSASTKGPSVF PLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYASTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG K	SEQ ID 2299	CAGATGCAGCTGGTGCAGTCTGGGG GAGTCTTGCTTCAGCCAGGGCGGTC CCTGAGACTCTCCTGTACAGCTTCT GGATTCACCTTTGCTGCTTATAATAT CAACTGGTTCCGCCAGGGTCCTGGG GGGGGGCTGGAGTGGGTAGGTTTCA TTAGAGCCAACGCTGATAGTGGGAC AACAGAGTACGCCGCGTCTGTGAAA GGCAGATTCTTCATCTCAAGAGATG ATTCCAGAAGCACCGCCTACCTGCA AATGACTAGCCTTAAAACCGAGGAC ACAGCCGTTTATTACTGTGCCAGAG ATGATCGGGGTCGGGGAGATGACTT TGACTACTGGGGCCAGGGCACCCTG GTCACCGTCTCCTCAGCATCCACCA AGGGGCCTTCCGTGTTCCCCCTGGC CCCTTCATCCAAGTCGACCTCTGGT GGAACCGCCGCACTCGGTTGCCTGG TCAAAGACTACTTCCCCGAGCCCGT GACTGTCTCGTGGAACTCGGGCGCC CTCACATCCGGAGTGCATACCTTTC CCGCCGTGTTGCAGTCCAGCGGCCT GTACAGCCTGAGCTCCGTCGTGACA GTGCCGTCCTCCTCCCTTGGAACCC AGACCTATATCTGCAACGTCAATCA CAAGCCCTCCAACACCAAAGTGGAC AAGAAGGTCGAACCCAAGTCCTGCG ACAAGACTCACACCTGTCCGCCTTG TCCAGCCCCTGAGCTGCTGGGTGGT CCGTCCGTGTTCCTCTTCCCGCCCAA GCCGAAGGACACTCTGATGATTTCA CGCACCCCGGAAGTCACTTGCGTGG TCGTGGACGTGTCGCACGAAGATCC CGAAGTGAAATTCAATTGGTACGTG GATGGGGTCGAAGTGCACAACGCC AAGACCAAGCCTAGGGAAGAACAG TACgccTCTACGTACCGGGTGGTGTC CGTGCTGACCGTGCTGCACCAGGAC TGGCTGAACGGAAAGGAGTACAAG TGCAAAGTGTCAAACAAGGCTCTCC CTGCCCCTATCGAAAAGACCATCAG CAAGGCCAAGGGTCAACCTAGGGA GCCCCAGGTCTACACTTTGCCGCCT AGCCGGGAAGAAATGACTAAGAAC

			CAAGTGTCCCTGACTTGCCTTGTCA AGGGCTTTTATCCGTCCGACATCGC CGTGGAGTGGGAGTCCAACGGACA ACCGGAGAACAACTACAAGACCAC CCCACCGGTGCTCGATTCCGATGGC TCCTTCTTCCTGTACTCCAAGCTGAC TGTGGACAAGTCAAGATGGCAGCA GGGAAACGTGTTCTCCTGCTCCGTG ATGCACGAAGCGCTGCACAACCATT ACACCCAGAAATCACTGTCACTTTC GCCGGGAAAA
SEQ ID 2192	QVQLVQSGGGLVQPGGSLRLSCAASG FTFSSYGMTWVRQAPGKGLEWVSTIS GNGVGTYYPDSVKDRFTISRDSSKNTV YLQMNSLRAEDTAVYYCVKHGRAGIN WYFDLWGRGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2300	CAGGTGCAGCTGGTGCAATCTGGGG GAGGCTTGGTACAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTTAGCAGCTATGGCA TGACGTGGGTCCGCCAGGCTCCAGG GAAGGGGCTGGAGTGGGTCTCAACT ATTAGTGGTAATGGTGTTGGCACAT ACTACCCAGACTCCGTGAAGGACCG GTTCACCATCTCCAGAGACAGTTCC AAGAACACGGTGTATCTGCAAATGA ACAGCCTGAGAGCCGAGGACACGG CCGTATATTACTGTGTGAAACATGG TAGGGCCGGAATAAACTGGTACTTC GATCTCTGGGGCCGTGGCACCCTGG TGACCGTCTCCTCAGCATCCACCAA GGGGCCTTCCGTGTTCCCCCTGGCC CCTTCATCCAAGTCGACCTCTGGTG GAACCGCCGCACTCGGTTGCCTGGT CAAAGACTACTTCCCCGAGCCCGTG ACTGTCTCGTGGAACTCGGGCGCCC TCACATCCGGAGTGCATACCTTTCC CGCCGTGTTGCAGTCCAGCGGCCTG TACAGCCTGAGCTCCGTCGTGACAG TGCCGTCCTCCTCCCTTGGAACCCA GACCTATATCTGCAACGTCAATCAC AAGCCCTCCAACACCAAAGTGGACA AGAAGGTCGAACCCAAGTCCTGCGA CAAGACTCACACCTGTCCGCCTTGT CCAGCCCCTGAGCTGCTGGGTGGTC CGTCCGTGTTCCTCTTCCCGCCCAAG CCGAAGGACACTCTGATGATTTCAC GCACCCCGGAAGTCACTTGCGTGGT CGTGGACGTGTCGCACGAAGATCCC GAAGTGAAATTCAATTGGTACGTGG ATGGGGTCGAAGTGCACAACGCCA AGACCAAGCCTAGGGAAGAACAGT ACgccTCTACGTACCGGGTGGTGTCC GTGCTGACCGTGCTGCACCAGGACT GGCTGAACGGAAAGGAGTACAAGT GCAAAGTGTCAAACAAGGCTCTCCC TGCCCCTATCGAAAAGACCATCAGC AAGGCCAAGGGTCAACCTAGGGAG CCCCAGGTCTACACTTTGCCGCCTA GCCGGGAAGAAATGACTAAGAACC

			AAGTGTCCCTGACTTGCCTTGTCAA GGGCTTTTATCCGTCCGACATCGCC GTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACC CCACCGGTGCTCGATTCCGATGGCT CCTTCTTCCTGTACTCCAAGCTGACT GTGGACAAGTCAAGATGGCAGCAG GGAAACGTGTTCTCCTGCTCCGTGA TGCACGAAGCGCTGCACAACCATTA CACCCAGAAATCACTGTCACTTTCG CCGGGAAAA
SEQ ID 2193	QVQLQQSGPGLVKPSQTLSLTCAISGD SVSSNSAAWNWIRQSPSRGLEWLGRT YYRSKWYNDYAVSVKSRITINPDTSKN QFSLQLNSVTPEDTAVYYCARGGGLW AFDIWGQGTTVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTK PREEQYASTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2301	CAGGTACAGCTGCAGCAGTCAGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCAACAGTGC TGCTTGGAACTGGATCAGGCAGTCC CCATCGAGAGGCCTTGAGTGGCTGG GAAGGACATACTACAGGTCCAAGTG GTATAATGATTATGCAGTATCTGTG AAAAGTCGAATAACCATCAACCCAG ACACATCCAAGAACCAGTTCTCCCT GCAGCTGAACTCTGTGACTCCCGAG GACACGGCTGTGTATTACTGTGCAA GAGGGGGAGGGCTTTGGGCTTTTGA TATCTGGGGCCAAGGGACCACGGTC ACCGTCTCCTCAGCATCCACCAAGG GGCCTTCCGTGTTCCCCCTGGCCCCT TCATCCAAGTCGACCTCTGGTGGAA CCGCCGCACTCGGTTGCCTGGTCAA AGACTACTTCCCCGAGCCCGTGACT GTCTCGTGGAACTCGGGCGCCCTCA CATCCGGAGTGCATACCTTTCCCGC CGTGTTGCAGTCCAGCGGCCTGTAC AGCCTGAGCTCCGTCGTGACAGTGC CGTCCTCCTCCCTTGGAACCCAGAC CTATATCTGCAACGTCAATCACAAG CCCTCCAACACCAAAGTGGACAAGA AGGTCGAACCCAAGTCCTGCGACAA GACTCACACCTGTCCGCCTTGTCCA GCCCCTGAGCTGCTGGGTGGTCCGT CCGTGTTCCTCTTCCCGCCCAAGCC GAAGGACACTCTGATGATTTCACGC ACCCCGGAAGTCACTTGCGTGGTCG TGGACGTGTCGCACGAAGATCCCGA AGTGAAATTCAATTGGTACGTGGAT GGGGTCGAAGTGCACAACGCCAAG ACCAAGCCTAGGGAAGAACAGTACg ccTCTACGTACCGGGTGGTGTCCGTG CTGACCGTGCTGCACCAGGACTGGC TGAACGGAAAGGAGTACAAGTGCA AAGTGTCAAACAAGGCTCTCCCTGC CCCTATCGAAAAGACCATCAGCAAG GCCAAGGGTCAACCTAGGGAGCCCC AGGTCTACACTTTGCCGCCTAGCCG GGAAGAAATGACTAAGAACCAAGT

			GTCCCTGACTTGCCTTGTCAAGGGC TTTTATCCGTCCGACATCGCCGTGG AGTGGGAGTCCAACGGACAACCGG AGAACAACTACAAGACCACCCCACC GGTGCTCGATTCCGATGGCTCCTTCT TCCTGTACTCCAAGCTGACTGTGGA CAAGTCAAGATGGCAGCAGGGAAA CGTGTTCTCCTGCTCCGTGATGCAC GAAGCGCTGCACAACCATTACACCC AGAAATCACTGTCACTTTCGCCGGG AAAA
SEQ ID 2194	EVQLVQSGAEVKKPGASVKVSCKASG YTFTGYYMHWVRQAPGQGLEWMGW INPNSGGTNYAQKFQGRVTMTRDTSIS TAYMELSRLRSDDTAVYYCARDKIGS CPYWGQGTLVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTK PREEQYASTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2302	GAGGTCCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTCTCCTGCAAGGCTTCT GGATACACCTTCACCGGCTACTATA TGCACTGGGTGCGACAGGCCCCTGG ACAAGGGCTTGAGTGGATGGGATG GATCAACCCTAACAGTGGTGGCACA AACTATGCACAGAAGTTTCAGGGCA GGGTCACCATGACCAGGGACACGTC CATCAGCACAGCCTACATGGAGCTG AGCAGGCTGAGATCTGACGACACG GCCGTGTATTACTGTGCGAGAGACA AGATCGGCAGCTGTCCTTACTGGGG CCAGGGAACCCTGGTCACCGTCTCC TCAGCATCCACCAAGGGGCCTTCCG TGTTCCCCCTGGCCCCTTCATCCAAG TCGACCTCTGGTGGAACCGCCGCAC TCGGTTGCCTGGTCAAAGACTACTT CCCCGAGCCCGTGACTGTCTCGTGG AACTCGGGCGCCCTCACATCCGGAG TGCATACCTTTCCCGCCGTGTTGCA GTCCAGCGGCCTGTACAGCCTGAGC TCCGTCGTGACAGTGCCGTCCTCCT CCCTTGGAACCCAGACCTATATCTG CAACGTCAATCACAAGCCCTCCAAC ACCAAAGTGGACAAGAAGGTCGAA CCCAAGTCCTGCGACAAGACTCACA CCTGTCCGCCTTGTCCAGCCCCTGA GCTGCTGGGTGGTCCGTCCGTGTTC CTCTTCCCGCCCAAGCCGAAGGACA CTCTGATGATTTCACGCACCCCGGA AGTCACTTGCGTGGTCGTGGACGTG TCGCACGAAGATCCCGAAGTGAAAT TCAATTGGTACGTGGATGGGGTCGA AGTGCACAACGCCAAGACCAAGCCT AGGGAAGAACAGTACgccTCTACGTA CCGGGTGGTGTCCGTGCTGACCGTG CTGCACCAGGACTGGCTGAACGGAA AGGAGTACAAGTGCAAAGTGTCAA ACAAGGCTCTCCCTGCCCCTATCGA AAAGACCATCAGCAAGGCCAAGGG TCAACCTAGGGAGCCCCAGGTCTAC ACTTTGCCGCCTAGCCGGGAAGAAA TGACTAAGAACCAAGTGTCCCTGAC

			TTGCCTTGTCAAGGGCTTTTATCCGT CCGACATCGCCGTGGAGTGGGAGTC CAACGGACAACCGGAGAACAACTA CAAGACCACCCCACCGGTGCTCGAT TCCGATGGCTCCTTCTTCCTGTACTC CAAGCTGACTGTGGACAAGTCAAGA TGGCAGCAGGGAAACGTGTTCTCCT GCTCCGTGATGCACGAAGCGCTGCA CAACCATTACACCCAGAAATCACTG TCACTTTCGCCGGGAAAA
SEQ ID 2195	QVTLKESGPTLVKPTQTLTLTCTFSGFS LSTSGVGVGWIRQPPGKALEWLALIY WDDDKRYSPSLKSRLTITKDTSKNQV VLTMTNMDPVDTATYYCAHRPDSSSQ CFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTK PREEQYASTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2303	CAGGTCACCTTGAAGGAGTCTGGTC CTACGCTGGTGAAACCCACACAGAC CCTCACGCTGACCTGCACCTTCTCTG GGTTCTCACTCAGCACTAGTGGAGT GGGTGTGGGCTGGATCCGTCAGCCC CCAGGAAAGGCCCTGGAGTGGCTTG CACTCATTTATTGGGATGATGATAA GCGCTACAGCCCATCTCTGAAGAGC AGGCTCACCATCACCAAGGACACCT CCAAAAACCAGGTGGTCCTTACAAT GACCAACATGGACCCTGTGGACACA GCCACATATTACTGTGCACACAGAC CGGATAGCAGCAGTCAATGTTTTGA CTACTGGGGCCAGGGAACCCTGGTC ACCGTCTCCTCAGCATCCACCAAGG GGCCTTCCGTGTTCCCCCTGGCCCCT TCATCCAAGTCGACCTCTGGTGGAA CCGCCGCACTCGGTTGCCTGGTCAA AGACTACTTCCCCGAGCCCGTGACT GTCTCGTGGAACTCGGGCGCCCTCA CATCCGGAGTGCATACCTTTCCCGC CGTGTTGCAGTCCAGCGGCCTGTAC AGCCTGAGCTCCGTCGTGACAGTGC CGTCCTCCTCCCTTGGAACCCAGAC CTATATCTGCAACGTCAATCACAAG CCCTCCAACACCAAAGTGGACAAGA AGGTCGAACCCAAGTCCTGCGACAA GACTCACACCTGTCCGCCTTGTCCA GCCCCTGAGCTGCTGGGTGGTCCGT CCGTGTTCCTCTTCCCGCCCAAGCC GAAGGACACTCTGATGATTTCACGC ACCCCGGAAGTCACTTGCGTGGTCG TGGACGTGTCGCACGAAGATCCCGA AGTGAAATTCAATTGGTACGTGGAT GGGGTCGAAGTGCACAACGCCAAG ACCAAGCCTAGGGAAGAACAGTACg ccTCTACGTACCGGGTGGTGTCCGTG CTGACCGTGCTGCACCAGGACTGGC TGAACGGAAAGGAGTACAAGTGCA AAGTGTCAAACAAGGCTCTCCCTGC CCCTATCGAAAAGACCATCAGCAAG GCCAAGGGTCAACCTAGGGAGCCCC AGGTCTACACTTTGCCGCCTAGCCG GGAAGAAATGACTAAGAACCAAGT

			GTCCCTGACTTGCCTTGTCAAGGGC TTTTATCCGTCCGACATCGCCGTGG AGTGGGAGTCCAACGGACAACCGG AGAACAACTACAAGACCACCCCACC GGTGCTCGATTCCGATGGCTCCTTCT TCCTGTACTCCAAGCTGACTGTGGA CAAGTCAAGATGGCAGCAGGGAAA CGTGTTCTCCTGCTCCGTGATGCAC GAAGCGCTGCACAACCATTACACCC AGAAATCACTGTCACTTTCGCCGGG AAAA
SEQ ID 2196	QVTLKESGGGVVQPGRSLRLSCAASGF TFSSYAMHWVRQAPGKGLEWVAVISY DGSNKYYADSVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCARSSGWSLP EDYWGQGTLVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTK PREEQYASTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2304	CAGGTCACCTTGAAGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTCAGTAGCTATGCTA TGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTT ATATCATATGATGGAAGTAATAAAT ACTACGCAGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCTGAGGACACGG CTGTGTATTACTGTGCGAGAAGCAG TGGCTGGTCACTGCCTGAAGACTAC TGGGGCCAGGGAACCCTGGTCACCG TCTCCTCAGCATCCACCAAGGGGCC TTCCGTGTTCCCCCTGGCCCCTTCAT CCAAGTCGACCTCTGGTGGAACCGC CGCACTCGGTTGCCTGGTCAAAGAC TACTTCCCCGAGCCCGTGACTGTCT CGTGGAACTCGGGCGCCCTCACATC CGGAGTGCATACCTTTCCCGCCGTG TTGCAGTCCAGCGGCCTGTACAGCC TGAGCTCCGTCGTGACAGTGCCGTC CTCCTCCCTTGGAACCCAGACCTAT ATCTGCAACGTCAATCACAAGCCCT CCAACACCAAAGTGGACAAGAAGG TCGAACCCAAGTCCTGCGACAAGAC TCACACCTGTCCGCCTTGTCCAGCC CCTGAGCTGCTGGGTGGTCCGTCCG TGTTCCTCTTCCCGCCCAAGCCGAA GGACACTCTGATGATTTCACGCACC CCGGAAGTCACTTGCGTGGTCGTGG ACGTGTCGCACGAAGATCCCGAAGT GAAATTCAATTGGTACGTGGATGGG GTCGAAGTGCACAACGCCAAGACC AAGCCTAGGGAAGAACAGTACgccT CTACGTACCGGGTGGTGTCCGTGCT GACCGTGCTGCACCAGGACTGGCTG AACGGAAAGGAGTACAAGTGCAAA GTGTCAAACAAGGCTCTCCCTGCCC CTATCGAAAAGACCATCAGCAAGGC CAAGGGTCAACCTAGGGAGCCCCA GGTCTACACTTTGCCGCCTAGCCGG GAAGAAATGACTAAGAACCAAGTG

			TCCCTGACTTGCCTTGTCAAGGGCTT TTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCAAGCTGACTGTGGACA AGTCAAGATGGCAGCAGGGAAACG TGTTCTCCTGCTCCGTGATGCACGA AGCGCTGCACAACCATTACACCCAG AAATCACTGTCACTTTCGCCGGGAA AA
SEQ ID 2197	QVQLVQSGAEVKKPGASVKVSCKVSG YTLTELSMHWVRQAPGKGLEWMGGF DPEDGETIYAQKFQGRVTMTEDTSTDT AYMELSSLRSEDTAVYYCATDVNPEL LGAGFDYWGQGTLVTVSSASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYASTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG K	SEQ ID 2305	CAGGTCCAGCTGGTACAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTCTCCTGCAAGGTTTCC GGATACACCCTCACTGAATTATCCA TGCACTGGGTGCGACAGGCTCCTGG AAAAGGGCTTGAGTGGATGGGAGG TTTTGATCCTGAAGATGGTGAAACA ATCTACGCACAGAAGTTCCAGGGCA GAGTCACCATGACCGAGGACACATC TACAGACACAGCCTACATGGAGCTG AGCAGCCTGAGATCTGAGGACACG GCCGTGTATTACTGTGCAACGGATG TGAACCCGGAGCTACTGGGGGCGG GATTTGACTACTGGGGCCAGGGCAC CCTGGTCACCGTCTCCTCAGCATCC ACCAAGGGGCCTTCCGTGTTCCCCC TGGCCCCTTCATCCAAGTCGACCTC TGGTGGAACCGCCGCACTCGGTTGC CTGGTCAAAGACTACTTCCCCGAGC CCGTGACTGTCTCGTGGAACTCGGG CGCCCTCACATCCGGAGTGCATACC TTTCCCGCCGTGTTGCAGTCCAGCG GCCTGTACAGCCTGAGCTCCGTCGT GACAGTGCCGTCCTCCTCCCTTGGA ACCCAGACCTATATCTGCAACGTCA ATCACAAGCCCTCCAACACCAAAGT GGACAAGAAGGTCGAACCCAAGTC CTGCGACAAGACTCACACCTGTCCG CCTTGTCCAGCCCCTGAGCTGCTGG GTGGTCCGTCCGTGTTCCTCTTCCCG CCCAAGCCGAAGGACACTCTGATGA TTTCACGCACCCCGGAAGTCACTTG CGTGGTCGTGGACGTGTCGCACGAA GATCCCGAAGTGAAATTCAATTGGT ACGTGGATGGGGTCGAAGTGCACA ACGCCAAGACCAAGCCTAGGGAAG AACAGTACgccTCTACGTACCGGGTG GTGTCCGTGCTGACCGTGCTGCACC AGGACTGGCTGAACGGAAAGGAGT ACAAGTGCAAAGTGTCAAACAAGG CTCTCCCTGCCCCTATCGAAAAGAC CATCAGCAAGGCCAAGGGTCAACCT AGGGAGCCCCAGGTCTACACTTTGC CGCCTAGCCGGGAAGAAATGACTA

			AGAACCAAGTGTCCCTGACTTGCCT TGTCAAGGGCTTTTATCCGTCCGAC ATCGCCGTGGAGTGGGAGTCCAACG GACAACCGGAGAACAACTACAAGA CCACCCCACCGGTGCTCGATTCCGA TGGCTCCTTCTTCCTGTACTCCAAGC TGACTGTGGACAAGTCAAGATGGCA GCAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACT TTCGCCGGGAAAA
SEQ ID 2198	QVTLKESGGGLVQPGGSLRLSCAASGF TFSDQYMDWVRQAPGKGLEWVGRVR NKANSYTTEYAASVKGRFTISRDDSKN SLYLQMNSLNTEDTAMYFCASSLNSG GYRCFHHWGQGTLVTVSSASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYASTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG K	SEQ ID 2306	CAGGTCACCTTGAAGGAGTCTGGGG GAGGCTTGGTCCAGCCTGGAGGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTCAGTGACCAGTACA TGGACTGGGTCCGCCAGGCTCCAGG GAAGGGGCTGGAGTGGGTTGGCCGT GTTAGAAACAAAGCTAACAGTTACA CCACAGAATACGCCGCGTCTGTGAA AGGCAGATTCACCATCTCAAGAGAT GATTCAAAGAACTCACTGTATCTGC AAATGAATAGTCTGAACACCGAGG ACACGGCCATGTATTTCTGTGCTAG TAGTCTCAATAGTGGGGGCTACCGA TGCTTCCATCACTGGGGCCAGGGCA CCCTGGTGACCGTCTCCTCAGCATC CACCAAGGGGCCTTCCGTGTTCCCC CTGGCCCCTTCATCCAAGTCGACCT CTGGTGGAACCGCCGCACTCGGTTG CCTGGTCAAAGACTACTTCCCCGAG CCCGTGACTGTCTCGTGGAACTCGG GCGCCCTCACATCCGGAGTGCATAC CTTTCCCGCCGTGTTGCAGTCCAGC GGCCTGTACAGCCTGAGCTCCGTCG TGACAGTGCCGTCCTCCTCCCTTGG AACCCAGACCTATATCTGCAACGTC AATCACAAGCCCTCCAACACCAAAG TGGACAAGAAGGTCGAACCCAAGT CCTGCGACAAGACTCACACCTGTCC GCCTTGTCCAGCCCCTGAGCTGCTG GGTGGTCCGTCCGTGTTCCTCTTCCC GCCCAAGCCGAAGGACACTCTGATG ATTTCACGCACCCCGGAAGTCACTT GCGTGGTCGTGGACGTGTCGCACGA AGATCCCGAAGTGAAATTCAATTGG TACGTGGATGGGGTCGAAGTGCACA ACGCCAAGACCAAGCCTAGGGAAG AACAGTACgccTCTACGTACCGGGTG GTGTCCGTGCTGACCGTGCTGCACC AGGACTGGCTGAACGGAAAGGAGT ACAAGTGCAAAGTGTCAAACAAGG CTCTCCCTGCCCCTATCGAAAAGAC CATCAGCAAGGCCAAGGGTCAACCT AGGGAGCCCCAGGTCTACACTTTGC CGCCTAGCCGGGAAGAAATGACTA

			AGAACCAAGTGTCCCTGACTTGCCT TGTCAAGGGCTTTTATCCGTCCGAC ATCGCCGTGGAGTGGGAGTCCAACG GACAACCGGAGAACAACTACAAGA CCACCCCACCGGTGCTCGATTCCGA TGGCTCCTTCTTCCTGTACTCCAAGC TGACTGTGGACAAGTCAAGATGGCA GCAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACT TTCGCCGGGAAAA
SEQ ID 2199	QVQLVQSGGGLVQPGGSLRLSCSASGF TFSSYAMHWVRQAPGKGLEYVSAISS NGGSTYYADSVKGRFTISRDNSKNTLY LQMSSLRAEDTAVYYCVKAPRGVVPA AMRGGYWGQGTLVTVSSASTKGPSVF PLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYASTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG K	SEQ ID 2307	CAGGTCCAGCTGGTGCAGTCTGGGG GAGGCTTGGTCCAGCCTGGGGGGTC CCTGAGACTCTCCTGTTCAGCCTCTG GATTCACCTTCAGTAGCTATGCTAT GCACTGGGTCCGCCAGGCTCCAGGG AAGGGACTGGAATATGTTTCAGCTA TTAGTAGTAATGGGGGTAGCACATA CTACGCAGACTCAGTGAAGGGCAG ATTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTTCAAATGA GCAGTCTGAGAGCTGAGGACACGG CTGTGTATTACTGTGTGAAAGCGCC GAGGGGTGTAGTACCAGCTGCTATG CGGGGGGGCTACTGGGGCCAGGGA ACCCTGGTCACCGTCTCCTCAGCAT CCACCAAGGGGCCTTCCGTGTTCCC CCTGGCCCCTTCATCCAAGTCGACC TCTGGTGGAACCGCCGCACTCGGTT GCCTGGTCAAAGACTACTTCCCCGA GCCCGTGACTGTCTCGTGGAACTCG GGCGCCCTCACATCCGGAGTGCATA CCTTTCCCGCCGTGTTGCAGTCCAG CGGCCTGTACAGCCTGAGCTCCGTC GTGACAGTGCCGTCCTCCTCCCTTG GAACCCAGACCTATATCTGCAACGT CAATCACAAGCCCTCCAACACCAAA GTGGACAAGAAGGTCGAACCCAAG TCCTGCGACAAGACTCACACCTGTC CGCCTTGTCCAGCCCCTGAGCTGCT GGGTGGTCCGTCCGTGTTCCTCTTCC CGCCCAAGCCGAAGGACACTCTGAT GATTTCACGCACCCCGGAAGTCACT TGCGTGGTCGTGGACGTGTCGCACG AAGATCCCGAAGTGAAATTCAATTG GTACGTGGATGGGGTCGAAGTGCAC AACGCCAAGACCAAGCCTAGGGAA GAACAGTACgccTCTACGTACCGGGT GGTGTCCGTGCTGACCGTGCTGCAC CAGGACTGGCTGAACGGAAAGGAG TACAAGTGCAAAGTGTCAAACAAG GCTCTCCCTGCCCCTATCGAAAAGA CCATCAGCAAGGCCAAGGGTCAACC TAGGGAGCCCCAGGTCTACACTTTG CCGCCTAGCCGGGAAGAAATGACTA

			AGAACCAAGTGTCCCTGACTTGCCT TGTCAAGGGCTTTTATCCGTCCGAC ATCGCCGTGGAGTGGGAGTCCAACG GACAACCGGAGAACAACTACAAGA CCACCCCACCGGTGCTCGATTCCGA TGGCTCCTTCTTCCTGTACTCCAAGC TGACTGTGGACAAGTCAAGATGGCA GCAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACT TTCGCCGGGAAAA
SEQ ID 2200	QVQLQESGGGLVQPGRSLRLSCTASGF TFGDYAMSWFRQAPGKGLEWVGFIRS KAYGGTTEYAASVKGRFTISRDDSKSI AYLQMNSLKTEDTAVYYCTRLVGNSG SYYPFGYWGQGTLVTVSSASTKGPSVF PLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYASTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG K	SEQ ID 2308	CAGGTGCAGCTGCAGGAGTCGGGG GGAGGCTTGGTACAGCCAGGGCGGT CCCTGAGACTCTCCTGTACAGCTTCT GGATTCACCTTTGGTGATTATGCTAT GAGCTGGTTCCGCCAGGCTCCAGGG AAGGGGCTGGAGTGGGTAGGTTTCA TTAGAAGCAAAGCTTATGGTGGGAC AACAGAATACGCCGCGTCTGTGAAA GGCAGATTCACCATCTCAAGAGATG ATTCCAAAAGCATCGCCTATCTGCA AATGAACAGCCTGAAAACCGAGGA CACAGCCGTGTATTACTGTACTAGA TTGGTGGGCAATAGTGGGAGCTACT ATCCGTTTGGGTACTGGGGCCAGGG AACCCTGGTGACCGTCTCCTCAGCA TCCACCAAGGGGCCTTCCGTGTTCC CCCTGGCCCCTTCATCCAAGTCGAC CTCTGGTGGAACCGCCGCACTCGGT TGCCTGGTCAAAGACTACTTCCCCG AGCCCGTGACTGTCTCGTGGAACTC GGGCGCCCTCACATCCGGAGTGCAT ACCTTTCCCGCCGTGTTGCAGTCCA GCGGCCTGTACAGCCTGAGCTCCGT CGTGACAGTGCCGTCCTCCTCCCTT GGAACCCAGACCTATATCTGCAACG TCAATCACAAGCCCTCCAACACCAA AGTGGACAAGAAGGTCGAACCCAA GTCCTGCGACAAGACTCACACCTGT CCGCCTTGTCCAGCCCCTGAGCTGC TGGGTGGTCCGTCCGTGTTCCTCTTC CCGCCCAAGCCGAAGGACACTCTGA TGATTTCACGCACCCCGGAAGTCAC TTGCGTGGTCGTGGACGTGTCGCAC GAAGATCCCGAAGTGAAATTCAATT GGTACGTGGATGGGGTCGAAGTGCA CAACGCCAAGACCAAGCCTAGGGA AGAACAGTACgccTCTACGTACCGGG TGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGA GTACAAGTGCAAAGTGTCAAACAA GGCTCTCCCTGCCCCTATCGAAAAG ACCATCAGCAAGGCCAAGGGTCAA CCTAGGGAGCCCCAGGTCTACACTT TGCCGCCTAGCCGGGAAGAAATGAC

			TAAGAACCAAGTGTCCCTGACTTGC CTTGTCAAGGGCTTTTATCCGTCCG ACATCGCCGTGGAGTGGGAGTCCAA CGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCC GATGGCTCCTTCTTCCTGTACTCCAA GCTGACTGTGGACAAGTCAAGATGG CAGCAGGGAAACGTGTTCTCCTGCT CCGTGATGCACGAAGCGCTGCACAA CCATTACACCCAGAAATCACTGTCA CTTTCGCCGGGAAAA
SEQ ID 2201	QVQLQQWGAGLLKPSETLSLTCAVYG GSFSGYYWSWIRQPPGKGLEWIGEINH SGSTNYNPSLKSRVTISVDTSKNQFSLK LSSVTAADTAVYYCARGRSLPYRGLA PRSFGGYYFDYWGQGTLVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCP APELLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYASTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSL SLSPGK	SEQ ID 2309	CAGGTGCAGCTACAGCAGTGGGGC GCAGGACTGTTGAAGCCTTCGGAGA CCCTGTCCCTCACCTGCGCTGTCTAT GGTGGGTCCTTCAGTGGTTACTACT GGAGCTGGATCCGCCAGCCCCCAGG GAAGGGGCTGGAGTGGATTGGGGA AATCAATCATAGTGGAAGCACCAAC TACAACCCGTCCCTCAAGAGTCGAG TCACCATATCAGTAGACACGTCCAA GAACCAGTTCTCCCTGAAGCTGAGC TCGGTGACCGCCGCGGACACGGCTG TGTATTACTGTGCGAGAGGCCGGTC CCTTCCCTACCGGGGGTTGGCTCCT AGATCTTTCGGAGGATACTACTTTG ACTACTGGGGCCAGGGAACCCTGGT CACCGTCTCCTCAGCATCCACCAAG GGGCCTTCCGTGTTCCCCCTGGCCC CTTCATCCAAGTCGACCTCTGGTGG AACCGCCGCACTCGGTTGCCTGGTC AAAGACTACTTCCCCGAGCCCGTGA CTGTCTCGTGGAACTCGGGCGCCCT CACATCCGGAGTGCATACCTTTCCC GCCGTGTTGCAGTCCAGCGGCCTGT ACAGCCTGAGCTCCGTCGTGACAGT GCCGTCCTCCTCCCTTGGAACCCAG ACCTATATCTGCAACGTCAATCACA AGCCCTCCAACACCAAAGTGGACAA GAAGGTCGAACCCAAGTCCTGCGAC AAGACTCACACCTGTCCGCCTTGTC CAGCCCCTGAGCTGCTGGGTGGTCC GTCCGTGTTCCTCTTCCCGCCCAAGC CGAAGGACACTCTGATGATTTCACG CACCCCGGAAGTCACTTGCGTGGTC GTGGACGTGTCGCACGAAGATCCCG AAGTGAAATTCAATTGGTACGTGGA TGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTA CgccTCTACGTACCGGGTGGTGTCCG TGCTGACCGTGCTGCACCAGGACTG GCTGAACGGAAAGGAGTACAAGTG CAAAGTGTCAAACAAGGCTCTCCCT GCCCCTATCGAAAAGACCATCAGCA AGGCCAAGGGTCAACCTAGGGAGC CCCAGGTCTACACTTTGCCGCCTAG

			CCGGGAAGAAATGACTAAGAACCA AGTGTCCCTGACTTGCCTTGTCAAG GGCTTTTATCCGTCCGACATCGCCG TGGAGTGGGAGTCCAACGGACAAC CGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTC CTTCTTCCTGTACTCCAAGCTGACTG TGGACAAGTCAAGATGGCAGCAGG GAAACGTGTTCTCCTGCTCCGTGAT GCACGAAGCGCTGCACAACCATTAC ACCCAGAAATCACTGTCACTTTCGC CGGGAAAA
SEQ ID 2202	QVQLQESGGGLVRPGGSLRLSCGDSGF NFSGYEMNWVRQAPGKGLEWVSYVS TSGSTRYYADSVKGRFTISRDNAKNTL YLQMNSLRVEDTAVYYCARGRTHWG PQDFDYWGQGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2310	CAGGTGCAGCTGCAGGAGTCGGGG GGAGGCTTGGTACGGCCTGGAGGGT CCCTGAGACTCTCCTGTGGAGACTC TGGATTCAACTTCAGTGGATATGAA ATGAACTGGGTCCGCCAGGCTCCAG GGAAGGGGCTGGAGTGGGTTTCATA CGTCAGTACTAGTGGTAGTACCAGA TACTACGCAGACTCTGTGAAGGGCC GATTTACCATCTCCAGAGACAACGC CAAGAACACCCTGTATTTGCAAATG AACAGTCTGAGAGTCGAGGACACG GCTGTGTATTACTGTGCAAGAGGAC GGACTCACTGGGGCCCCCAGGACTT TGACTACTGGGGCCAGGGAACCCTG GTCACCGTCTCCTCAGCATCCACCA AGGGGCCTTCCGTGTTCCCCCTGGC CCCTTCATCCAAGTCGACCTCTGGT GGAACCGCCGCACTCGGTTGCCTGG TCAAAGACTACTTCCCCGAGCCCGT GACTGTCTCGTGGAACTCGGGCGCC CTCACATCCGGAGTGCATACCTTTC CCGCCGTGTTGCAGTCCAGCGGCCT GTACAGCCTGAGCTCCGTCGTGACA GTGCCGTCCTCCTCCCTTGGAACCC AGACCTATATCTGCAACGTCAATCA CAAGCCCTCCAACACCAAAGTGGAC AAGAAGGTCGAACCCAAGTCCTGCG ACAAGACTCACACCTGTCCGCCTTG TCCAGCCCCTGAGCTGCTGGGTGGT CCGTCCGTGTTCCTCTTCCCGCCCAA GCCGAAGGACACTCTGATGATTTCA CGCACCCCGGAAGTCACTTGCGTGG TCGTGGACGTGTCGCACGAAGATCC CGAAGTGAAATTCAATTGGTACGTG GATGGGGTCGAAGTGCACAACGCC AAGACCAAGCCTAGGGAAGAACAG TACgccTCTACGTACCGGGTGGTGTC CGTGCTGACCGTGCTGCACCAGGAC TGGCTGAACGGAAAGGAGTACAAG TGCAAAGTGTCAAACAAGGCTCTCC CTGCCCCTATCGAAAAGACCATCAG CAAGGCCAAGGGTCAACCTAGGGA GCCCCAGGTCTACACTTTGCCGCCT AGCCGGGAAGAAATGACTAAGAAC

			CAAGTGTCCCTGACTTGCCTTGTCA AGGGCTTTTATCCGTCCGACATCGC CGTGGAGTGGGAGTCCAACGGACA ACCGGAGAACAACTACAAGACCAC CCCACCGGTGCTCGATTCCGATGGC TCCTTCTTCCTGTACTCCAAGCTGAC TGTGGACAAGTCAAGATGGCAGCA GGGAAACGTGTTCTCCTGCTCCGTG ATGCACGAAGCGCTGCACAACCATT ACACCCAGAAATCACTGTCACTTTC GCCGGGAAAA
SEQ ID 2203	QVQLQESGGGLVQPGGSLRLSCAASG FTFSSYAMSWVRQAPGKGLEWVSAIS GSGGSTYYADSVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCAKGGMYYY GSGSSYFDYWGQGTLVTVSSASTKGPS VFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSG LYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCDKTHTCPPCPAPE LLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHN AKTKPREEQYASTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSP GK	SEQ ID 2311	CAGGTGCAGCTGCAGGAGTCGGGG GGAGGCTTGGTACAGCCTGGGGGGT CCCTGAGACTCTCCTGTGCAGCCTC TGGATTCACCTTTAGCAGCTATGCC ATGAGCTGGGTCCGCCAGGCTCCAG GGAAGGGGCTGGAGTGGGTCTCAG CTATTAGTGGTAGTGGTGGTAGCAC ATACTACGCAGACTCCGTGAAGGGC CGGTTCACCATCTCCAGAGACAATT CCAAGAACACGCTGTATCTGCAAAT GAACAGCCTGAGAGCCGAGGACAC GGCCGTATATTACTGTGCGAAAGGA GGAATGTATTACTATGGTTCGGGGA GCTCGTACTTTGACTACTGGGGCCA GGGAACCCTGGTGACCGTCTCCTCA GCATCCACCAAGGGGCCTTCCGTGT TCCCCCTGGCCCCTTCATCCAAGTC GACCTCTGGTGGAACCGCCGCACTC GGTTGCCTGGTCAAAGACTACTTCC CCGAGCCCGTGACTGTCTCGTGGAA CTCGGGCGCCCTCACATCCGGAGTG CATACCTTTCCCGCCGTGTTGCAGTC CAGCGGCCTGTACAGCCTGAGCTCC GTCGTGACAGTGCCGTCCTCCTCCC TTGGAACCCAGACCTATATCTGCAA CGTCAATCACAAGCCCTCCAACACC AAAGTGGACAAGAAGGTCGAACCC AAGTCCTGCGACAAGACTCACACCT GTCCGCCTTGTCCAGCCCCTGAGCT GCTGGGTGGTCCGTCCGTGTTCCTCT TCCCGCCCAAGCCGAAGGACACTCT GATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGC ACGAAGATCCCGAAGTGAAATTCAA TTGGTACGTGGATGGGGTCGAAGTG CACAACGCCAAGACCAAGCCTAGG GAAGAACAGTACgccTCTACGTACCG GGTGGTGTCCGTGCTGACCGTGCTG CACCAGGACTGGCTGAACGGAAAG GAGTACAAGTGCAAAGTGTCAAAC AAGGCTCTCCCTGCCCCTATCGAAA AGACCATCAGCAAGGCCAAGGGTC AACCTAGGGAGCCCCAGGTCTACAC TTTGCCGCCTAGCCGGGAAGAAATG

			ACTAAGAACCAAGTGTCCCTGACTT GCCTTGTCAAGGGCTTTTATCCGTCC GACATCGCCGTGGAGTGGGAGTCCA ACGGACAACCGGAGAACAACTACA AGACCACCCCACCGGTGCTCGATTC CGATGGCTCCTTCTTCCTGTACTCCA AGCTGACTGTGGACAAGTCAAGATG GCAGCAGGGAAACGTGTTCTCCTGC TCCGTGATGCACGAAGCGCTGCACA ACCATTACACCCAGAAATCACTGTC ACTTTCGCCGGGAAAA
SEQ ID 2204	QVQLVQSGGGLVQPGGSLRLSCAASG FTFSSYAMSWVRQAPGKGLEWVSGIS GSGGSTYYADSVKGRFTISRDNSKNM LFLQMNSPRAEDTAVYYCAKKIAAAG KQPVDYWGQGTLVTVSSASTKGPSVF PLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYASTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG K	SEQ ID 2312	CAGGTGCAGCTGGTGCAATCTGGGG GAGGCTTGGTACAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTTAGCAGCTATGCCA TGAGCTGGGTCCGCCAGGCTCCAGG GAAGGGGCTGGAATGGGTCTCAGGT ATTAGTGGTAGTGGTGGTAGCACAT ACTACGCAGACTCCGTGAAGGGCCG GTTCACCATCTCCAGAGACAATTCC AAGAACATGCTGTTTCTGCAAATGA ACAGCCCGAGAGCCGAGGACACGG CCGTATATTACTGTGCGAAGAAAAT AGCAGCAGCTGGTAAGCAACCTGTT GACTACTGGGGCCAGGGAACCCTGG TCACCGTCTCCTCAGCATCCACCAA GGGGCCTTCCGTGTTCCCCCTGGCC CCTTCATCCAAGTCGACCTCTGGTG GAACCGCCGCACTCGGTTGCCTGGT CAAAGACTACTTCCCCGAGCCCGTG ACTGTCTCGTGGAACTCGGGCGCCC TCACATCCGGAGTGCATACCTTTCC CGCCGTGTTGCAGTCCAGCGGCCTG TACAGCCTGAGCTCCGTCGTGACAG TGCCGTCCTCCTCCCTTGGAACCCA GACCTATATCTGCAACGTCAATCAC AAGCCCTCCAACACCAAAGTGGACA AGAAGGTCGAACCCAAGTCCTGCGA CAAGACTCACACCTGTCCGCCTTGT CCAGCCCCTGAGCTGCTGGGTGGTC CGTCCGTGTTCCTCTTCCCGCCCAAG CCGAAGGACACTCTGATGATTTCAC GCACCCCGGAAGTCACTTGCGTGGT CGTGGACGTGTCGCACGAAGATCCC GAAGTGAAATTCAATTGGTACGTGG ATGGGGTCGAAGTGCACAACGCCA AGACCAAGCCTAGGGAAGAACAGT ACgccTCTACGTACCGGGTGGTGTCC GTGCTGACCGTGCTGCACCAGGACT GGCTGAACGGAAAGGAGTACAAGT GCAAAGTGTCAAACAAGGCTCTCCC TGCCCCTATCGAAAAGACCATCAGC AAGGCCAAGGGTCAACCTAGGGAG CCCCAGGTCTACACTTTGCCGCCTA GCCGGGAAGAAATGACTAAGAACC

			AAGTGTCCCTGACTTGCCTTGTCAA GGGCTTTTATCCGTCCGACATCGCC GTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACC CCACCGGTGCTCGATTCCGATGGCT CCTTCTTCCTGTACTCCAAGCTGACT GTGGACAAGTCAAGATGGCAGCAG GGAAACGTGTTCTCCTGCTCCGTGA TGCACGAAGCGCTGCACAACCATTA CACCCAGAAATCACTGTCACTTTCG CCGGGAAAA
SEQ ID 2205	QVQLQQWGAGLLKPSETLSLTCAVYG GSFSGYYWSWIRQPPGKGLEWIGEINH SGSTNYNPSLKSRVTISVDTSKNQFSLK LSSVTAADTAVYYCARRKVYDYVWG SYRLPGSVSYYFDYWGQGTLVTVSSA STKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAP IEKTISKAKGQPREPQVYTLPPSREEMT KNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	SEQ ID 2313	CAGGTGCAGCTACAGCAGTGGGGC GCAGGACTGTTGAAGCCTTCGGAGA CCCTGTCCCTCACCTGCGCTGTCTAT GGTGGGTCCTTCAGTGGTTACTACT GGAGCTGGATCCGCCAGCCCCCAGG GAAGGGGCTGGAGTGGATTGGGGA AATCAATCATAGTGGAAGCACCAAC TACAACCCGTCCCTCAAGAGTCGAG TCACCATATCAGTAGACACGTCCAA GAACCAGTTCTCCCTGAAGCTGAGC TCTGTGACCGCCGCGGACACGGCTG TGTATTACTGTGCGAGAAGGAAGGT GTATGATTACGTTTGGGGGAGTTAT CGCCTCCCCGGGTCGGTATCGTACT ACTTTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTCTCCTCAGCATCC ACCAAGGGGCCTTCCGTGTTCCCCC TGGCCCCTTCATCCAAGTCGACCTC TGGTGGAACCGCCGCACTCGGTTGC CTGGTCAAAGACTACTTCCCCGAGC CCGTGACTGTCTCGTGGAACTCGGG CGCCCTCACATCCGGAGTGCATACC TTTCCCGCCGTGTTGCAGTCCAGCG GCCTGTACAGCCTGAGCTCCGTCGT GACAGTGCCGTCCTCCTCCCTTGGA ACCCAGACCTATATCTGCAACGTCA ATCACAAGCCCTCCAACACCAAAGT GGACAAGAAGGTCGAACCCAAGTC CTGCGACAAGACTCACACCTGTCCG CCTTGTCCAGCCCCTGAGCTGCTGG GTGGTCCGTCCGTGTTCCTCTTCCCG CCCAAGCCGAAGGACACTCTGATGA TTTCACGCACCCCGGAAGTCACTTG CGTGGTCGTGGACGTGTCGCACGAA GATCCCGAAGTGAAATTCAATTGGT ACGTGGATGGGGTCGAAGTGCACA ACGCCAAGACCAAGCCTAGGGAAG AACAGTACgccTCTACGTACCGGGTG GTGTCCGTGCTGACCGTGCTGCACC AGGACTGGCTGAACGGAAAGGAGT ACAAGTGCAAAGTGTCAAACAAGG CTCTCCCTGCCCCTATCGAAAAGAC CATCAGCAAGGCCAAGGGTCAACCT AGGGAGCCCCAGGTCTACACTTTGC

			CGCCTAGCCGGGAAGAAATGACTA AGAACCAAGTGTCCCTGACTTGCCT TGTCAAGGGCTTTTATCCGTCCGAC ATCGCCGTGGAGTGGGAGTCCAACG GACAACCGGAGAACAACTACAAGA CCACCCCACCGGTGCTCGATTCCGA TGGCTCCTTCTTCCTGTACTCCAAGC TGACTGTGGACAAGTCAAGATGGCA GCAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACT TTCGCCGGGAAAA
SEQ ID 2206	QVQLVQSGAEVKKPGESLKISCKGSGY SFTSYWIGWVRQMPGKGLEWMGIIYP GDSDTRYSPSFQGQVTISADKSISTAYL QWSSLKASDTAMYYCARLPGRAARPD YWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVD KKVEPKSCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKP REEQYASTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2314	CAGGTCCAGCTGGTACAGTCTGGAG CAGAGGTGAAAAAGCCCGGGGAGT CTCTGAAGATCTCCTGTAAGGGTTC TGGATACAGCTTTACCAGCTACTGG ATCGGCTGGGTGCGCCAGATGCCCG GGAAAGGCCTGGAGTGGATGGGGA TCATCTATCCTGGTGACTCTGATACC AGATACAGCCCGTCCTTCCAAGGCC AGGTCACCATCTCAGCCGACAAGTC CATCAGCACCGCCTACCTGCAGTGG AGCAGCCTGAAGGCCTCGGACACCG CCATGTATTACTGTGCGAGACTCCC GGGGAGAGCAGCTCGTCCAGACTAC TGGGGCCAGGGCACCCTGGTCACCG TCTCCTCAGCATCCACCAAGGGGCC TTCCGTGTTCCCCCTGGCCCCTTCAT CCAAGTCGACCTCTGGTGGAACCGC CGCACTCGGTTGCCTGGTCAAAGAC TACTTCCCCGAGCCCGTGACTGTCT CGTGGAACTCGGGCGCCCTCACATC CGGAGTGCATACCTTTCCCGCCGTG TTGCAGTCCAGCGGCCTGTACAGCC TGAGCTCCGTCGTGACAGTGCCGTC CTCCTCCCTTGGAACCCAGACCTAT ATCTGCAACGTCAATCACAAGCCCT CCAACACCAAAGTGGACAAGAAGG TCGAACCCAAGTCCTGCGACAAGAC TCACACCTGTCCGCCTTGTCCAGCC CCTGAGCTGCTGGGTGGTCCGTCCG TGTTCCTCTTCCCGCCCAAGCCGAA GGACACTCTGATGATTTCACGCACC CCGGAAGTCACTTGCGTGGTCGTGG ACGTGTCGCACGAAGATCCCGAAGT GAAATTCAATTGGTACGTGGATGGG GTCGAAGTGCACAACGCCAAGACC AAGCCTAGGGAAGAACAGTACgccT CTACGTACCGGGTGGTGTCCGTGCT GACCGTGCTGCACCAGGACTGGCTG AACGGAAAGGAGTACAAGTGCAAA GTGTCAAACAAGGCTCTCCCTGCCC CTATCGAAAAGACCATCAGCAAGGC CAAGGGTCAACCTAGGGAGCCCCA GGTCTACACTTTGCCGCCTAGCCGG

			GAAGAAATGACTAAGAACCAAGTG TCCCTGACTTGCCTTGTCAAGGGCTT TTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCAAGCTGACTGTGGACA AGTCAAGATGGCAGCAGGGAAACG TGTTCTCCTGCTCCGTGATGCACGA AGCGCTGCACAACCATTACACCCAG AAATCACTGTCACTTTCGCCGGGAA AA
SEQ ID 2207	QVTLKESGGGVVQPGRSLRLSCAASGF TFSSYAMHWVRQAPGKGLEWVAVISY DGSNKYYADSVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCARGPGAVA GTKPKYYFDYWGQGTLVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYASTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSL SPGK	SEQ ID 2315	CAGGTCACCTTGAAGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTCAGTAGCTATGCTA TGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTT ATATCATATGATGGAAGTAATAAAT ACTACGCAGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCTGAGGACACGG CTGTGTATTACTGTGCGAGAGGCCC CGGGGCAGTGGCTGGTACTAAGCCA AAGTACTACTTTGACTACTGGGGCC AGGGAACCCTGGTCACCGTCTCCTC AGCATCCACCAAGGGGCCTTCCGTG TTCCCCCTGGCCCCTTCATCCAAGTC GACCTCTGGTGGAACCGCCGCACTC GGTTGCCTGGTCAAAGACTACTTCC CCGAGCCCGTGACTGTCTCGTGGAA CTCGGGCGCCCTCACATCCGGAGTG CATACCTTTCCCGCCGTGTTGCAGTC CAGCGGCCTGTACAGCCTGAGCTCC GTCGTGACAGTGCCGTCCTCCTCCC TTGGAACCCAGACCTATATCTGCAA CGTCAATCACAAGCCCTCCAACACC AAAGTGGACAAGAAGGTCGAACCC AAGTCCTGCGACAAGACTCACACCT GTCCGCCTTGTCCAGCCCCTGAGCT GCTGGGTGGTCCGTCCGTGTTCCTCT TCCCGCCCAAGCCGAAGGACACTCT GATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGC ACGAAGATCCCGAAGTGAAATTCAA TTGGTACGTGGATGGGGTCGAAGTG CACAACGCCAAGACCAAGCCTAGG GAAGAACAGTACgccTCTACGTACCG GGTGGTGTCCGTGCTGACCGTGCTG CACCAGGACTGGCTGAACGGAAAG GAGTACAAGTGCAAAGTGTCAAAC AAGGCTCTCCCTGCCCCTATCGAAA AGACCATCAGCAAGGCCAAGGGTC AACCTAGGGAGCCCCAGGTCTACAC TTTGCCGCCTAGCCGGGAAGAAATG

			ACTAAGAACCAAGTGTCCCTGACTT GCCTTGTCAAGGGCTTTTATCCGTCC GACATCGCCGTGGAGTGGGAGTCCA ACGGACAACCGGAGAACAACTACA AGACCACCCCACCGGTGCTCGATTC CGATGGCTCCTTCTTCCTGTACTCCA AGCTGACTGTGGACAAGTCAAGATG GCAGCAGGGAAACGTGTTCTCCTGC TCCGTGATGCACGAAGCGCTGCACA ACCATTACACCCAGAAATCACTGTC ACTTTCGCCGGGAAAA
SEQ ID 2208	EVQLVQSGGGVVQPGRSLRLSCAASG FTFSSYAMHWVRQAPGKGLEWVAVIS YDGSNKYYADSVKGRFTISRDNSKNT LYLQMNSLRAEDTAVYYCARATYYY DSSGYRFDYWGQGTLVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYASTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSL SPGK	SEQ ID 2316	GAGGTCCAGCTGGTGCAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTCAGTAGCTATGCTA TGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTT ATATCATATGATGGAAGTAATAAAT ACTACGCAGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCTGAGGACACGG CTGTGTATTACTGTGCGAGGGCCAC GTATTACTATGATAGTAGTGGTTAT AGGTTTGACTACTGGGGCCAGGGAA CCCTGGTCACCGTCTCCTCAGCATC CACCAAGGGGCCTTCCGTGTTCCCC CTGGCCCCTTCATCCAAGTCGACCT CTGGTGGAACCGCCGCACTCGGTTG CCTGGTCAAAGACTACTTCCCCGAG CCCGTGACTGTCTCGTGGAACTCGG GCGCCCTCACATCCGGAGTGCATAC CTTTCCCGCCGTGTTGCAGTCCAGC GGCCTGTACAGCCTGAGCTCCGTCG TGACAGTGCCGTCCTCCTCCCTTGG AACCCAGACCTATATCTGCAACGTC AATCACAAGCCCTCCAACACCAAAG TGGACAAGAAGGTCGAACCCAAGT CCTGCGACAAGACTCACACCTGTCC GCCTTGTCCAGCCCCTGAGCTGCTG GGTGGTCCGTCCGTGTTCCTCTTCCC GCCCAAGCCGAAGGACACTCTGATG ATTTCACGCACCCCGGAAGTCACTT GCGTGGTCGTGGACGTGTCGCACGA AGATCCCGAAGTGAAATTCAATTGG TACGTGGATGGGGTCGAAGTGCACA ACGCCAAGACCAAGCCTAGGGAAG AACAGTACgccTCTACGTACCGGGTG GTGTCCGTGCTGACCGTGCTGCACC AGGACTGGCTGAACGGAAAGGAGT ACAAGTGCAAAGTGTCAAACAAGG CTCTCCCTGCCCCTATCGAAAAGAC CATCAGCAAGGCCAAGGGTCAACCT AGGGAGCCCCAGGTCTACACTTTGC CGCCTAGCCGGGAAGAAATGACTA

			AGAACCAAGTGTCCCTGACTTGCCT TGTCAAGGGCTTTTATCCGTCCGAC ATCGCCGTGGAGTGGGAGTCCAACG GACAACCGGAGAACAACTACAAGA CCACCCCACCGGTGCTCGATTCCGA TGGCTCCTTCTTCCTGTACTCCAAGC TGACTGTGGACAAGTCAAGATGGCA GCAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACT TTCGCCGGGAAAA
SEQ ID 2209	EVQLVQSGGGLVEPGGSLRLSCAASRF TFSDAWMSWVRQAPGKGLEWVGRIK SKISGGTTDYAAPVQGRFTISRDDSKN TLYLQMDSLKTEDTAVYYCANRNLGY WGQGTLVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPR EEQYASTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK	SEQ ID 2317	GAGGTCCAGCTGGTACAGTCTGGGG GAGGCTTGGTAGAACCGGGGGGGT CCCTTAGACTCTCCTGTGCAGCCTCT CGATTCACTTTCAGTGACGCCTGGA TGAGCTGGGTCCGCCAGGCTCCAGG TAAGGGGCTGGAGTGGGTTGGCCGT ATTAAAAGCAAAATAAGTGGTGGG ACAACAGACTACGCTGCACCCGTGC AAGGCAGATTCACCATCTCAAGAGA TGATTCAAAAAACACGCTGTATCTG CAAATGGACAGCCTGAAAACCGAG GACACAGCCGTGTATTACTGTGCGA ACCGAAACTTAGGCTACTGGGGCCA GGGCACCCTGGTGACCGTCTCCTCA GCATCCACCAAGGGGCCTTCCGTGT TCCCCCTGGCCCCTTCATCCAAGTC GACCTCTGGTGGAACCGCCGCACTC GGTTGCCTGGTCAAAGACTACTTCC CCGAGCCCGTGACTGTCTCGTGGAA CTCGGGCGCCCTCACATCCGGAGTG CATACCTTTCCCGCCGTGTTGCAGTC CAGCGGCCTGTACAGCCTGAGCTCC GTCGTGACAGTGCCGTCCTCCTCCC TTGGAACCCAGACCTATATCTGCAA CGTCAATCACAAGCCCTCCAACACC AAAGTGGACAAGAAGGTCGAACCC AAGTCCTGCGACAAGACTCACACCT GTCCGCCTTGTCCAGCCCCTGAGCT GCTGGGTGGTCCGTCCGTGTTCCTCT TCCCGCCCAAGCCGAAGGACACTCT GATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGC ACGAAGATCCCGAAGTGAAATTCAA TTGGTACGTGGATGGGGTCGAAGTG CACAACGCCAAGACCAAGCCTAGG GAAGAACAGTACgccTCTACGTACCG GGTGGTGTCCGTGCTGACCGTGCTG CACCAGGACTGGCTGAACGGAAAG GAGTACAAGTGCAAAGTGTCAAAC AAGGCTCTCCCTGCCCCTATCGAAA AGACCATCAGCAAGGCCAAGGGTC AACCTAGGGAGCCCCAGGTCTACAC TTTGCCGCCTAGCCGGGAAGAAATG ACTAAGAACCAAGTGTCCCTGACTT

			GCCTTGTCAAGGGCTTTTATCCGTCC GACATCGCCGTGGAGTGGGAGTCCA ACGGACAACCGGAGAACAACTACA AGACCACCCCACCGGTGCTCGATTC CGATGGCTCCTTCTTCCTGTACTCCA AGCTGACTGTGGACAAGTCAAGATG GCAGCAGGGAAACGTGTTCTCCTGC TCCGTGATGCACGAAGCGCTGCACA ACCATTACACCCAGAAATCACTGTC ACTTTCGCCGGGAAAA
SEQ ID 2210	EVQLVQSGAEVKKPGASVKVSCKASG YTFTSYAMHWVRQAPGQRLEWMGWI NAGNGNTKYSQKFQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARARYYD SSGYIAPSGYFDYWGQGTLVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPP CPAPELLGGPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYASTYRVVSVLT VLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK	SEQ ID 2318	GAGGTCCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTTTCCTGCAAGGCTTCT GGATACACCTTCACTAGCTATGCTA TGCATTGGGTGCGCCAGGCCCCCGG ACAAAGGCTTGAGTGGATGGGATG GATCAACGCTGGCAATGGTAACACA AAATATTCACAGAAGTTCCAGGGCA GAGTCACCATGACCACAGACACATC CACGAGCACAGCCTACATGGAGCTG AGGAGCCTGAGATCTGACGACACG GCCGTGTATTACTGTGCGAGAGCTC GTTACTATGATAGTAGTGGTTATAT TGCCCCATCGGGTTACTTTGACTACT GGGGCCAGGGAACCCTGGTCACCGT CTCCTCAGCATCCACCAAGGGGCCT TCCGTGTTCCCCCTGGCCCCTTCATC CAAGTCGACCTCTGGTGGAACCGCC GCACTCGGTTGCCTGGTCAAAGACT ACTTCCCCGAGCCCGTGACTGTCTC GTGGAACTCGGGCGCCCTCACATCC GGAGTGCATACCTTTCCCGCCGTGT TGCAGTCCAGCGGCCTGTACAGCCT GAGCTCCGTCGTGACAGTGCCGTCC TCCTCCCTTGGAACCCAGACCTATA TCTGCAACGTCAATCACAAGCCCTC CAACACCAAAGTGGACAAGAAGGT CGAACCCAAGTCCTGCGACAAGACT CACACCTGTCCGCCTTGTCCAGCCC CTGAGCTGCTGGGTGGTCCGTCCGT GTTCCTCTTCCCGCCCAAGCCGAAG GACACTCTGATGATTTCACGCACCC CGGAAGTCACTTGCGTGGTCGTGGA CGTGTCGCACGAAGATCCCGAAGTG AAATTCAATTGGTACGTGGATGGGG TCGAAGTGCACAACGCCAAGACCA AGCCTAGGGAAGAACAGTACgccTCT ACGTACCGGGTGGTGTCCGTGCTGA CCGTGCTGCACCAGGACTGGCTGAA CGGAAAGGAGTACAAGTGCAAAGT GTCAAACAAGGCTCTCCCTGCCCCT ATCGAAAAGACCATCAGCAAGGCC AAGGGTCAACCTAGGGAGCCCCAG GTCTACACTTTGCCGCCTAGCCGGG

			AAGAAATGACTAAGAACCAAGTGT CCCTGACTTGCCTTGTCAAGGGCTTT TATCCGTCCGACATCGCCGTGGAGT GGGAGTCCAACGGACAACCGGAGA ACAACTACAAGACCACCCCACCGGT GCTCGATTCCGATGGCTCCTTCTTCC TGTACTCCAAGCTGACTGTGGACAA GTCAAGATGGCAGCAGGGAAACGT GTTCTCCTGCTCCGTGATGCACGAA GCGCTGCACAACCATTACACCCAGA AATCACTGTCACTTTCGCCGGGAAA A
SEQ ID 2211	QVQLVQSGAEVKKPGASVKVSCKASG YTFTSYAMHWVRQAPGQRLEWMGWI NAGNGNTKYSQKFQGRVTITRDTSAST AYMELSSLRSEDTAVYYCARDGPAVD GAEYFQHWGQGTLVTVSSASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYASTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG K	SEQ ID 2319	CAGGTGCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTTTCCTGCAAGGCTTCT GGATACACCTTCACTAGCTATGCTA TGCATTGGGTGCGCCAGGCCCCCGG ACAAAGGCTTGAGTGGATGGGATG GATCAACGCTGGCAATGGTAACACA AAATATTCACAGAAGTTCCAGGGCA GAGTCACCATTACCAGGGACACATC CGCGAGCACAGCCTACATGGAGCTG AGCAGCCTGAGATCTGAAGACACG GCTGTGTATTACTGTGCGAGAGATG GCCCCGCCGTTGATGGTGCTGAATA CTTCCAGCACTGGGGCCAGGGCACC CTGGTCACCGTCTCCTCAGCATCCA CCAAGGGGCCTTCCGTGTTCCCCCT GGCCCCTTCATCCAAGTCGACCTCT GGTGGAACCGCCGCACTCGGTTGCC TGGTCAAAGACTACTTCCCCGAGCC CGTGACTGTCTCGTGGAACTCGGGC GCCCTCACATCCGGAGTGCATACCT TTCCCGCCGTGTTGCAGTCCAGCGG CCTGTACAGCCTGAGCTCCGTCGTG ACAGTGCCGTCCTCCTCCCTTGGAA CCCAGACCTATATCTGCAACGTCAA TCACAAGCCCTCCAACACCAAAGTG GACAAGAAGGTCGAACCCAAGTCCT GCGACAAGACTCACACCTGTCCGCC TTGTCCAGCCCCTGAGCTGCTGGGT GGTCCGTCCGTGTTCCTCTTCCCGCC CAAGCCGAAGGACACTCTGATGATT TCACGCACCCCGGAAGTCACTTGCG TGGTCGTGGACGTGTCGCACGAAGA TCCCGAAGTGAAATTCAATTGGTAC GTGGATGGGGTCGAAGTGCACAAC GCCAAGACCAAGCCTAGGGAAGAA CAGTACgccTCTACGTACCGGGTGGT GTCCGTGCTGACCGTGCTGCACCAG GACTGGCTGAACGGAAAGGAGTAC AAGTGCAAAGTGTCAAACAAGGCTC TCCCTGCCCCTATCGAAAAGACCAT CAGCAAGGCCAAGGGTCAACCTAG GGAGCCCCAGGTCTACACTTTGCCG CCTAGCCGGGAAGAAATGACTAAG

			AACCAAGTGTCCCTGACTTGCCTTG TCAAGGGCTTTTATCCGTCCGACAT CGCCGTGGAGTGGGAGTCCAACGG ACAACCGGAGAACAACTACAAGAC CACCCCACCGGTGCTCGATTCCGAT GGCTCCTTCTTCCTGTACTCCAAGCT GACTGTGGACAAGTCAAGATGGCA GCAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACT TTCGCCGGGAAAA
SEQ ID 2212	QLQLQESGPGLVKPSQTLSLTCAISGDS VSSNSAAWNWIRQSPSRGLEWLGRTY YRSKWYNDYAVSLKSRITINPDTSKNQ FSLQLNSVTPEDTAVYYCASLASGSPP PGDYWGQGTLVTVSSASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2320	CAGCTGCAGCTGCAGGAGTCGGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCAACAGTGC TGCTTGGAACTGGATCAGGCAGTCC CCATCGCGAGGCCTTGAGTGGCTGG GAAGGACTTACTACAGGTCCAAGTG GTATAATGATTATGCAGTATCTCTG AAAAGTCGAATAACCATCAACCCGG ACACATCCAAGAACCAGTTCTCCCT GCAGCTGAACTCTGTGACTCCCGAG GACACGGCTGTATATTACTGTGCAA GTTTGGCGAGTGGTTCCCCCCCTCC GGGGGACTACTGGGGCCAGGGAAC CCTGGTGACCGTCTCCTCAGCATCC ACCAAGGGGCCTTCCGTGTTCCCCC TGGCCCCTTCATCCAAGTCGACCTC TGGTGGAACCGCCGCACTCGGTTGC CTGGTCAAAGACTACTTCCCCGAGC CCGTGACTGTCTCGTGGAACTCGGG CGCCCTCACATCCGGAGTGCATACC TTTCCCGCCGTGTTGCAGTCCAGCG GCCTGTACAGCCTGAGCTCCGTCGT GACAGTGCCGTCCTCCTCCCTTGGA ACCCAGACCTATATCTGCAACGTCA ATCACAAGCCCTCCAACACCAAAGT GGACAAGAAGGTCGAACCCAAGTC CTGCGACAAGACTCACACCTGTCCG CCTTGTCCAGCCCCTGAGCTGCTGG GTGGTCCGTCCGTGTTCCTCTTCCCG CCCAAGCCGAAGGACACTCTGATGA TTTCACGCACCCCGGAAGTCACTTG CGTGGTCGTGGACGTGTCGCACGAA GATCCCGAAGTGAAATTCAATTGGT ACGTGGATGGGGTCGAAGTGCACA ACGCCAAGACCAAGCCTAGGGAAG AACAGTACgccTCTACGTACCGGGTG GTGTCCGTGCTGACCGTGCTGCACC AGGACTGGCTGAACGGAAAGGAGT ACAAGTGCAAAGTGTCAAACAAGG CTCTCCCTGCCCCTATCGAAAAGAC CATCAGCAAGGCCAAGGGTCAACCT AGGGAGCCCCAGGTCTACACTTTGC CGCCTAGCCGGGAAGAAATGACTA

			AGAACCAAGTGTCCCTGACTTGCCT TGTCAAGGGCTTTTATCCGTCCGAC ATCGCCGTGGAGTGGGAGTCCAACG GACAACCGGAGAACAACTACAAGA CCACCCCACCGGTGCTCGATTCCGA TGGCTCCTTCTTCCTGTACTCCAAGC TGACTGTGGACAAGTCAAGATGGCA GCAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACT TTCGCCGGGAAAA
SEQ ID 2213	QVTLKESGGGVVQPGRSLRLSCAASGF TFSTYGMHWVRQAPGKGLEWVALISY DGSKKYYANSVKGRFTISRDNSKNTL YLQMKSLRAEDTAMYYCAKGPIVGAT MDYWGQGALVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTK PREEQYASTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2321	CAGGTCACCTTGAAGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTCAGTACCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCACTT ATATCATATGATGGAAGTAAAAAAT ACTATGCAAACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCC AAGAACACGTTGTATCTGCAAATGA AAAGTCTGAGAGCTGAGGACACGG CTATGTATTACTGTGCGAAAGGCCC TATAGTGGGAGCGACTATGGACTAC TGGGGCCAGGGAGCCCTGGTCACCG TCTCCTCAGCATCCACCAAGGGGCC TTCCGTGTTCCCCCTGGCCCCTTCAT CCAAGTCGACCTCTGGTGGAACCGC CGCACTCGGTTGCCTGGTCAAAGAC TACTTCCCCGAGCCCGTGACTGTCT CGTGGAACTCGGGCGCCCTCACATC CGGAGTGCATACCTTTCCCGCCGTG TTGCAGTCCAGCGGCCTGTACAGCC TGAGCTCCGTCGTGACAGTGCCGTC CTCCTCCCTTGGAACCCAGACCTAT ATCTGCAACGTCAATCACAAGCCCT CCAACACCAAAGTGGACAAGAAGG TCGAACCCAAGTCCTGCGACAAGAC TCACACCTGTCCGCCTTGTCCAGCC CCTGAGCTGCTGGGTGGTCCGTCCG TGTTCCTCTTCCCGCCCAAGCCGAA GGACACTCTGATGATTTCACGCACC CCGGAAGTCACTTGCGTGGTCGTGG ACGTGTCGCACGAAGATCCCGAAGT GAAATTCAATTGGTACGTGGATGGG GTCGAAGTGCACAACGCCAAGACC AAGCCTAGGGAAGAACAGTACgccT CTACGTACCGGGTGGTGTCCGTGCT GACCGTGCTGCACCAGGACTGGCTG AACGGAAAGGAGTACAAGTGCAAA GTGTCAAACAAGGCTCTCCCTGCCC CTATCGAAAAGACCATCAGCAAGGC CAAGGGTCAACCTAGGGAGCCCCA GGTCTACACTTTGCCGCCTAGCCGG GAAGAAATGACTAAGAACCAAGTG

			TCCCTGACTTGCCTTGTCAAGGGCTT TTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCAAGCTGACTGTGGACA AGTCAAGATGGCAGCAGGGAAACG TGTTCTCCTGCTCCGTGATGCACGA AGCGCTGCACAACCATTACACCCAG AAATCACTGTCACTTTCGCCGGGAA AA
SEQ ID 2214	EVQLVQSGAEVKKPGSSVKVSCKASG GTFSSYAISWVRQAPGQGLEWMGWIS AYNGNTNYAQKLQGRVTMTTDTSTST AYMELRSLRSDDTAVYYCARWYGDY GLDYWGQGTLVTVSSASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2322	GAGGTGCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGTCCTC GGTGAAGGTCTCCTGCAAGGCTTCT GGAGGCACCTTCAGCAGCTATGCTA TCAGCTGGGTGCGACAGGCCCCTGG ACAAGGGCTTGAGTGGATGGGATG GATCAGCGCTTACAATGGTAACACA AACTATGCACAGAAGCTCCAGGGCA GAGTCACCATGACCACAGACACATC CACGAGCACAGCCTACATGGAGCTG AGGAGCCTGAGATCTGACGACACG GCCGTGTATTACTGTGCGAGATGGT ACGGTGACTACGGCCTTGACTACTG GGGCCAGGGAACCCTGGTCACCGTC TCCTCAGCATCCACCAAGGGGCCTT CCGTGTTCCCCCTGGCCCCTTCATCC AAGTCGACCTCTGGTGGAACCGCCG CACTCGGTTGCCTGGTCAAAGACTA CTTCCCCGAGCCCGTGACTGTCTCG TGGAACTCGGGCGCCCTCACATCCG GAGTGCATACCTTTCCCGCCGTGTT GCAGTCCAGCGGCCTGTACAGCCTG AGCTCCGTCGTGACAGTGCCGTCCT CCTCCCTTGGAACCCAGACCTATAT CTGCAACGTCAATCACAAGCCCTCC AACACCAAAGTGGACAAGAAGGTC GAACCCAAGTCCTGCGACAAGACTC ACACCTGTCCGCCTTGTCCAGCCCC TGAGCTGCTGGGTGGTCCGTCCGTG TTCCTCTTCCCGCCCAAGCCGAAGG ACACTCTGATGATTTCACGCACCCC GGAAGTCACTTGCGTGGTCGTGGAC GTGTCGCACGAAGATCCCGAAGTGA AATTCAATTGGTACGTGGATGGGGT CGAAGTGCACAACGCCAAGACCAA GCCTAGGGAAGAACAGTACgccTCTA CGTACCGGGTGGTGTCCGTGCTGAC CGTGCTGCACCAGGACTGGCTGAAC GGAAAGGAGTACAAGTGCAAAGTG TCAAACAAGGCTCTCCCTGCCCCTA TCGAAAAGACCATCAGCAAGGCCA AGGGTCAACCTAGGGAGCCCCAGGT CTACACTTTGCCGCCTAGCCGGGAA GAAATGACTAAGAACCAAGTGTCCC

			TGACTTGCCTTGTCAAGGGCTTTTAT CCGTCCGACATCGCCGTGGAGTGGG AGTCCAACGGACAACCGGAGAACA ACTACAAGACCACCCCACCGGTGCT CGATTCCGATGGCTCCTTCTTCCTGT ACTCCAAGCTGACTGTGGACAAGTC AAGATGGCAGCAGGGAAACGTGTT CTCCTGCTCCGTGATGCACGAAGCG CTGCACAACCATTACACCCAGAAAT CACTGTCACTTTCGCCGGGAAAA
SEQ ID 2215	EVQLVQSGAEVKKPGASVKVSCKASG YTFTSYAMHWVRQAPGQRLAWMGWI NAGNGNTKYSEKFEGRVTITRDTSAST AYMELSSLRSEDTAVYYCARVAKYYY ESGGYRASNWFDPWGQGTLVTVSSAS TKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVL TVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMT KNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	SEQ ID 2323	GAGGTCCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTTTCCTGCAAGGCTTCT GGATACACCTTCACTAGCTATGCTA TGCATTGGGTGCGCCAGGCCCCCGG ACAAAGGCTTGCGTGGATGGGATGG ATCAACGCTGGCAATGGTAACACAA AATATTCAGAGAAGTTCGAAGGCAG AGTCACCATCACCAGGGACACATCC GCGAGCACAGCCTACATGGAGCTGA GCAGCCTGAGATCTGAAGACACGGC TGTGTATTACTGTGCGAGGGTCGCC AAATATTATTACGAGAGTGGTGGTT ATCGGGCCTCCAACTGGTTCGACCC CTGGGGCCAGGGCACCCTGGTCACC GTCTCCTCAGCATCCACCAAGGGGC CTTCCGTGTTCCCCCTGGCCCCTTCA TCCAAGTCGACCTCTGGTGGAACCG CCGCACTCGGTTGCCTGGTCAAAGA CTACTTCCCCGAGCCCGTGACTGTC TCGTGGAACTCGGGCGCCCTCACAT CCGGAGTGCATACCTTTCCCGCCGT GTTGCAGTCCAGCGGCCTGTACAGC CTGAGCTCCGTCGTGACAGTGCCGT CCTCCTCCCTTGGAACCCAGACCTA TATCTGCAACGTCAATCACAAGCCC TCCAACACCAAAGTGGACAAGAAG GTCGAACCCAAGTCCTGCGACAAGA CTCACACCTGTCCGCCTTGTCCAGC CCCTGAGCTGCTGGGTGGTCCGTCC GTGTTCCTCTTCCCGCCCAAGCCGA AGGACACTCTGATGATTTCACGCAC CCCGGAAGTCACTTGCGTGGTCGTG GACGTGTCGCACGAAGATCCCGAAG TGAAATTCAATTGGTACGTGGATGG GGTCGAAGTGCACAACGCCAAGAC CAAGCCTAGGGAAGAACAGTACgcc TCTACGTACCGGGTGGTGTCCGTGC TGACCGTGCTGCACCAGGACTGGCT GAACGGAAAGGAGTACAAGTGCAA AGTGTCAAACAAGGCTCTCCCTGCC CCTATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTACACTTTGCCGCCTAGCCGG

			GAAGAAATGACTAAGAACCAAGTG TCCCTGACTTGCCTTGTCAAGGGCTT TTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCAAGCTGACTGTGGACA AGTCAAGATGGCAGCAGGGAAACG TGTTCTCCTGCTCCGTGATGCACGA AGCGCTGCACAACCATTACACCCAG AAATCACTGTCACTTTCGCCGGGAA AA
SEQ ID 2216	QVQLQESGPGLVKPSQTLSLTCAISGD SVSSNSAAWNWIRQSPSRGLEWLGRT YYRSKWYNDYAVSVKSRITINPDTSKN QFSLQLNSVTPEDTAVYYCARAPPPTV GWYAPVFDYWGQGTLVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYASTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSL SPGK	SEQ ID 2324	CAGGTGCAGCTGCAGGAGTCAGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCAACAGTGC TGCTTGGAACTGGATCAGGCAGTCC CCATCGAGAGGCCTTGAGTGGCTGG GAAGGACATACTACAGGTCCAAGTG GTATAATGATTATGCAGTATCTGTG AAAAGTCGAATAACCATCAACCCAG ACACATCCAAGAACCAGTTCTCCCT GCAGCTGAACTCTGTGACTCCCGAG GACACGGCTGTGTATTACTGTGCAA GAGCGCCCCCTCCGACTGTTGGCTG GTACGCCCCCGTCTTTGACTACTGG GGCCAGGGAACCCTGGTCACCGTCT CCTCAGCATCCACCAAGGGGCCTTC CGTGTTCCCCCTGGCCCCTTCATCCA AGTCGACCTCTGGTGGAACCGCCGC ACTCGGTTGCCTGGTCAAAGACTAC TTCCCCGAGCCCGTGACTGTCTCGT GGAACTCGGGCGCCCTCACATCCGG AGTGCATACCTTTCCCGCCGTGTTG CAGTCCAGCGGCCTGTACAGCCTGA GCTCCGTCGTGACAGTGCCGTCCTC CTCCCTTGGAACCCAGACCTATATC TGCAACGTCAATCACAAGCCCTCCA ACACCAAAGTGGACAAGAAGGTCG AACCCAAGTCCTGCGACAAGACTCA CACCTGTCCGCCTTGTCCAGCCCCT GAGCTGCTGGGTGGTCCGTCCGTGT TCCTCTTCCCGCCCAAGCCGAAGGA CACTCTGATGATTTCACGCACCCCG GAAGTCACTTGCGTGGTCGTGGACG TGTCGCACGAAGATCCCGAAGTGAA ATTCAATTGGTACGTGGATGGGGTC GAAGTGCACAACGCCAAGACCAAG CCTAGGGAAGAACAGTACgccTCTAC GTACCGGGTGGTGTCCGTGCTGACC GTGCTGCACCAGGACTGGCTGAACG GAAAGGAGTACAAGTGCAAAGTGT CAAACAAGGCTCTCCCTGCCCCTAT CGAAAAGACCATCAGCAAGGCCAA GGGTCAACCTAGGGAGCCCCAGGTC TACACTTTGCCGCCTAGCCGGGAAG

			AAATGACTAAGAACCAAGTGTCCCT GACTTGCCTTGTCAAGGGCTTTTATC CGTCCGACATCGCCGTGGAGTGGGA GTCCAACGGACAACCGGAGAACAA CTACAAGACCACCCCACCGGTGCTC GATTCCGATGGCTCCTTCTTCCTGTA CTCCAAGCTGACTGTGGACAAGTCA AGATGGCAGCAGGGAAACGTGTTCT CCTGCTCCGTGATGCACGAAGCGCT GCACAACCATTACACCCAGAAATCA CTGTCACTTTCGCCGGGAAAA
SEQ ID 2217	QLQLQESGGGLVQPGGSLRLSCSASGI SFRDYWMHWIRQTPGKGLVWVSRINP DGSSTSYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKVTGRRVG AHDYWGQGTLVTVSSASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2325	CAGCTGCAGCTGCAGGAGTCCGGGG GAGGCTTAGTTCAGCCGGGGGGGTC CCTGAGACTCTCCTGCTCAGCCTCT GGAATCAGCTTCAGAGATTACTGGA TGCACTGGATCCGCCAAACTCCAGG GAAGGGGCTGGTGTGGGTCTCACGT ATTAATCCTGATGGGAGTAGCACAA GCTACGCGGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCTGAGGACACGG CTGTGTATTACTGTGCGAAAGTTAC GGGACGGAGAGTGGGAGCCCATGA CTACTGGGGCCAGGGAACCCTGGTC ACCGTCTCCTCAGCATCCACCAAGG GGCCTTCCGTGTTCCCCCTGGCCCCT TCATCCAAGTCGACCTCTGGTGGAA CCGCCGCACTCGGTTGCCTGGTCAA AGACTACTTCCCCGAGCCCGTGACT GTCTCGTGGAACTCGGGCGCCCTCA CATCCGGAGTGCATACCTTTCCCGC CGTGTTGCAGTCCAGCGGCCTGTAC AGCCTGAGCTCCGTCGTGACAGTGC CGTCCTCCTCCCTTGGAACCCAGAC CTATATCTGCAACGTCAATCACAAG CCCTCCAACACCAAAGTGGACAAGA AGGTCGAACCCAAGTCCTGCGACAA GACTCACACCTGTCCGCCTTGTCCA GCCCCTGAGCTGCTGGGTGGTCCGT CCGTGTTCCTCTTCCCGCCCAAGCC GAAGGACACTCTGATGATTTCACGC ACCCCGGAAGTCACTTGCGTGGTCG TGGACGTGTCGCACGAAGATCCCGA AGTGAAATTCAATTGGTACGTGGAT GGGGTCGAAGTGCACAACGCCAAG ACCAAGCCTAGGGAAGAACAGTACg ccTCTACGTACCGGGTGGTGTCCGTG CTGACCGTGCTGCACCAGGACTGGC TGAACGGAAAGGAGTACAAGTGCA AAGTGTCAAACAAGGCTCTCCCTGC CCCTATCGAAAAGACCATCAGCAAG GCCAAGGGTCAACCTAGGGAGCCCC AGGTCTACACTTTGCCGCCTAGCCG GGAAGAAATGACTAAGAACCAAGT

			GTCCCTGACTTGCCTTGTCAAGGGC TTTTATCCGTCCGACATCGCCGTGG AGTGGGAGTCCAACGGACAACCGG AGAACAACTACAAGACCACCCCACC GGTGCTCGATTCCGATGGCTCCTTCT TCCTGTACTCCAAGCTGACTGTGGA CAAGTCAAGATGGCAGCAGGGAAA CGTGTTCTCCTGCTCCGTGATGCAC GAAGCGCTGCACAACCATTACACCC AGAAATCACTGTCACTTTCGCCGGG AAAA
SEQ ID 2218	QVQLVQSGAEVKKPGASVKVSCKASG YTFTGYYMHWVRQAPGQGLEWMGW INPNSGGTNYAQKFQGRVTMTRDTSIS TAYMELSRLRSDDTAVYYCAFAQPGA ETLNFDLWGRGTLVTVSSASTKGPSVF PLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYASTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG K	SEQ ID 2326	CAGGTGCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTCTCCTGCAAGGCTTCT GGATACACCTTCACCGGCTACTATA TGCACTGGGTGCGACAGGCCCCTGG ACAAGGGCTTGAGTGGATGGGATG GATCAACCCTAACAGTGGTGGCACA AACTATGCACAGAAGTTTCAGGGCA GGGTCACCATGACCAGGGACACGTC CATCAGCACAGCCTACATGGAGCTG AGCAGGCTGAGATCTGACGACACG GCCGTGTATTACTGTGCCTTTGCCCA GCCGGGCGCTGAGACGTTGAACTTC GATCTCTGGGGCCGTGGCACCCTGG TCACCGTCTCCTCAGCATCCACCAA GGGGCCTTCCGTGTTCCCCCTGGCC CCTTCATCCAAGTCGACCTCTGGTG GAACCGCCGCACTCGGTTGCCTGGT CAAAGACTACTTCCCCGAGCCCGTG ACTGTCTCGTGGAACTCGGGCGCCC TCACATCCGGAGTGCATACCTTTCC CGCCGTGTTGCAGTCCAGCGGCCTG TACAGCCTGAGCTCCGTCGTGACAG TGCCGTCCTCCTCCCTTGGAACCCA GACCTATATCTGCAACGTCAATCAC AAGCCCTCCAACACCAAAGTGGACA AGAAGGTCGAACCCAAGTCCTGCGA CAAGACTCACACCTGTCCGCCTTGT CCAGCCCCTGAGCTGCTGGGTGGTC CGTCCGTGTTCCTCTTCCCGCCCAAG CCGAAGGACACTCTGATGATTTCAC GCACCCCGGAAGTCACTTGCGTGGT CGTGGACGTGTCGCACGAAGATCCC GAAGTGAAATTCAATTGGTACGTGG ATGGGGTCGAAGTGCACAACGCCA AGACCAAGCCTAGGGAAGAACAGT ACgccTCTACGTACCGGGTGGTGTCC GTGCTGACCGTGCTGCACCAGGACT GGCTGAACGGAAAGGAGTACAAGT GCAAAGTGTCAAACAAGGCTCTCCC TGCCCCTATCGAAAAGACCATCAGC AAGGCCAAGGGTCAACCTAGGGAG CCCCAGGTCTACACTTTGCCGCCTA GCCGGGAAGAAATGACTAAGAACC

			AAGTGTCCCTGACTTGCCTTGTCAA GGGCTTTTATCCGTCCGACATCGCC GTGGAGTGGGAGTCCAACGGACAA CCGGAGAACAACTACAAGACCACC CCACCGGTGCTCGATTCCGATGGCT CCTTCTTCCTGTACTCCAAGCTGACT GTGGACAAGTCAAGATGGCAGCAG GGAAACGTGTTCTCCTGCTCCGTGA TGCACGAAGCGCTGCACAACCATTA CACCCAGAAATCACTGTCACTTTCG CCGGGAAAA
SEQ ID 2219	QVQLQQSGPGLVKPSQTLSLTCAISGD SVSSKSAAWNWIRQSPSRGLEWLGRT YYRSKWNNDYALSVKSRITINPDTSKN QFSLQLKSVTPEDTALYYCVRQVAGG MDVWGQGTTVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTK PREEQYASTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2327	CAGGTACAGCTGCAGCAGTCAGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCAAAAGTGC TGCTTGGAACTGGATCAGGCAGTCC CCATCGAGAGGCCTTGAGTGGCTGG GAAGGACATACTACAGGTCCAAATG GAATAATGATTATGCATTATCTGTG AAAAGTCGAATAACCATCAACCCAG ACACATCCAAGAACCAGTTCTCCCT GCAGCTGAAGTCTGTGACTCCCGAG GACACGGCTCTGTATTACTGTGTAA GACAAGTCGCGGGCGGTATGGACGT CTGGGGCCAAGGGACCACGGTCACC GTCTCCTCAGCATCCACCAAGGGGC CTTCCGTGTTCCCCCTGGCCCCTTCA TCCAAGTCGACCTCTGGTGGAACCG CCGCACTCGGTTGCCTGGTCAAAGA CTACTTCCCCGAGCCCGTGACTGTC TCGTGGAACTCGGGCGCCCTCACAT CCGGAGTGCATACCTTTCCCGCCGT GTTGCAGTCCAGCGGCCTGTACAGC CTGAGCTCCGTCGTGACAGTGCCGT CCTCCTCCCTTGGAACCCAGACCTA TATCTGCAACGTCAATCACAAGCCC TCCAACACCAAAGTGGACAAGAAG GTCGAACCCAAGTCCTGCGACAAGA CTCACACCTGTCCGCCTTGTCCAGC CCCTGAGCTGCTGGGTGGTCCGTCC GTGTTCCTCTTCCCGCCCAAGCCGA AGGACACTCTGATGATTTCACGCAC CCCGGAAGTCACTTGCGTGGTCGTG GACGTGTCGCACGAAGATCCCGAAG TGAAATTCAATTGGTACGTGGATGG GGTCGAAGTGCACAACGCCAAGAC CAAGCCTAGGGAAGAACAGTACgcc TCTACGTACCGGGTGGTGTCCGTGC TGACCGTGCTGCACCAGGACTGGCT GAACGGAAAGGAGTACAAGTGCAA AGTGTCAAACAAGGCTCTCCCTGCC CCTATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTACACTTTGCCGCCTAGCCGG GAAGAAATGACTAAGAACCAAGTG

			TCCCTGACTTGCCTTGTCAAGGGCTT TTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCAAGCTGACTGTGGACA AGTCAAGATGGCAGCAGGGAAACG TGTTCTCCTGCTCCGTGATGCACGA AGCGCTGCACAACCATTACACCCAG AAATCACTGTCACTTTCGCCGGGAA AA
SEQ ID 2220	QVQLVQSGGGLVQPGRSLRLSCTASGF TFGDYAMSWFRQAPGKGLEWVSAISG SGGSTYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKGSVYSGSY YMLIDYWGQGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2328	CAGGTGCAGCTGGTGCAATCTGGGG GAGGCTTGGTACAGCCAGGGCGGTC CCTGAGACTCTCCTGTACAGCTTCT GGATTCACCTTTGGTGATTATGCTAT GAGCTGGTTCCGCCAGGCTCCAGGG AAGGGGCTGGAGTGGGTCTCAGCTA TTAGTGGTAGTGGTGGTAGCACATA CTATGCAGACTCCGTGAAGGGCCGA TTCACCATCTCCAGAGACAATTCCA AGAACACGCTGTATCTGCAAATGAA CAGCCTGAGAGCTGAGGACACGGCT GTGTATTACTGTGCGAAAGGATCGG TATATAGTGGGAGCTACTATATGCT CATTGACTACTGGGGCCAGGGCACC CTGGTCACCGTCTCCTCAGCATCCA CCAAGGGGCCTTCCGTGTTCCCCCT GGCCCCTTCATCCAAGTCGACCTCT GGTGGAACCGCCGCACTCGGTTGCC TGGTCAAAGACTACTTCCCCGAGCC CGTGACTGTCTCGTGGAACTCGGGC GCCCTCACATCCGGAGTGCATACCT TTCCCGCCGTGTTGCAGTCCAGCGG CCTGTACAGCCTGAGCTCCGTCGTG ACAGTGCCGTCCTCCTCCCTTGGAA CCCAGACCTATATCTGCAACGTCAA TCACAAGCCCTCCAACACCAAAGTG GACAAGAAGGTCGAACCCAAGTCCT GCGACAAGACTCACACCTGTCCGCC TTGTCCAGCCCCTGAGCTGCTGGGT GGTCCGTCCGTGTTCCTCTTCCCGCC CAAGCCGAAGGACACTCTGATGATT TCACGCACCCCGGAAGTCACTTGCG TGGTCGTGGACGTGTCGCACGAAGA TCCCGAAGTGAAATTCAATTGGTAC GTGGATGGGGTCGAAGTGCACAAC GCCAAGACCAAGCCTAGGGAAGAA CAGTACgccTCTACGTACCGGGTGGT GTCCGTGCTGACCGTGCTGCACCAG GACTGGCTGAACGGAAAGGAGTAC AAGTGCAAAGTGTCAAACAAGGCTC TCCCTGCCCCTATCGAAAAGACCAT CAGCAAGGCCAAGGGTCAACCTAG GGAGCCCCAGGTCTACACTTTGCCG CCTAGCCGGGAAGAAATGACTAAG

			AACCAAGTGTCCCTGACTTGCCTTG TCAAGGGCTTTTATCCGTCCGACAT CGCCGTGGAGTGGGAGTCCAACGG ACAACCGGAGAACAACTACAAGAC CACCCCACCGGTGCTCGATTCCGAT GGCTCCTTCTTCCTGTACTCCAAGCT GACTGTGGACAAGTCAAGATGGCA GCAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACT TTCGCCGGGAAAA
SEQ ID 2221	QVQLQQSGPGLVRPSQTLSLTCVISGD SVSSGSAAWNWIRQSPSRGLEWLGRT YYRAKWYNEYAGSVKSRITISPDTSKN QFSLQLNSVTPEDTAVYFCTRQDKDNT RYSGLGVWGQGTTVTVSSASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYASTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG K	SEQ ID 2329	CAGGTACAGCTGCAGCAGTCAGGTC CAGGACTGGTGAGGCCCTCGCAGAC CCTCTCACTCACCTGTGTCATCTCCG GGGACAGTGTCTCTAGCGGCAGTGC TGCTTGGAACTGGATCAGGCAGTCC CCATCGAGAGGCCTTGAGTGGCTGG GAAGGACATATTATAGGGCCAAGTG GTATAATGAATATGCAGGGTCTGTG AAAAGCCGAATAACCATCAGTCCGG ACACATCCAAGAACCAGTTCTCCCT GCAACTGAACTCTGTGACTCCCGAG GACACGGCTGTGTATTTCTGTACAA GACAAGACAAAGACAACACGAGAT ATTCCGGTTTGGGCGTCTGGGGCCA AGGGACCACGGTGACCGTCTCCTCA GCATCCACCAAGGGGCCTTCCGTGT TCCCCCTGGCCCCTTCATCCAAGTC GACCTCTGGTGGAACCGCCGCACTC GGTTGCCTGGTCAAAGACTACTTCC CCGAGCCCGTGACTGTCTCGTGGAA CTCGGGCGCCCTCACATCCGGAGTG CATACCTTTCCCGCCGTGTTGCAGTC CAGCGGCCTGTACAGCCTGAGCTCC GTCGTGACAGTGCCGTCCTCCTCCC TTGGAACCCAGACCTATATCTGCAA CGTCAATCACAAGCCCTCCAACACC AAAGTGGACAAGAAGGTCGAACCC AAGTCCTGCGACAAGACTCACACCT GTCCGCCTTGTCCAGCCCCTGAGCT GCTGGGTGGTCCGTCCGTGTTCCTCT TCCCGCCCAAGCCGAAGGACACTCT GATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGC ACGAAGATCCCGAAGTGAAATTCAA TTGGTACGTGGATGGGGTCGAAGTG CACAACGCCAAGACCAAGCCTAGG GAAGAACAGTACgccTCTACGTACCG GGTGGTGTCCGTGCTGACCGTGCTG CACCAGGACTGGCTGAACGGAAAG GAGTACAAGTGCAAAGTGTCAAAC AAGGCTCTCCCTGCCCCTATCGAAA AGACCATCAGCAAGGCCAAGGGTC AACCTAGGGAGCCCCAGGTCTACAC TTTGCCGCCTAGCCGGGAAGAAATG

			ACTAAGAACCAAGTGTCCCTGACTT GCCTTGTCAAGGGCTTTTATCCGTCC GACATCGCCGTGGAGTGGGAGTCCA ACGGACAACCGGAGAACAACTACA AGACCACCCCACCGGTGCTCGATTC CGATGGCTCCTTCTTCCTGTACTCCA AGCTGACTGTGGACAAGTCAAGATG GCAGCAGGGAAACGTGTTCTCCTGC TCCGTGATGCACGAAGCGCTGCACA ACCATTACACCCAGAAATCACTGTC ACTTTCGCCGGGAAAA
SEQ ID 2222	EVQLVETGGGLVQPGGSLRLSCAASEF TLRNYGVSWVRQAPGKGLEWVSGMS GSGYSTYYADSVKGRFTISRDSSKNTL FLQMDSLRAEDTAIYYCARGPRMWSS GIDAFDIWGHGTMVTVSSASTKGPSVF PLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYASTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG K	SEQ ID 2330	GAGGTGCAGCTGGTGGAGACCGGG GGAGGCTTAGTTCAGCCTGGGGGGT CCCTGAGACTCTCCTGTGCAGCCTC TGAATTCACCCTTAGGAACTATGGC GTGAGCTGGGTCCGCCAGGCTCCAG GGAAGGGGCTGGAGTGGGTCTCAG GTATGAGTGGTAGTGGTTATAGTAC ATACTACGCAGACTCCGTGAAGGGC CGGTTCACCATCTCCAGAGACAGTT CCAAGAACACGCTGTTTCTGCAAAT GGACAGCCTGAGAGCCGAGGACAC GGCCATATATTACTGTGCGAGAGGG CCCCGAATGTGGAGCAGTGGCATTG ATGCTTTTGATATCTGGGGCCACGG GACAATGGTGACCGTCTCTTCAGCA TCCACCAAGGGGCCTTCCGTGTTCC CCCTGGCCCCTTCATCCAAGTCGAC CTCTGGTGGAACCGCCGCACTCGGT TGCCTGGTCAAAGACTACTTCCCCG AGCCCGTGACTGTCTCGTGGAACTC GGGCGCCCTCACATCCGGAGTGCAT ACCTTTCCCGCCGTGTTGCAGTCCA GCGGCCTGTACAGCCTGAGCTCCGT CGTGACAGTGCCGTCCTCCTCCCTT GGAACCCAGACCTATATCTGCAACG TCAATCACAAGCCCTCCAACACCAA AGTGGACAAGAAGGTCGAACCCAA GTCCTGCGACAAGACTCACACCTGT CCGCCTTGTCCAGCCCCTGAGCTGC TGGGTGGTCCGTCCGTGTTCCTCTTC CCGCCCAAGCCGAAGGACACTCTGA TGATTTCACGCACCCCGGAAGTCAC TTGCGTGGTCGTGGACGTGTCGCAC GAAGATCCCGAAGTGAAATTCAATT GGTACGTGGATGGGGTCGAAGTGCA CAACGCCAAGACCAAGCCTAGGGA AGAACAGTACgccTCTACGTACCGGG TGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGA GTACAAGTGCAAAGTGTCAAACAA GGCTCTCCCTGCCCCTATCGAAAAG ACCATCAGCAAGGCCAAGGGTCAA CCTAGGGAGCCCCAGGTCTACACTT TGCCGCCTAGCCGGGAAGAAATGAC

			TAAGAACCAAGTGTCCCTGACTTGC CTTGTCAAGGGCTTTTATCCGTCCG ACATCGCCGTGGAGTGGGAGTCCAA CGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCC GATGGCTCCTTCTTCCTGTACTCCAA GCTGACTGTGGACAAGTCAAGATGG CAGCAGGGAAACGTGTTCTCCTGCT CCGTGATGCACGAAGCGCTGCACAA CCATTACACCCAGAAATCACTGTCA CTTTCGCCGGGAAAA
SEQ ID 2223	QVQLQQWGAGLLKPSETLSLTCAVYG GSVSGYYWSWIRQPPGKGLEWMGEIH HSGSTNYNPSLKSRVTISLDTPKNQFSL KLSSVTAADTAVYYCARRDWAGKRV WGQGTLVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPR EEQYASTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK	SEQ ID 2331	CAGGTGCAGCTACAGCAGTGGGGC GCAGGACTGTTGAAGCCTTCGGAGA CCCTGTCCCTCACCTGCGCTGTCTAT GGTGGGTCCGTCAGTGGTTACTACT GGAGCTGGATCCGCCAGCCCCCAGG GAAGGGGCTGGAGTGGATGGGGGA AATCCATCATAGTGGAAGCACCAAC TACAACCCGTCCCTCAAGAGTCGAG TCACCATATCACTAGACACGCCCAA GAACCAGTTCTCCCTGAAGCTAAGC TCTGTGACCGCCGCGGACACGGCTG TATATTACTGTGCGAGACGGGATTG GGCAGGAAAAAGGGTCTGGGGCCA GGGAACCCTGGTCACCGTCTCCTCA GCATCCACCAAGGGGCCTTCCGTGT TCCCCCTGGCCCCTTCATCCAAGTC GACCTCTGGTGGAACCGCCGCACTC GGTTGCCTGGTCAAAGACTACTTCC CCGAGCCCGTGACTGTCTCGTGGAA CTCGGGCGCCCTCACATCCGGAGTG CATACCTTTCCCGCCGTGTTGCAGTC CAGCGGCCTGTACAGCCTGAGCTCC GTCGTGACAGTGCCGTCCTCCTCCC TTGGAACCCAGACCTATATCTGCAA CGTCAATCACAAGCCCTCCAACACC AAAGTGGACAAGAAGGTCGAACCC AAGTCCTGCGACAAGACTCACACCT GTCCGCCTTGTCCAGCCCCTGAGCT GCTGGGTGGTCCGTCCGTGTTCCTCT TCCCGCCCAAGCCGAAGGACACTCT GATGATTTCACGCACCCCGGAAGTC ACTTGCGTGGTCGTGGACGTGTCGC ACGAAGATCCCGAAGTGAAATTCAA TTGGTACGTGGATGGGGTCGAAGTG CACAACGCCAAGACCAAGCCTAGG GAAGAACAGTACgccTCTACGTACCG GGTGGTGTCCGTGCTGACCGTGCTG CACCAGGACTGGCTGAACGGAAAG GAGTACAAGTGCAAAGTGTCAAAC AAGGCTCTCCCTGCCCCTATCGAAA AGACCATCAGCAAGGCCAAGGGTC AACCTAGGGAGCCCCAGGTCTACAC TTTGCCGCCTAGCCGGGAAGAAATG ACTAAGAACCAAGTGTCCCTGACTT

			GCCTTGTCAAGGGCTTTTATCCGTCC GACATCGCCGTGGAGTGGGAGTCCA ACGGACAACCGGAGAACAACTACA AGACCACCCCACCGGTGCTCGATTC CGATGGCTCCTTCTTCCTGTACTCCA AGCTGACTGTGGACAAGTCAAGATG GCAGCAGGGAAACGTGTTCTCCTGC TCCGTGATGCACGAAGCGCTGCACA ACCATTACACCCAGAAATCACTGTC ACTTTCGCCGGGAAAA
SEQ ID 2224	QVQLQQSGPGLLKPSQTLSLTCAISGD SVSSNTATWNWIRQSPSRGLEWLGRT YYRSKWYKDNALSVKSRITINPDTSKN QFSLQLNSVTPEDTAVYYCAGGRAGIA AFDIWGQGTTVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTK PREEQYASTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2332	CAGGTACAGCTGCAGCAGTCAGGTC CAGGACTATTAAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCAACACTGC TACTTGGAACTGGATCAGGCAGTCC CCATCGAGAGGCCTTGAGTGGCTGG GAAGGACATACTACAGGTCCAAGTG GTATAAGGATAATGCACTGTCTGTG AAAAGTCGAATAACCATCAACCCAG ACACATCCAAGAACCAGTTCTCCCT GCAGCTGAACTCTGTGACTCCCGAG GACACGGCTGTGTATTACTGTGCAG GAGGTCGGGCTGGTATTGCCGCTTT TGATATCTGGGGCCAAGGGACCACG GTCACCGTCTCCTCAGCATCCACCA AGGGGCCTTCCGTGTTCCCCCTGGC CCCTTCATCCAAGTCGACCTCTGGT GGAACCGCCGCACTCGGTTGCCTGG TCAAAGACTACTTCCCCGAGCCCGT GACTGTCTCGTGGAACTCGGGCGCC CTCACATCCGGAGTGCATACCTTTC CCGCCGTGTTGCAGTCCAGCGGCCT GTACAGCCTGAGCTCCGTCGTGACA GTGCCGTCCTCCTCCCTTGGAACCC AGACCTATATCTGCAACGTCAATCA CAAGCCCTCCAACACCAAAGTGGAC AAGAAGGTCGAACCCAAGTCCTGCG ACAAGACTCACACCTGTCCGCCTTG TCCAGCCCCTGAGCTGCTGGGTGGT CCGTCCGTGTTCCTCTTCCCGCCCAA GCCGAAGGACACTCTGATGATTTCA CGCACCCCGGAAGTCACTTGCGTGG TCGTGGACGTGTCGCACGAAGATCC CGAAGTGAAATTCAATTGGTACGTG GATGGGGTCGAAGTGCACAACGCC AAGACCAAGCCTAGGGAAGAACAG TACgccTCTACGTACCGGGTGGTGTC CGTGCTGACCGTGCTGCACCAGGAC TGGCTGAACGGAAAGGAGTACAAG TGCAAAGTGTCAAACAAGGCTCTCC CTGCCCCTATCGAAAAGACCATCAG CAAGGCCAAGGGTCAACCTAGGGA GCCCCAGGTCTACACTTTGCCGCCT AGCCGGGAAGAAATGACTAAGAAC

			CAAGTGTCCCTGACTTGCCTTGTCA AGGGCTTTTATCCGTCCGACATCGC CGTGGAGTGGGAGTCCAACGGACA ACCGGAGAACAACTACAAGACCAC CCCACCGGTGCTCGATTCCGATGGC TCCTTCTTCCTGTACTCCAAGCTGAC TGTGGACAAGTCAAGATGGCAGCA GGGAAACGTGTTCTCCTGCTCCGTG ATGCACGAAGCGCTGCACAACCATT ACACCCAGAAATCACTGTCACTTTC GCCGGGAAAA
SEQ ID 2225	QVQLVQSGGGLIQPGGSLRLSCAASGF TVSSNYMSWVRQAPGKGLEWVSLIYS DGRTNYADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCAKGALQGEWR RFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTK PREEQYASTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2333	CAGGTGCAGCTGGTGCAATCTGGAG GAGGCTTGATCCAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGGTTCACCGTCAGTAGCAACTACA TGAGCTGGGTCCGCCAGGCTCCAGG GAAGGGGCTGGAATGGGTCTCACTT ATTTATAGTGATGGTCGCACAAACT ATGCAGACTCCGTGAAGGGCCGATT CACCATCTCCAGAGACAATTCCAAG AACACGCTGTATCTGCAAATGAACA GCCTGAGAGCCGAGGACACGGCCG TATATTACTGTGCGAAGGGGGCCCT ACAGGGCGAATGGCGGAGATTTGA CTACTGGGGCCAGGGCACCCTGGTC ACCGTCTCCTCAGCATCCACCAAGG GGCCTTCCGTGTTCCCCCTGGCCCCT TCATCCAAGTCGACCTCTGGTGGAA CCGCCGCACTCGGTTGCCTGGTCAA AGACTACTTCCCCGAGCCCGTGACT GTCTCGTGGAACTCGGGCGCCCTCA CATCCGGAGTGCATACCTTTCCCGC CGTGTTGCAGTCCAGCGGCCTGTAC AGCCTGAGCTCCGTCGTGACAGTGC CGTCCTCCTCCCTTGGAACCCAGAC CTATATCTGCAACGTCAATCACAAG CCCTCCAACACCAAAGTGGACAAGA AGGTCGAACCCAAGTCCTGCGACAA GACTCACACCTGTCCGCCTTGTCCA GCCCCTGAGCTGCTGGGTGGTCCGT CCGTGTTCCTCTTCCCGCCCAAGCC GAAGGACACTCTGATGATTTCACGC ACCCCGGAAGTCACTTGCGTGGTCG TGGACGTGTCGCACGAAGATCCCGA AGTGAAATTCAATTGGTACGTGGAT GGGGTCGAAGTGCACAACGCCAAG ACCAAGCCTAGGGAAGAACAGTACg ccTCTACGTACCGGGTGGTGTCCGTG CTGACCGTGCTGCACCAGGACTGGC TGAACGGAAAGGAGTACAAGTGCA AAGTGTCAAACAAGGCTCTCCCTGC CCCTATCGAAAAGACCATCAGCAAG GCCAAGGGTCAACCTAGGGAGCCCC AGGTCTACACTTTGCCGCCTAGCCG GGAAGAAATGACTAAGAACCAAGT

			GTCCCTGACTTGCCTTGTCAAGGGC TTTTATCCGTCCGACATCGCCGTGG AGTGGGAGTCCAACGGACAACCGG AGAACAACTACAAGACCACCCCACC GGTGCTCGATTCCGATGGCTCCTTCT TCCTGTACTCCAAGCTGACTGTGGA CAAGTCAAGATGGCAGCAGGGAAA CGTGTTCTCCTGCTCCGTGATGCAC GAAGCGCTGCACAACCATTACACCC AGAAATCACTGTCACTTTCGCCGGG AAAA
SEQ ID 2226	QVQLQQSGPGLVKPSQTLSLTCAISGD SVSSNSAAWNWIRQSPSRGLEWLGRT YYRSKWYNDYAVSVKSRITINPDTSKN QFSLQLNSVTPEDTAVYYCTRTNQGY GGNSGVFDYWGQGTLVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYASTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSL SPGK	SEQ ID 2334	CAGGTGCAGCTACAGCAGTCAGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTAGCAACAGTGC TGCTTGGAACTGGATCAGGCAGTCC CCATCGAGAGGCCTTGAGTGGCTGG GAAGGACATATTACAGGTCCAAGTG GTATAATGATTATGCAGTATCTGTG AAAAGTCGAATAACCATCAACCCAG ACACATCCAAGAACCAGTTCTCCCT GCAGCTGAACTCTGTGACTCCCGAG GACACGGCTGTGTATTACTGTACAA GAACCAACCAGGGATACGGTGGTA ACTCCGGGGTATTTGACTACTGGGG CCAGGGAACCCTGGTCACCGTCTCC TCAGCATCCACCAAGGGGCCTTCCG TGTTCCCCCTGGCCCCTTCATCCAAG TCGACCTCTGGTGGAACCGCCGCAC TCGGTTGCCTGGTCAAAGACTACTT CCCCGAGCCCGTGACTGTCTCGTGG AACTCGGGCGCCCTCACATCCGGAG TGCATACCTTTCCCGCCGTGTTGCA GTCCAGCGGCCTGTACAGCCTGAGC TCCGTCGTGACAGTGCCGTCCTCCT CCCTTGGAACCCAGACCTATATCTG CAACGTCAATCACAAGCCCTCCAAC ACCAAAGTGGACAAGAAGGTCGAA CCCAAGTCCTGCGACAAGACTCACA CCTGTCCGCCTTGTCCAGCCCCTGA GCTGCTGGGTGGTCCGTCCGTGTTC CTCTTCCCGCCCAAGCCGAAGGACA CTCTGATGATTTCACGCACCCCGGA AGTCACTTGCGTGGTCGTGGACGTG TCGCACGAAGATCCCGAAGTGAAAT TCAATTGGTACGTGGATGGGGTCGA AGTGCACAACGCCAAGACCAAGCCT AGGGAAGAACAGTACgccTCTACGTA CCGGGTGGTGTCCGTGCTGACCGTG CTGCACCAGGACTGGCTGAACGGAA AGGAGTACAAGTGCAAAGTGTCAA ACAAGGCTCTCCCTGCCCCTATCGA AAAGACCATCAGCAAGGCCAAGGG TCAACCTAGGGAGCCCCAGGTCTAC ACTTTGCCGCCTAGCCGGGAAGAAA

			TGACTAAGAACCAAGTGTCCCTGAC TTGCCTTGTCAAGGGCTTTTATCCGT CCGACATCGCCGTGGAGTGGGAGTC CAACGGACAACCGGAGAACAACTA CAAGACCACCCCACCGGTGCTCGAT TCCGATGGCTCCTTCTTCCTGTACTC CAAGCTGACTGTGGACAAGTCAAGA TGGCAGCAGGGAAACGTGTTCTCCT GCTCCGTGATGCACGAAGCGCTGCA CAACCATTACACCCAGAAATCACTG TCACTTTCGCCGGGAAAA
SEQ ID 2227	QVQLQQSGPGLVKPSQTLSLTCAISGD SVSGNSAAWNWIRQSPSRGLEWLGRT YYRSKWYNDYAVSVKSRITINPDTSKN QFSLQLNSVTPEDTAVYYCARIVGGAV DCWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTK PREEQYASTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2335	CAGGTGCAGCTACAGCAGTCAGGTC CAGGACTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCCG GGGACAGTGTCTCTGGCAACAGTGC TGCTTGGAACTGGATCAGGCAGTCC CCATCGAGAGGCCTTGAGTGGCTGG GAAGGACATACTACAGGTCCAAGTG GTATAATGATTATGCAGTATCTGTG AAAAGTCGAATAACCATCAACCCAG ACACATCCAAGAACCAGTTCTCCCT GCAGTTGAATTCTGTGACTCCCGAG GACACGGCTGTGTATTACTGTGCGA GGATAGTGGGAGGTGCCGTTGACTG CTGGGGCCAGGGAACCCTGGTGACC GTCTCCTCAGCATCCACCAAGGGGC CTTCCGTGTTCCCCCTGGCCCCTTCA TCCAAGTCGACCTCTGGTGGAACCG CCGCACTCGGTTGCCTGGTCAAAGA CTACTTCCCCGAGCCCGTGACTGTC TCGTGGAACTCGGGCGCCCTCACAT CCGGAGTGCATACCTTTCCCGCCGT GTTGCAGTCCAGCGGCCTGTACAGC CTGAGCTCCGTCGTGACAGTGCCGT CCTCCTCCCTTGGAACCCAGACCTA TATCTGCAACGTCAATCACAAGCCC TCCAACACCAAAGTGGACAAGAAG GTCGAACCCAAGTCCTGCGACAAGA CTCACACCTGTCCGCCTTGTCCAGC CCCTGAGCTGCTGGGTGGTCCGTCC GTGTTCCTCTTCCCGCCCAAGCCGA AGGACACTCTGATGATTTCACGCAC CCCGGAAGTCACTTGCGTGGTCGTG GACGTGTCGCACGAAGATCCCGAAG TGAAATTCAATTGGTACGTGGATGG GGTCGAAGTGCACAACGCCAAGAC CAAGCCTAGGGAAGAACAGTACgcc TCTACGTACCGGGTGGTGTCCGTGC TGACCGTGCTGCACCAGGACTGGCT GAACGGAAAGGAGTACAAGTGCAA AGTGTCAAACAAGGCTCTCCCTGCC CCTATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTACACTTTGCCGCCTAGCCGG GAAGAAATGACTAAGAACCAAGTG

			TCCCTGACTTGCCTTGTCAAGGGCTT TTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCAAGCTGACTGTGGACA AGTCAAGATGGCAGCAGGGAAACG TGTTCTCCTGCTCCGTGATGCACGA AGCGCTGCACAACCATTACACCCAG AAATCACTGTCACTTTCGCCGGGAA AA
SEQ ID 2228	EVQLVQSGAEVKKPGASVKVSCKASG YTFTSYAMHWVRQAPGQRLEWMGWI NAGNGNTKYSQKFQGRVTITRDTSAST AYMELSSLRSEDTAVYYCARVRVGAT TVYDSWFDPWGQGTLVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYASTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSL SPGK	SEQ ID 2336	GAGGTGCAGCTGGTGCAGTCTGGGG CTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTTTCCTGCAAGGCTTCT GGATACACCTTCACTAGCTATGCTA TGCATTGGGTGCGCCAGGCCCCCGG ACAAAGGCTTGAGTGGATGGGATG GATCAACGCTGGCAATGGTAACACA AAATATTCACAGAAGTTCCAGGGCA GAGTCACCATTACCAGGGACACATC CGCGAGCACAGCCTACATGGAGCTG AGCAGCCTGAGATCTGAAGACACG GCTGTGTATTACTGTGCGAGAGTTA GAGTGGGAGCTACTACTGTTTACGA CAGCTGGTTCGACCCCTGGGGCCAG GGAACCCTGGTGACCGTCTCCTCAG CATCCACCAAGGGGCCTTCCGTGTT CCCCCTGGCCCCTTCATCCAAGTCG ACCTCTGGTGGAACCGCCGCACTCG GTTGCCTGGTCAAAGACTACTTCCC CGAGCCCGTGACTGTCTCGTGGAAC TCGGGCGCCCTCACATCCGGAGTGC ATACCTTTCCCGCCGTGTTGCAGTCC AGCGGCCTGTACAGCCTGAGCTCCG TCGTGACAGTGCCGTCCTCCTCCCTT GGAACCCAGACCTATATCTGCAACG TCAATCACAAGCCCTCCAACACCAA AGTGGACAAGAAGGTCGAACCCAA GTCCTGCGACAAGACTCACACCTGT CCGCCTTGTCCAGCCCCTGAGCTGC TGGGTGGTCCGTCCGTGTTCCTCTTC CCGCCCAAGCCGAAGGACACTCTGA TGATTTCACGCACCCCGGAAGTCAC TTGCGTGGTCGTGGACGTGTCGCAC GAAGATCCCGAAGTGAAATTCAATT GGTACGTGGATGGGGTCGAAGTGCA CAACGCCAAGACCAAGCCTAGGGA AGAACAGTACgccTCTACGTACCGGG TGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGA GTACAAGTGCAAAGTGTCAAACAA GGCTCTCCCTGCCCCTATCGAAAAG ACCATCAGCAAGGCCAAGGGTCAA CCTAGGGAGCCCCAGGTCTACACTT TGCCGCCTAGCCGGGAAGAAATGAC

			TAAGAACCAAGTGTCCCTGACTTGC CTTGTCAAGGGCTTTTATCCGTCCG ACATCGCCGTGGAGTGGGAGTCCAA CGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCC GATGGCTCCTTCTTCCTGTACTCCAA GCTGACTGTGGACAAGTCAAGATGG CAGCAGGGAAACGTGTTCTCCTGCT CCGTGATGCACGAAGCGCTGCACAA CCATTACACCCAGAAATCACTGTCA CTTTCGCCGGGAAAA
SEQ ID 2229	QVQLVQSGGGLVQPGGSLRLSCAASG FTFSSYAMSWVRQAPGKGLEWVSAIS GSGGSTYYADSVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCAKDGGSSPY YDSSGLLPWYFDLWGRGTLVTVSSAS TKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVL TVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMT KNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	SEQ ID 2337	CAGGTGCAGCTGGTGCAGTCTGGGG GAGGCTTGGTACAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTTAGCAGCTATGCCA TGAGCTGGGTCCGCCAGGCTCCAGG GAAGGGGCTGGAGTGGGTCTCAGCT ATTAGTGGTAGTGGTGGTAGCACAT ACTACGCAGACTCCGTGAAGGGCCG GTTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCCGAGGACACGG CCGTATATTACTGTGCGAAAGATGG GGGGTCCAGCCCATACTATGATAGT AGTGGTTTACTACCCTGGTACTTCG ATCTCTGGGGCCGTGGCACCCTGGT CACCGTCTCCTCAGCATCCACCAAG GGGCCTTCCGTGTTCCCCCTGGCCC CTTCATCCAAGTCGACCTCTGGTGG AACCGCCGCACTCGGTTGCCTGGTC AAAGACTACTTCCCCGAGCCCGTGA CTGTCTCGTGGAACTCGGGCGCCCT CACATCCGGAGTGCATACCTTTCCC GCCGTGTTGCAGTCCAGCGGCCTGT ACAGCCTGAGCTCCGTCGTGACAGT GCCGTCCTCCTCCCTTGGAACCCAG ACCTATATCTGCAACGTCAATCACA AGCCCTCCAACACCAAAGTGGACAA GAAGGTCGAACCCAAGTCCTGCGAC AAGACTCACACCTGTCCGCCTTGTC CAGCCCCTGAGCTGCTGGGTGGTCC GTCCGTGTTCCTCTTCCCGCCCAAGC CGAAGGACACTCTGATGATTTCACG CACCCCGGAAGTCACTTGCGTGGTC GTGGACGTGTCGCACGAAGATCCCG AAGTGAAATTCAATTGGTACGTGGA TGGGGTCGAAGTGCACAACGCCAA GACCAAGCCTAGGGAAGAACAGTA CgccTCTACGTACCGGGTGGTGTCCG TGCTGACCGTGCTGCACCAGGACTG GCTGAACGGAAAGGAGTACAAGTG CAAAGTGTCAAACAAGGCTCTCCCT GCCCCTATCGAAAAGACCATCAGCA AGGCCAAGGGTCAACCTAGGGAGC CCCAGGTCTACACTTTGCCGCCTAG

			CCGGGAAGAAATGACTAAGAACCA AGTGTCCCTGACTTGCCTTGTCAAG GGCTTTTATCCGTCCGACATCGCCG TGGAGTGGGAGTCCAACGGACAAC CGGAGAACAACTACAAGACCACCC CACCGGTGCTCGATTCCGATGGCTC CTTCTTCCTGTACTCCAAGCTGACTG TGGACAAGTCAAGATGGCAGCAGG GAAACGTGTTCTCCTGCTCCGTGAT GCACGAAGCGCTGCACAACCATTAC ACCCAGAAATCACTGTCACTTTCGC CGGGAAAA
SEQ ID 2230	QVQLQESGGGLVQPGGSLRLSCAASG FTFSSYAMHWVRQAPGKGLEYVSAISS NGGSTYYANSVKGRFTISRDNSKNTLY LQMGSLRAEDMAVYYCARAKFWTYY FDYWGQGTLVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTK PREEQYASTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2338	CAGGTGCAGCTGCAGGAGTCGGGG GGAGGCTTGGTCCAGCCTGGGGGGT CCCTGAGACTCTCCTGTGCAGCCTC TGGATTCACCTTCAGTAGCTATGCT ATGCACTGGGTCCGCCAGGCTCCAG GGAAGGGACTGGAATATGTTTCAGC TATTAGTAGTAATGGGGGTAGCACA TATTATGCAAACTCTGTGAAGGGCA GATTCACCATCTCCAGAGACAATTC CAAGAACACGCTGTATCTTCAAATG GGCAGCCTGAGAGCTGAGGACATG GCTGTGTATTACTGTGCGAGAGCTA AGTTTTGGACATACTACTTTGACTA CTGGGGCCAGGGAACCCTGGTGACC GTCTCCTCAGCATCCACCAAGGGGC CTTCCGTGTTCCCCCTGGCCCCTTCA TCCAAGTCGACCTCTGGTGGAACCG CCGCACTCGGTTGCCTGGTCAAAGA CTACTTCCCCGAGCCCGTGACTGTC TCGTGGAACTCGGGCGCCCTCACAT CCGGAGTGCATACCTTTCCCGCCGT GTTGCAGTCCAGCGGCCTGTACAGC CTGAGCTCCGTCGTGACAGTGCCGT CCTCCTCCCTTGGAACCCAGACCTA TATCTGCAACGTCAATCACAAGCCC TCCAACACCAAAGTGGACAAGAAG GTCGAACCCAAGTCCTGCGACAAGA CTCACACCTGTCCGCCTTGTCCAGC CCCTGAGCTGCTGGGTGGTCCGTCC GTGTTCCTCTTCCCGCCCAAGCCGA AGGACACTCTGATGATTTCACGCAC CCCGGAAGTCACTTGCGTGGTCGTG GACGTGTCGCACGAAGATCCCGAAG TGAAATTCAATTGGTACGTGGATGG GGTCGAAGTGCACAACGCCAAGAC CAAGCCTAGGGAAGAACAGTACgcc TCTACGTACCGGGTGGTGTCCGTGC TGACCGTGCTGCACCAGGACTGGCT GAACGGAAAGGAGTACAAGTGCAA AGTGTCAAACAAGGCTCTCCCTGCC CCTATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTACACTTTGCCGCCTAGCCGG GAAGAAATGACTAAGAACCAAGTG

			TCCCTGACTTGCCTTGTCAAGGGCTT TTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCAAGCTGACTGTGGACA AGTCAAGATGGCAGCAGGGAAACG TGTTCTCCTGCTCCGTGATGCACGA AGCGCTGCACAACCATTACACCCAG AAATCACTGTCACTTTCGCCGGGAA AA
SEQ ID 2231	QVQLQQWGAGLLKPSETLSLTCAVYG GSFSGYYWSWIRQPPGKGLEWIGEINH SGSTNYNPSLKSRVTISVDTSKNQFSLK LSSVTAADTAVYYCARGGGSGSYYKR FFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTK PREEQYASTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2339	CAGGTGCAGCTACAGCAGTGGGGC GCAGGACTGTTGAAGCCTTCGGAGA CCCTGTCCCTCACCTGCGCTGTCTAT GGTGGGTCCTTCAGTGGTTACTACT GGAGCTGGATCCGCCAGCCCCCAGG GAAGGGGCTGGAGTGGATTGGGGA AATCAATCATAGTGGAAGCACCAAC TACAACCCGTCCCTCAAGAGTCGAG TCACCATATCAGTAGACACGTCCAA GAACCAGTTCTCCCTGAAGCTGAGC TCTGTGACCGCCGCGGACACGGCTG TGTATTACTGTGCGAGAGGCGGTGG TTCGGGGAGTTATTATAAGAGGTTC TTTGACTACTGGGGCCAGGGAACCC TGGTCACCGTCTCCTCAGCATCCAC CAAGGGGCCTTCCGTGTTCCCCCTG GCCCCTTCATCCAAGTCGACCTCTG GTGGAACCGCCGCACTCGGTTGCCT GGTCAAAGACTACTTCCCCGAGCCC GTGACTGTCTCGTGGAACTCGGGCG CCCTCACATCCGGAGTGCATACCTT TCCCGCCGTGTTGCAGTCCAGCGGC CTGTACAGCCTGAGCTCCGTCGTGA CAGTGCCGTCCTCCTCCCTTGGAAC CCAGACCTATATCTGCAACGTCAAT CACAAGCCCTCCAACACCAAAGTGG ACAAGAAGGTCGAACCCAAGTCCTG CGACAAGACTCACACCTGTCCGCCT TGTCCAGCCCCTGAGCTGCTGGGTG GTCCGTCCGTGTTCCTCTTCCCGCCC AAGCCGAAGGACACTCTGATGATTT CACGCACCCCGGAAGTCACTTGCGT GGTCGTGGACGTGTCGCACGAAGAT CCCGAAGTGAAATTCAATTGGTACG TGGATGGGGTCGAAGTGCACAACGC CAAGACCAAGCCTAGGGAAGAACA GTACgccTCTACGTACCGGGTGGTGT CCGTGCTGACCGTGCTGCACCAGGA CTGGCTGAACGGAAAGGAGTACAA GTGCAAAGTGTCAAACAAGGCTCTC CCTGCCCCTATCGAAAAGACCATCA GCAAGGCCAAGGGTCAACCTAGGG AGCCCCAGGTCTACACTTTGCCGCC TAGCCGGGAAGAAATGACTAAGAA

			CCAAGTGTCCCTGACTTGCCTTGTC AAGGGCTTTTATCCGTCCGACATCG CCGTGGAGTGGGAGTCCAACGGAC AACCGGAGAACAACTACAAGACCA CCCCACCGGTGCTCGATTCCGATGG CTCCTTCTTCCTGTACTCCAAGCTGA CTGTGGACAAGTCAAGATGGCAGCA GGGAAACGTGTTCTCCTGCTCCGTG ATGCACGAAGCGCTGCACAACCATT ACACCCAGAAATCACTGTCACTTTC GCCGGGAAAA
SEQ ID 2232	EVQLVQSGAEVRKPGASVKVSCKASG YTFTSYAISWVRQAPGQGLEWMGWIS AYDGNTNYAQKLQGRVTMTTDTSTST AYMEVRSLRSDDTAVYYCARDGTVR RVVGATTPGNFDYRGQGTLVTVSSAS TKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVL TVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMT KNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	SEQ ID 2340	GAGGTGCAGCTGGTGCAGTCTGGAG CTGAGGTGAGGAAGCCTGGGGCCTC AGTGAAGGTCTCCTGCAAGGCTTCT GGTTACACATTTACCAGTTATGCCA TCAGCTGGGTGCGACAGGCCCCTGG ACAAGGGCTTGAGTGGATGGGGTG GATCAGCGCTTACGACGGTAACACA AACTATGCACAGAAGCTCCAGGGCA GAGTCACCATGACCACAGACACATC CACGAGCACAGCCTACATGGAGGTG AGGAGCCTGAGATCTGACGACACG GCCGTGTATTACTGTGCGAGAGATG GTACGGTCCGAAGGGTAGTGGGAG CTACTACCCCTGGAAACTTTGACTA CAGGGGCCAGGGAACCCTGGTCACC GTCTCCTCAGCATCCACCAAGGGGC CTTCCGTGTTCCCCCTGGCCCCTTCA TCCAAGTCGACCTCTGGTGGAACCG CCGCACTCGGTTGCCTGGTCAAAGA CTACTTCCCCGAGCCCGTGACTGTC TCGTGGAACTCGGGCGCCCTCACAT CCGGAGTGCATACCTTTCCCGCCGT GTTGCAGTCCAGCGGCCTGTACAGC CTGAGCTCCGTCGTGACAGTGCCGT CCTCCTCCCTTGGAACCCAGACCTA TATCTGCAACGTCAATCACAAGCCC TCCAACACCAAAGTGGACAAGAAG GTCGAACCCAAGTCCTGCGACAAGA CTCACACCTGTCCGCCTTGTCCAGC CCCTGAGCTGCTGGGTGGTCCGTCC GTGTTCCTCTTCCCGCCCAAGCCGA AGGACACTCTGATGATTTCACGCAC CCCGGAAGTCACTTGCGTGGTCGTG GACGTGTCGCACGAAGATCCCGAAG TGAAATTCAATTGGTACGTGGATGG GGTCGAAGTGCACAACGCCAAGAC CAAGCCTAGGGAAGAACAGTACgcc TCTACGTACCGGGTGGTGTCCGTGC TGACCGTGCTGCACCAGGACTGGCT GAACGGAAAGGAGTACAAGTGCAA AGTGTCAAACAAGGCTCTCCCTGCC CCTATCGAAAAGACCATCAGCAAGG CCAAGGGTCAACCTAGGGAGCCCCA GGTCTACACTTTGCCGCCTAGCCGG

			GAAGAAATGACTAAGAACCAAGTG TCCCTGACTTGCCTTGTCAAGGGCTT TTATCCGTCCGACATCGCCGTGGAG TGGGAGTCCAACGGACAACCGGAG AACAACTACAAGACCACCCCACCGG TGCTCGATTCCGATGGCTCCTTCTTC CTGTACTCCAAGCTGACTGTGGACA AGTCAAGATGGCAGCAGGGAAACG TGTTCTCCTGCTCCGTGATGCACGA AGCGCTGCACAACCATTACACCCAG AAATCACTGTCACTTTCGCCGGGAA AA
SEQ ID 2233	EVQLVQSGGGVVQPGRSLRLSCAASG FTFSSYGMHWVRQAPGKGLEWVAVI WYDGSNKYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARDLNRG YCSGGSCFGYWGQGTLVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYASTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSL SPGK	SEQ ID 2341	GAGGTGCAGCTGGTGCAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCGTCT GGATTCACCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTT ATATGGTATGATGGAAGTAATAAAT ACTATGCAGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCCGAGGACACGG CTGTGTATTACTGTGCGAGAGATCT GAATCGAGGATATTGTAGTGGTGGT AGCTGCTTTGGCTACTGGGGCCAGG GAACCCTGGTCACCGTCTCCTCAGC ATCCACCAAGGGGCCTTCCGTGTTC CCCCTGGCCCCTTCATCCAAGTCGA CCTCTGGTGGAACCGCCGCACTCGG TTGCCTGGTCAAAGACTACTTCCCC GAGCCCGTGACTGTCTCGTGGAACT CGGGCGCCCTCACATCCGGAGTGCA TACCTTTCCCGCCGTGTTGCAGTCCA GCGGCCTGTACAGCCTGAGCTCCGT CGTGACAGTGCCGTCCTCCTCCCTT GGAACCCAGACCTATATCTGCAACG TCAATCACAAGCCCTCCAACACCAA AGTGGACAAGAAGGTCGAACCCAA GTCCTGCGACAAGACTCACACCTGT CCGCCTTGTCCAGCCCCTGAGCTGC TGGGTGGTCCGTCCGTGTTCCTCTTC CCGCCCAAGCCGAAGGACACTCTGA TGATTTCACGCACCCCGGAAGTCAC TTGCGTGGTCGTGGACGTGTCGCAC GAAGATCCCGAAGTGAAATTCAATT GGTACGTGGATGGGGTCGAAGTGCA CAACGCCAAGACCAAGCCTAGGGA AGAACAGTACgccTCTACGTACCGGG TGGTGTCCGTGCTGACCGTGCTGCA CCAGGACTGGCTGAACGGAAAGGA GTACAAGTGCAAAGTGTCAAACAA GGCTCTCCCTGCCCCTATCGAAAAG ACCATCAGCAAGGCCAAGGGTCAA CCTAGGGAGCCCCAGGTCTACACTT TGCCGCCTAGCCGGGAAGAAATGAC

			TAAGAACCAAGTGTCCCTGACTTGC CTTGTCAAGGGCTTTTATCCGTCCG ACATCGCCGTGGAGTGGGAGTCCAA CGGACAACCGGAGAACAACTACAA GACCACCCCACCGGTGCTCGATTCC GATGGCTCCTTCTTCCTGTACTCCAA GCTGACTGTGGACAAGTCAAGATGG CAGCAGGGAAACGTGTTCTCCTGCT CCGTGATGCACGAAGCGCTGCACAA CCATTACACCCAGAAATCACTGTCA CTTTCGCCGGGAAAA
SEQ ID 2234	QVQLQESGGGLVQPGGSLRLSCAASG FTFSSYAMSWVRQAPGKGLEWVSYIS SSGTTIYYADSVKGRFTVSRDNAKNSL YLQMNSLRAEDTAVYYCARDYSSSGE CFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLS SVVTVPSSSLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTK PREEQYASTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK	SEQ ID 2342	CAGGTGCAGCTGCAGGAGTCTGGGG GAGGCTTGGTACAGCCGGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCACCTTTAGCAGCTATGCCA TGAGCTGGGTCCGCCAGGCTCCAGG GAAGGGGCTGGAGTGGGTTTCATAC ATTAGTAGTAGTGGTACTACCATAT ACTACGCAGACTCTGTGAAGGGCCG ATTCACCGTCTCCAGAGACAATGCC AAGAACTCACTGTATCTGCAAATGA ACAGCCTGAGAGCCGAGGACACGG CCGTGTATTACTGTGCGAGGGATTA TAGCAGCTCGGGGGAGTGCTTTGAC TACTGGGGCCAGGGAACCCTGGTCA CCGTCTCCTCAGCATCCACCAAGGG GCCTTCCGTGTTCCCCCTGGCCCCTT CATCCAAGTCGACCTCTGGTGGAAC CGCCGCACTCGGTTGCCTGGTCAAA GACTACTTCCCCGAGCCCGTGACTG TCTCGTGGAACTCGGGCGCCCTCAC ATCCGGAGTGCATACCTTTCCCGCC GTGTTGCAGTCCAGCGGCCTGTACA GCCTGAGCTCCGTCGTGACAGTGCC GTCCTCCTCCCTTGGAACCCAGACC TATATCTGCAACGTCAATCACAAGC CCTCCAACACCAAAGTGGACAAGA AGGTCGAACCCAAGTCCTGCGACAA GACTCACACCTGTCCGCCTTGTCCA GCCCCTGAGCTGCTGGGTGGTCCGT CCGTGTTCCTCTTCCCGCCCAAGCC GAAGGACACTCTGATGATTTCACGC ACCCCGGAAGTCACTTGCGTGGTCG TGGACGTGTCGCACGAAGATCCCGA AGTGAAATTCAATTGGTACGTGGAT GGGGTCGAAGTGCACAACGCCAAG ACCAAGCCTAGGGAAGAACAGTACg ccTCTACGTACCGGGTGGTGTCCGTG CTGACCGTGCTGCACCAGGACTGGC TGAACGGAAAGGAGTACAAGTGCA AAGTGTCAAACAAGGCTCTCCCTGC CCCTATCGAAAAGACCATCAGCAAG GCCAAGGGTCAACCTAGGGAGCCCC AGGTCTACACTTTGCCGCCTAGCCG GGAAGAAATGACTAAGAACCAAGT

			GTCCCTGACTTGCCTTGTCAAGGGC TTTTATCCGTCCGACATCGCCGTGG AGTGGGAGTCCAACGGACAACCGG AGAACAACTACAAGACCACCCCACC GGTGCTCGATTCCGATGGCTCCTTCT TCCTGTACTCCAAGCTGACTGTGGA CAAGTCAAGATGGCAGCAGGGAAA CGTGTTCTCCTGCTCCGTGATGCAC GAAGCGCTGCACAACCATTACACCC AGAAATCACTGTCACTTTCGCCGGG AAAA
SEQ ID 2235	EVQLVQSGGGVVQPGRSLRLSCAASG FTFSSYGMHWVRQAPGKGLEWVAVI WYDGSNKYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARDQAA MVGYFDYWGQGTLVTVSSASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYASTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG K	SEQ ID 2343	GAGGTGCAGCTGGTGCAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCGTCT GGATTCACCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTT ATATGGTATGATGGAAGTAATAAAT ACTATGCAGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCCGAGGACACGG CTGTGTATTACTGTGCGAGAGATCA GGCAGCTATGGTAGGCTACTTTGAC TACTGGGGCCAGGGAACCCTGGTCA CCGTCTCCTCAGCATCCACCAAGGG GCCTTCCGTGTTCCCCCTGGCCCCTT CATCCAAGTCGACCTCTGGTGGAAC CGCCGCACTCGGTTGCCTGGTCAAA GACTACTTCCCCGAGCCCGTGACTG TCTCGTGGAACTCGGGCGCCCTCAC ATCCGGAGTGCATACCTTTCCCGCC GTGTTGCAGTCCAGCGGCCTGTACA GCCTGAGCTCCGTCGTGACAGTGCC GTCCTCCTCCCTTGGAACCCAGACC TATATCTGCAACGTCAATCACAAGC CCTCCAACACCAAAGTGGACAAGA AGGTCGAACCCAAGTCCTGCGACAA GACTCACACCTGTCCGCCTTGTCCA GCCCCTGAGCTGCTGGGTGGTCCGT CCGTGTTCCTCTTCCCGCCCAAGCC GAAGGACACTCTGATGATTTCACGC ACCCCGGAAGTCACTTGCGTGGTCG TGGACGTGTCGCACGAAGATCCCGA AGTGAAATTCAATTGGTACGTGGAT GGGGTCGAAGTGCACAACGCCAAG ACCAAGCCTAGGGAAGAACAGTACg ccTCTACGTACCGGGTGGTGTCCGTG CTGACCGTGCTGCACCAGGACTGGC TGAACGGAAAGGAGTACAAGTGCA AAGTGTCAAACAAGGCTCTCCCTGC CCCTATCGAAAAGACCATCAGCAAG GCCAAGGGTCAACCTAGGGAGCCCC AGGTCTACACTTTGCCGCCTAGCCG GGAAGAAATGACTAAGAACCAAGT

			GTCCCTGACTTGCCTTGTCAAGGGC TTTTATCCGTCCGACATCGCCGTGG AGTGGGAGTCCAACGGACAACCGG AGAACAACTACAAGACCACCCCACC GGTGCTCGATTCCGATGGCTCCTTCT TCCTGTACTCCAAGCTGACTGTGGA CAAGTCAAGATGGCAGCAGGGAAA CGTGTTCTCCTGCTCCGTGATGCAC GAAGCGCTGCACAACCATTACACCC AGAAATCACTGTCACTTTCGCCGGG AAAA
SEQ ID 2236	QVTLKESGGGVVQPGRSLRLSCAASGF IFSNYAIHWVRQAPGKGLEWVAVISY DGSNKYYADSVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCARTFAGYSS KLGYFDLWGRGTLVTVSSASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYASTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG K	SEQ ID 2344	CAGGTCACCTTGAAGGAGTCTGGGG GAGGCGTGGTCCAGCCTGGGAGGTC CCTGAGACTCTCCTGTGCAGCCTCT GGATTCATCTTCAGTAACTATGCTA TACACTGGGTCCGCCAGGCTCCAGG CAAGGGGCTGGAGTGGGTGGCAGTT ATATCATATGATGGAAGTAATAAAT ACTACGCAGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCC AAGAACACGCTGTATCTGCAAATGA ACAGCCTGAGAGCTGAGGACACGG CTGTGTATTACTGTGCGAGGACTTTT GCGGGGTATAGCAGCAAACTGGGG TACTTCGATCTCTGGGGCCGTGGCA CCCTGGTCACCGTCTCCTCAGCATC CACCAAGGGGCCTTCCGTGTTCCCC CTGGCCCCTTCATCCAAGTCGACCT CTGGTGGAACCGCCGCACTCGGTTG CCTGGTCAAAGACTACTTCCCCGAG CCCGTGACTGTCTCGTGGAACTCGG GCGCCCTCACATCCGGAGTGCATAC CTTTCCCGCCGTGTTGCAGTCCAGC GGCCTGTACAGCCTGAGCTCCGTCG TGACAGTGCCGTCCTCCTCCCTTGG AACCCAGACCTATATCTGCAACGTC AATCACAAGCCCTCCAACACCAAAG TGGACAAGAAGGTCGAACCCAAGT CCTGCGACAAGACTCACACCTGTCC GCCTTGTCCAGCCCCTGAGCTGCTG GGTGGTCCGTCCGTGTTCCTCTTCCC GCCCAAGCCGAAGGACACTCTGATG ATTTCACGCACCCCGGAAGTCACTT GCGTGGTCGTGGACGTGTCGCACGA AGATCCCGAAGTGAAATTCAATTGG TACGTGGATGGGGTCGAAGTGCACA ACGCCAAGACCAAGCCTAGGGAAG AACAGTACgccTCTACGTACCGGGTG GTGTCCGTGCTGACCGTGCTGCACC AGGACTGGCTGAACGGAAAGGAGT ACAAGTGCAAAGTGTCAAACAAGG CTCTCCCTGCCCCTATCGAAAAGAC CATCAGCAAGGCCAAGGGTCAACCT AGGGAGCCCCAGGTCTACACTTTGC CGCCTAGCCGGGAAGAAATGACTA

			AGAACCAAGTGTCCCTGACTTGCCT TGTCAAGGGCTTTTATCCGTCCGAC ATCGCCGTGGAGTGGGAGTCCAACG GACAACCGGAGAACAACTACAAGA CCACCCCACCGGTGCTCGATTCCGA TGGCTCCTTCTTCCTGTACTCCAAGC TGACTGTGGACAAGTCAAGATGGCA GCAGGGAAACGTGTTCTCCTGCTCC GTGATGCACGAAGCGCTGCACAACC ATTACACCCAGAAATCACTGTCACT TTCGCCGGGAAAA

Table 41. Anti-CLEC2D IgG2 antibody amino acid and DNA sequence

SEQ ID	VH+CH IgG2 aa	SEQ ID	VH+IgG2 DNA
SEQ ID 2345	EVQLVQSGAEVKKPGA SVKVSCKASGYTFTSYA MHWVRQAPGQRLEWM GWINAGNGNTKYSQKF QGRVTITRDTSASTAYM ELSSLRSEDTAVYYCAR GSLSRSGWYAGLFDYW GQGTLVTVSSASTKGPS VFPLAPCSRSTSESTAA LGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSN FGTQTYTCNVDHKPSN TKVDKTVERKCCVECPP CPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVV VDVSHEDPEVQFNWYV DGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQD WLNGKEYKCKVSNKGL PAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPP MLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVM HEALHNHYTQKSLSLSP GK	SEQ ID 2453	GAAGTGCAGCTGGTGCAGTCTGG GGCTGAGGTGAAGAAGCCTGGGG CCTCAGTGAAGGTTTCCTGCAAGG CTTCTGGATACACCTTCACTAGCT ATGCTATGCATTGGGTGCGCCAG GCCCCCGGACAAAGGCTTGAGTG GATGGGATGGATCAACGCTGGCA ATGGTAACACAAAATATTCACAGA AGTTCCAGGGCAGAGTCACCATTA CCAGGGACACATCCGCGAGCACA GCCTACATGGAGCTGAGCAGCCT GAGATCTGAAGACACGGCTGTGTA TTACTGTGCGAGAGGCTCCTTGTC CCGAAGTGGCTGGTACGCCGGAC TCTTTGACTACTGGGGCCAGGGAA CCCTGGTCACCGTCTCCTCAGCAA GCACAAAAGGTCCTTCAGTGTTCC CTCTGGCACCTTGCTCACGCAGCA CCTCTGAGAGTACAGCCGCCCTG GGCTGCCTGGTAAAGGACTACTTT CCCGAACCAGTCACTGTGTCCTGG AATAGCGGGGCCTTGACCTCTGG AGTGCACACATTTCCAGCTGTACT GCAGTCATCTGGACTCTACAGCCT GTCCAGTGTGGTCACCGTACCTTC CTCCAACTTTGGCACTCAAACATA TACATGTAACGTGGATCATAAGCC CTCTAACACCAAAGTGGATAAAAC TGTGGAGCGTAAGTGTTGTGTCGA GTGTCCTCCTTGTCCTGCTCCTCC TGTGGCAGGCCCATCTGTGTTTCT CTTTCCCCCAAAGCCAAAGGACAC TTTGATGATATCCCGGACCCCTGA GGTGACTTGCGTCGTCGTAGATGT TTCACACGAAGATCCAGAGGTGCA GTTCAACTGGTACGTGGATGGCGT GGAAGTGCATAATGCCAAGACAAA GCCCCGCGAAGAGCAGTTTAATTC CACCTTCCGCGTGGTGTCTGTGCT

			GACCGTGGTACATCAGGATTGGCT TAACGGTAAGGAGTACAAGTGCAA GGTGAGTAACAAGGGGCTGCCCG CCCCTATCGAGAAGACTATCAGTA AAACCAAGGGCCAGCCAAGGGAG CCACAGGTGTACACACTTCCACCA TCTAGGGAGGAAATGACAAAGAAC CAGGTGAGTTTGACCTGTCTCGTG AAAGGCTTTTATCCCAGTGATATA GCCGTGGAATGGGAAAGTAACGG GCAGCCCGAGAACAACTATAAGAC CACACCACCCATGCTGGACTCCGA CGGTTCTTTCTTCCTTTATAGCAAG CTGACAGTGGATAAATCCAGGTGG CAGCAGGGTAACGTATTCAGTTGC AGTGTCATGCACGAGGCACTCCAC AACCACTATACTCAGAAAAGTCTTT CCCTGAGTCCAGGCAAG

SEQ ID 2346	QITLKESGGGVVQPGRS LRLSCAASGFTFSSYSM NWVRQAPGKGLQWVAI ISDDGSKSYYADSVQGR FTISRDNSRNTVFLQMN SLRAEDTAMYYCARDR GTKWNQLNDVFDMWG QGTMVTVSSASTKGPS VFPLAPCSRSTSESTAA LGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSN FGTQTYTCNVDHKPSN TKVDKTVERKCCVECPP CPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVV VDVSHEDPEVQFNWYV DGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQD WLNGKEYKCKVSNKGL PAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPP MLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVM HEALHNHYTQKSLSLSP GK	SEQ ID 2454	CAGATCACCTTGAAGGAGTCTGGG GGAGGCGTGGTCCAGCCTGGGAG GTCCCTGAGACTCTCCTGTGCAGC CTCTGGATTCACCTTCAGTAGTTAT AGCATGAACTGGGTCCGCCAGGC TCCAGGCAAGGGGCTGCAGTGGG TGGCAATTATATCAGATGATGGAA GTAAGAGTTACTACGCAGACTCCG TGCAGGGCCGATTCACCATCTCCA GAGACAATTCGAGGAACACAGTAT TTCTGCAAATGAACAGCCTGAGAG CTGAGGACACGGCTATGTATTACT GTGCGAGAGACAGGGGAACTAAA TGGAACCAATTGAATGATGTTTTTG ATATGTGGGGCCAAGGGACAATG GTCACCGTCTCTTCAGCAAGCACA AAAGGTCCTTCAGTGTTCCCTCTG GCACCTTGCTCACGCAGCACCTCT GAGAGTACAGCCGCCCTGGGCTG CCTGGTAAAGGACTACTTTCCCGA ACCAGTCACTGTGTCCTGGAATAG CGGGGCCTTGACCTCTGGAGTGC ACACATTTCCAGCTGTACTGCAGT CATCTGGACTCTACAGCCTGTCCA GTGTGGTCACCGTACCTTCCTCCA ACTTTGGCACTCAAACATATACAT GTAACGTGGATCATAAGCCCTCTA ACACCAAAGTGGATAAAACTGTGG AGCGTAAGTGTTGTGTCGAGTGTC CTCCTTGTCCTGCTCCTCCTGTGG CAGGCCCATCTGTGTTTCTCTTTC CCCCAAAGCCAAAGGACACTTTGA TGATATCCCGGACCCCTGAGGTGA CTTGCGTCGTCGTAGATGTTTCAC ACGAAGATCCAGAGGTGCAGTTCA ACTGGTACGTGGATGGCGTGGAA GTGCATAATGCCAAGACAAAGCCC CGCGAAGAGCAGTTTAATTCCACC TTCCGCGTGGTGTCTGTGCTGACC GTGGTACATCAGGATTGGCTTAAC GGTAAGGAGTACAAGTGCAAGGT GAGTAACAAGGGGCTGCCCGCCC CTATCGAGAAGACTATCAGTAAAA CCAAGGGCCAGCCAAGGGAGCCA CAGGTGTACACACTTCCACCATCT AGGGAGGAAATGACAAAGAACCA GGTGAGTTTGACCTGTCTCGTGAA AGGCTTTTATCCCAGTGATATAGC CGTGGAATGGGAAAGTAACGGGC AGCCCGAGAACAACTATAAGACCA CACCACCCATGCTGGACTCCGAC GGTTCTTTCTTCCTTTATAGCAAGC TGACAGTGGATAAATCCAGGTGGC AGCAGGGTAACGTATTCAGTTGCA GTGTCATGCACGAGGCACTCCACA

			ACCACTATACTCAGAAAAGTCTTTC CCTGAGTCCAGGCAAG

SEQ ID 2347	EVQLVQSGAEVKKPGA SVKVSCKASGYTFTSYY MHWVRQAPGQGLEWM GIINPSGGSTSYAQKFQ GRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCAR GRGYSSSRLYYFDYWG QGTLVTVSSASTKGPSV FPLAPCSRSTSESTAAL GCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSN FGTQTYTCNVDHKPSN TKVDKTVERKCCVECPP CPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVV VDVSHEDPEVQFNWYV DGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQD WLNGKEYKCKVSNKGL PAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPP MLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVM HEALHNHYTQKSLSLSP GK	SEQ ID 2455	GAAGTGCAGCTGGTGCAGTCTGG GGCTGAGGTGAAGAAGCCTGGGG CCTCAGTGAAGGTTTCCTGCAAGG CATCTGGATACACCTTCACCAGCT ACTATATGCACTGGGTGCGACAGG CCCCTGGACAAGGGCTTGAGTGG ATGGGAATAATCAACCCTAGTGGT GGTAGCACAAGCTACGCACAGAA GTTCCAGGGCAGAGTCACCATGA CCAGGGACACGTCCACGAGCACA GTCTACATGGAGCTGAGCAGCCT GAGATCTGAGGACACGGCCGTGT ATTACTGTGCGAGAGGCCGAGGG TATAGCAGCAGTCGGCTCTACTAC TTTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTCTCCTCAGCAAG CACAAAAGGTCCTTCAGTGTTCCC TCTGGCACCTTGCTCACGCAGCAC CTCTGAGAGTACAGCCGCCCTGG GCTGCCTGGTAAAGGACTACTTTC CCGAACCAGTCACTGTGTCCTGGA ATAGCGGGGCCTTGACCTCTGGA GTGCACACATTTCCAGCTGTACTG CAGTCATCTGGACTCTACAGCCTG TCCAGTGTGGTCACCGTACCTTCC TCCAACTTTGGCACTCAAACATATA CATGTAACGTGGATCATAAGCCCT CTAACACCAAAGTGGATAAAACTG TGGAGCGTAAGTGTTGTGTCGAGT GTCCTCCTTGTCCTGCTCCTCCTG TGGCAGGCCCATCTGTGTTTCTCT TTCCCCCAAAGCCAAAGGACACTT TGATGATATCCCGGACCCCTGAGG TGACTTGCGTCGTCGTAGATGTTT CACACGAAGATCCAGAGGTGCAG TTCAACTGGTACGTGGATGGCGTG GAAGTGCATAATGCCAAGACAAAG CCCCGCGAAGAGCAGTTTAATTCC ACCTTCCGCGTGGTGTCTGTGCTG ACCGTGGTACATCAGGATTGGCTT AACGGTAAGGAGTACAAGTGCAAG GTGAGTAACAAGGGGCTGCCCGC CCCTATCGAGAAGACTATCAGTAA AACCAAGGGCCAGCCAAGGGAGC CACAGGTGTACACACTTCCACCAT CTAGGGAGGAAATGACAAAGAACC AGGTGAGTTTGACCTGTCTCGTGA AAGGCTTTTATCCCAGTGATATAG CCGTGGAATGGGAAAGTAACGGG CAGCCCGAGAACAACTATAAGACC ACACCACCCATGCTGGACTCCGAC GGTTCTTTCTTCCTTTATAGCAAGC TGACAGTGGATAAATCCAGGTGGC AGCAGGGTAACGTATTCAGTTGCA GTGTCATGCACGAGGCACTCCACA

			ACCACTATACTCAGAAAAGTCTTTC CCTGAGTCCAGGCAAG

SEQ ID 2348	QVTLKESGGGLVRPGG SLRLSCEASGFTFSDPY MDWVRQAPGKGLEWV GRITNKRTGYATTYAAS VKDRFTISRDDSRKSVY LQMNSLKTEDTAVYYCA TDVSGSFAAYGGQGTL VTVSSASTKGPSVFPLA PCSRSTSESTAALGCLV KDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGL YSLSSVVTVPSSNFGTQ TYTCNVDHKPSNTKVDK TVERKCCVECPPCPAP PVAGPSVFLFPPKPKDT LMISRTPEVTCVVVDVS HEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTF RVVSVLTVVHQDWLNG KEYKCKVSNKGLPAPIE KTISKTKGQPREPQVYT LPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESN GQPENNYKTTPPMLDS DGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALH NHYTQKSLSLSPGK	SEQ ID 2456	CAGGTCACCTTGAAGGAGTCTGG GGGAGGCTTGGTCCGGCCTGGAG GGTCCCTGAGACTCTCCTGTGAAG CCTCTGGATTCACCTTCAGTGACC CCTACATGGACTGGGTCCGCCAG GCTCCAGGCAAGGGGCTGGAGTG GGTTGGCCGAATTACAAATAAGCG TACCGGTTACGCCACAACATATGC CGCGTCTGTGAAGGACAGATTCAC CATCTCAAGAGATGATTCAAGGAA GTCAGTATATCTGCAAATGAACAG CCTGAAGACCGAGGACACGGCCG TATATTATTGTGCAACAGATGTCAG TGGGTCCTTCGCGGCCTACGGGG GCCAGGGCACCCTGGTCACCGTC TCCTCAGCAAGCACAAAAGGTCCT TCAGTGTTCCCTCTGGCACCTTGC TCACGCAGCACCTCTGAGAGTACA GCCGCCCTGGGCTGCCTGGTAAA GGACTACTTTCCCGAACCAGTCAC TGTGTCCTGGAATAGCGGGGCCTT GACCTCTGGAGTGCACACATTTCC AGCTGTACTGCAGTCATCTGGACT CTACAGCCTGTCCAGTGTGGTCAC CGTACCTTCCTCCAACTTTGGCAC TCAAACATATACATGTAACGTGGA TCATAAGCCCTCTAACACCAAAGT GGATAAAACTGTGGAGCGTAAGTG TTGTGTCGAGTGTCCTCCTTGTCC TGCTCCTCCTGTGGCAGGCCCATC TGTGTTTCTCTTTCCCCCAAAGCC AAAGGACACTTTGATGATATCCCG GACCCCTGAGGTGACTTGCGTCG TCGTAGATGTTTCACACGAAGATC CAGAGGTGCAGTTCAACTGGTACG TGGATGGCGTGGAAGTGCATAATG CCAAGACAAAGCCCCGCGAAGAG CAGTTTAATTCCACCTTCCGCGTG GTGTCTGTGCTGACCGTGGTACAT CAGGATTGGCTTAACGGTAAGGAG TACAAGTGCAAGGTGAGTAACAAG GGGCTGCCCGCCCCTATCGAGAA GACTATCAGTAAAACCAAGGGCCA GCCAAGGGAGCCACAGGTGTACA CACTTCCACCATCTAGGGAGGAAA TGACAAAGAACCAGGTGAGTTTGA CCTGTCTCGTGAAAGGCTTTTATC CCAGTGATATAGCCGTGGAATGG GAAAGTAACGGGCAGCCCGAGAA CAACTATAAGACCACACCACCCAT GCTGGACTCCGACGGTTCTTTCTT CCTTTATAGCAAGCTGACAGTGGA TAAATCCAGGTGGCAGCAGGGTAA CGTATTCAGTTGCAGTGTCATGCA CGAGGCACTCCACAACCACTATAC

			TCAGAAAAGTCTTTCCCTGAGTCC AGGCAAG

SEQ ID 2349	EVQLVQSGGGVVQPGR SLRLSCAASGFTFSSYA MHWVRQAPGQRLEWM GWINAGNGNTKYSQKF QGRVTITRDTSASTAYM ELSSLRSEDTAVYYCAG EGGAVAGTVYWGQGTL VTVSSASTKGPSVFPLA PCSRSTSESTAALGCLV KDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGL YSLSSVVTVPSSNFGTQ TYTCNVDHKPSNTKVDK TVERKCCVECPPCPAP PVAGPSVFLFPPKPKDT LMISRTPEVTCVVVDVS HEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTF RVVSVLTVVHQDWLNG KEYKCKVSNKGLPAPIE KTISKTKGQPREPQVYT LPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESN GQPENNYKTTPPMLDS DGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALH NHYTQKSLSLSPGK	SEQ ID 2457	GAGGTCCAGCTGGTACAGTCTGG GGGAGGCGTGGTCCAGCCTGGGA GGTCCCTGAGACTCTCCTGTGCAG CGTCTGGATTCACCTTCAGTAGCT ATGCTATGCATTGGGTGCGCCAG GCCCCCGGACAAAGGCTTGAGTG GATGGGATGGATCAACGCTGGCA ATGGTAACACAAAATATTCACAGA AGTTCCAGGGCAGAGTCACCATTA CCAGGGACACATCCGCGAGCACA GCCTACATGGAGCTGAGCAGCCT GAGATCTGAAGACACGGCTGTGTA TTACTGTGCGGGAGAGGGCGGAG CAGTGGCTGGTACTGTCTACTGGG GCCAGGGAACCCTGGTCACCGTC TCCTCAGCAAGCACAAAAGGTCCT TCAGTGTTCCCTCTGGCACCTTGC TCACGCAGCACCTCTGAGAGTACA GCCGCCCTGGGCTGCCTGGTAAA GGACTACTTTCCCGAACCAGTCAC TGTGTCCTGGAATAGCGGGGCCTT GACCTCTGGAGTGCACACATTTCC AGCTGTACTGCAGTCATCTGGACT CTACAGCCTGTCCAGTGTGGTCAC CGTACCTTCCTCCAACTTTGGCAC TCAAACATATACATGTAACGTGGA TCATAAGCCCTCTAACACCAAAGT GGATAAAACTGTGGAGCGTAAGTG TTGTGTCGAGTGTCCTCCTTGTCC TGCTCCTCCTGTGGCAGGCCCATC TGTGTTTCTCTTTCCCCCAAAGCC AAAGGACACTTTGATGATATCCCG GACCCCTGAGGTGACTTGCGTCG TCGTAGATGTTTCACACGAAGATC CAGAGGTGCAGTTCAACTGGTACG TGGATGGCGTGGAAGTGCATAATG CCAAGACAAAGCCCCGCGAAGAG CAGTTTAATTCCACCTTCCGCGTG GTGTCTGTGCTGACCGTGGTACAT CAGGATTGGCTTAACGGTAAGGAG TACAAGTGCAAGGTGAGTAACAAG GGGCTGCCCGCCCCTATCGAGAA GACTATCAGTAAAACCAAGGGCCA GCCAAGGGAGCCACAGGTGTACA CACTTCCACCATCTAGGGAGGAAA TGACAAAGAACCAGGTGAGTTTGA CCTGTCTCGTGAAAGGCTTTTATC CCAGTGATATAGCCGTGGAATGG GAAAGTAACGGGCAGCCCGAGAA CAACTATAAGACCACACCACCCAT GCTGGACTCCGACGGTTCTTTCTT CCTTTATAGCAAGCTGACAGTGGA TAAATCCAGGTGGCAGCAGGGTAA CGTATTCAGTTGCAGTGTCATGCA CGAGGCACTCCACAACCACTATAC

			TCAGAAAAGTCTTTCCCTGAGTCC AGGCAAG

SEQ ID 2350	QVQLVQSGGGLVKPGG SLRLSCAASGFTFSNAW MSWVRQAPGKGLEWV GRIKSKTDGGTTDYAAP VKGRFTISRDDSKNTLY LQMNSLKTEDTAVYYCT TDEYFYWGQGTLVTVS SASTKGPSVFPLAPCSR STSESTAALGCLVKDYF PEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLS SVVTVPSSNFGTQTYTC NVDHKPSNTKVDKTVE RKCCVECPPCPAPPVA GPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHED PEVQFNWYVDGVEVHN AKTKPREEQFNSTFRVV SVLTVVHQDWLNGKEY KCKVSNKGLPAPIEKTIS KTKGQPREPQVYTLPPS REEMTKNQVSLTCLVK GFYPSDIAVEWESNGQ PENNYKTTPPMLDSDG SFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHN HYTQKSLSLSPGK	SEQ ID 2458	CAGGTCCAGCTGGTGCAGTCTGG GGGAGGCTTGGTAAAGCCTGGGG GGTCCCTTAGACTCTCCTGTGCAG CCTCTGGATTCACTTTCAGTAACG CCTGGATGAGCTGGGTCCGCCAG GCTCCAGGGAAGGGGCTGGAGTG GGTTGGCCGTATTAAAAGCAAAAC TGATGGTGGGACAACAGACTACG CTGCACCCGTGAAAGGCAGATTCA CCATCTCAAGAGATGATTCAAAAA ACACGCTGTATCTGCAAATGAACA GCCTGAAAACCGAGGACACAGCC GTGTATTACTGTACCACAGACGAG TATTTCTACTGGGGCCAGGGAACC CTGGTCACCGTCTCCTCAGCAAGC ACAAAAGGTCCTTCAGTGTTCCCT CTGGCACCTTGCTCACGCAGCAC CTCTGAGAGTACAGCCGCCCTGG GCTGCCTGGTAAAGGACTACTTTC CCGAACCAGTCACTGTGTCCTGGA ATAGCGGGGCCTTGACCTCTGGA GTGCACACATTTCCAGCTGTACTG CAGTCATCTGGACTCTACAGCCTG TCCAGTGTGGTCACCGTACCTTCC TCCAACTTTGGCACTCAAACATATA CATGTAACGTGGATCATAAGCCCT CTAACACCAAAGTGGATAAAACTG TGGAGCGTAAGTGTTGTGTCGAGT GTCCTCCTTGTCCTGCTCCTCCTG TGGCAGGCCCATCTGTGTTTCTCT TTCCCCCAAAGCCAAAGGACACTT TGATGATATCCCGGACCCCTGAGG TGACTTGCGTCGTCGTAGATGTTT CACACGAAGATCCAGAGGTGCAG TTCAACTGGTACGTGGATGGCGTG GAAGTGCATAATGCCAAGACAAAG CCCCGCGAAGAGCAGTTTAATTCC ACCTTCCGCGTGGTGTCTGTGCTG ACCGTGGTACATCAGGATTGGCTT AACGGTAAGGAGTACAAGTGCAAG GTGAGTAACAAGGGGCTGCCCGC CCCTATCGAGAAGACTATCAGTAA AACCAAGGGCCAGCCAAGGGAGC CACAGGTGTACACACTTCCACCAT CTAGGGAGGAAATGACAAAGAACC AGGTGAGTTTGACCTGTCTCGTGA AAGGCTTTTATCCCAGTGATATAG CCGTGGAATGGGAAAGTAACGGG CAGCCCGAGAACAACTATAAGACC ACACCACCCATGCTGGACTCCGAC GGTTCTTTCTTCCTTTATAGCAAGC TGACAGTGGATAAATCCAGGTGGC AGCAGGGTAACGTATTCAGTTGCA GTGTCATGCACGAGGCACTCCACA ACCACTATACTCAGAAAAGTCTTTC CCTGAGTCCAGGCAAG

SEQ ID 2351	QVQLQQWGAGLLKPSE TLSLTCAVYGGSFSGYY WSWIRQPPGKGLEWIG EINHSGSTNYNPSLKSR VTISVDTSKNQFSLKLSS VTAADTAVYYCARVNP GSYTREVSNFDYWGQG TLVTVSSASTKGPSVFP LAPCSRSTSESTAALGC LVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSS GLYSLSSVVTVPSSNFG TQTYTCNVDHKPSNTKV DKTVERKCCVECPPCP APPVAGPSVFLFPPKPK DTLMISRTPEVTCVVVD VSHEDPEVQFNWYVDG VEVHNAKTKPREEQFN STFRVVSVLTVVHQDWL NGKEYKCKVSNKGLPA PIEKTISKTKGQPREPQV YTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWE SNGQPENNYKTTPPML DSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK	SEQ ID 2459	CAGGTGCAGCTACAGCAGTGGGG CGCAGGACTGTTGAAGCCTTCGG AGACCCTGTCCCTCACCTGCGCTG TCTATGGTGGGTCCTTCAGTGGTT ACTACTGGAGCTGGATCCGCCAG CCCCCAGGGAAGGGGCTGGAGTG GATTGGGGAAATCAATCATAGTGG AAGCACCAACTACAACCCGTCCCT CAAGAGTCGAGTCACCATATCAGT AGACACGTCCAAGAACCAGTTCTC CCTGAAGCTGAGCTCTGTGACCG CCGCGGACACGGCTGTGTATTACT GTGCGAGAGTAAATCCGGGGAGT TATACGAGGGAGGTGAGCAACTTT GACTACTGGGGCCAGGGAACCCT GGTGACCGTCTCCTCAGCAAGCA CAAAAGGTCCTTCAGTGTTCCCTC TGGCACCTTGCTCACGCAGCACCT CTGAGAGTACAGCCGCCCTGGGC TGCCTGGTAAAGGACTACTTTCCC GAACCAGTCACTGTGTCCTGGAAT AGCGGGGCCTTGACCTCTGGAGT GCACACATTTCCAGCTGTACTGCA GTCATCTGGACTCTACAGCCTGTC CAGTGTGGTCACCGTACCTTCCTC CAACTTTGGCACTCAAACATATAC ATGTAACGTGGATCATAAGCCCTC TAACACCAAAGTGGATAAAACTGT GGAGCGTAAGTGTTGTGTCGAGT GTCCTCCTTGTCCTGCTCCTCCTG TGGCAGGCCCATCTGTGTTTCTCT TTCCCCCAAAGCCAAAGGACACTT TGATGATATCCCGGACCCCTGAGG TGACTTGCGTCGTCGTAGATGTTT CACACGAAGATCCAGAGGTGCAG TTCAACTGGTACGTGGATGGCGTG GAAGTGCATAATGCCAAGACAAAG CCCCGCGAAGAGCAGTTTAATTCC ACCTTCCGCGTGGTGTCTGTGCTG ACCGTGGTACATCAGGATTGGCTT AACGGTAAGGAGTACAAGTGCAAG GTGAGTAACAAGGGGCTGCCCGC CCCTATCGAGAAGACTATCAGTAA AACCAAGGGCCAGCCAAGGGAGC CACAGGTGTACACACTTCCACCAT CTAGGGAGGAAATGACAAAGAACC AGGTGAGTTTGACCTGTCTCGTGA AAGGCTTTTATCCCAGTGATATAG CCGTGGAATGGGAAAGTAACGGG CAGCCCGAGAACAACTATAAGACC ACACCACCCATGCTGGACTCCGAC GGTTCTTTCTTCCTTTATAGCAAGC TGACAGTGGATAAATCCAGGTGGC AGCAGGGTAACGTATTCAGTTGCA GTGTCATGCACGAGGCACTCCACA

			ACCACTATACTCAGAAAAGTCTTTC CCTGAGTCCAGGCAAG

SEQ ID 2352	QVQLQQSGPELVKPSQ TLTLTCGISGDSVSSNS VTWNWVRQSPSRGLE WLGRTYYRSQWYYNYA VSVKSRITISPDTSKNQF SLQLNSVTPEDTAVYYC ATRGHNYGVDYWGPGT TVTVSSASTKGPSVFPL APCSRSTSESTAALGCL VKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSG LYSLSSVVTVPSSNFGT QTYTCNVDHKPSNTKV DKTVERKCCVECPPCP APPVAGPSVFLFPPKPK DTLMISRTPEVTCVVVD VSHEDPEVQFNWYVDG VEVHNAKTKPREEQFN STFRVVSVLTVVHQDWL NGKEYKCKVSNKGLPA PIEKTISKTKGQPREPQV YTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWE SNGQPENNYKTTPPML DSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK	SEQ ID 2460	CAGGTACAGCTGCAGCAGTCAGG TCCAGAATTGGTGAAGCCCTCGCA GACCCTCACACTCACCTGTGGCAT CTCCGGGGACAGTGTCTCTAGCAA CAGTGTTACTTGGAACTGGGTCAG GCAGTCCCCATCGAGAGGCCTTG AGTGGCTGGGAAGGACTTACTACC GGTCCCAGTGGTATTATAATTATG CGGTGTCTGTGAAAAGTCGAATAA CCATCAGCCCAGACACATCCAAGA ACCAGTTCTCCCTGCAGTTGAATT CTGTGACTCCCGAGGACACGGCT GTCTATTACTGTGCAACCAGGGGA CATAACTACGGTGTAGATTACTGG GGCCCGGGGACCACGGTCACCGT CTCCTCAGCAAGCACAAAAGGTCC TTCAGTGTTCCCTCTGGCACCTTG CTCACGCAGCACCTCTGAGAGTAC AGCCGCCCTGGGCTGCCTGGTAA AGGACTACTTTCCCGAACCAGTCA CTGTGTCCTGGAATAGCGGGGCC TTGACCTCTGGAGTGCACACATTT CCAGCTGTACTGCAGTCATCTGGA CTCTACAGCCTGTCCAGTGTGGTC ACCGTACCTTCCTCCAACTTTGGC ACTCAAACATATACATGTAACGTG GATCATAAGCCCTCTAACACCAAA GTGGATAAAACTGTGGAGCGTAAG TGTTGTGTCGAGTGTCCTCCTTGT CCTGCTCCTCCTGTGGCAGGCCC ATCTGTGTTTCTCTTTCCCCCAAAG CCAAAGGACACTTTGATGATATCC CGGACCCCTGAGGTGACTTGCGT CGTCGTAGATGTTTCACACGAAGA TCCAGAGGTGCAGTTCAACTGGTA CGTGGATGGCGTGGAAGTGCATA ATGCCAAGACAAAGCCCCGCGAA GAGCAGTTTAATTCCACCTTCCGC GTGGTGTCTGTGCTGACCGTGGTA CATCAGGATTGGCTTAACGGTAAG GAGTACAAGTGCAAGGTGAGTAAC AAGGGGCTGCCCGCCCCTATCGA GAAGACTATCAGTAAAACCAAGGG CCAGCCAAGGGAGCCACAGGTGT ACACACTTCCACCATCTAGGGAGG AAATGACAAAGAACCAGGTGAGTT TGACCTGTCTCGTGAAAGGCTTTT ATCCCAGTGATATAGCCGTGGAAT GGGAAAGTAACGGGCAGCCCGAG AACAACTATAAGACCACACCACCC ATGCTGGACTCCGACGGTTCTTTC TTCCTTTATAGCAAGCTGACAGTG GATAAATCCAGGTGGCAGCAGGG TAACGTATTCAGTTGCAGTGTCAT GCACGAGGCACTCCACAACCACTA

			TACTCAGAAAAGTCTTTCCCTGAG TCCAGGCAAG

SEQ ID 2353	QVQLVQSGGGLVKPGG SLRLSCAASGFTFSNAW MSWVRQAPGKGLEWV CRIKSKTDGETTDYAAP VKGRFTISRDDSKNTLY LQMNSLKTEDTAVYHCT TGVGWSPFQYWGQGT LVTVSSASTKGPSVFPL APCSRSTSESTAALGCL VKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSG LYSLSSVVTVPSSNFGT QTYTCNVDHKPSNTKV DKTVERKCCVECPPCP APPVAGPSVFLFPPKPK DTLMISRTPEVTCVVVD VSHEDPEVQFNWYVDG VEVHNAKTKPREEQFN STFRVVSVLTVVHQDWL NGKEYKCKVSNKGLPA PIEKTISKTKGQPREPQV YTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWE SNGQPENNYKTTPPML DSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK	SEQ ID 2461	CAGGTGCAGCTGGTGCAGTCTGG GGGAGGCTTGGTAAAGCCTGGGG GGTCCCTTAGACTCTCCTGTGCAG CCTCTGGATTCACTTTCAGTAACG CCTGGATGAGCTGGGTCCGCCAG GCTCCAGGGAAGGGGCTGGAGTG GGTTTGCCGTATTAAAAGCAAAAC TGATGGTGAGACAACAGACTACGC TGCACCCGTGAAAGGCAGATTCAC CATCTCAAGAGATGATTCAAAAAA CACGCTGTATCTGCAAATGAACAG CCTGAAAACTGAGGACACAGCCGT GTATCACTGTACCACAGGGGTGG GATGGTCGCCCTTCCAATACTGGG GCCAGGGCACCCTGGTCACCGTC TCCTCAGCAAGCACAAAAGGTCCT TCAGTGTTCCCTCTGGCACCTTGC TCACGCAGCACCTCTGAGAGTACA GCCGCCCTGGGCTGCCTGGTAAA GGACTACTTTCCCGAACCAGTCAC TGTGTCCTGGAATAGCGGGGCCTT GACCTCTGGAGTGCACACATTTCC AGCTGTACTGCAGTCATCTGGACT CTACAGCCTGTCCAGTGTGGTCAC CGTACCTTCCTCCAACTTTGGCAC TCAAACATATACATGTAACGTGGA TCATAAGCCCTCTAACACCAAAGT GGATAAAACTGTGGAGCGTAAGTG TTGTGTCGAGTGTCCTCCTTGTCC TGCTCCTCCTGTGGCAGGCCCATC TGTGTTTCTCTTTCCCCCAAAGCC AAAGGACACTTTGATGATATCCCG GACCCCTGAGGTGACTTGCGTCG TCGTAGATGTTTCACACGAAGATC CAGAGGTGCAGTTCAACTGGTACG TGGATGGCGTGGAAGTGCATAATG CCAAGACAAAGCCCCGCGAAGAG CAGTTTAATTCCACCTTCCGCGTG GTGTCTGTGCTGACCGTGGTACAT CAGGATTGGCTTAACGGTAAGGAG TACAAGTGCAAGGTGAGTAACAAG GGGCTGCCCGCCCCTATCGAGAA GACTATCAGTAAAACCAAGGGCCA GCCAAGGGAGCCACAGGTGTACA CACTTCCACCATCTAGGGAGGAAA TGACAAAGAACCAGGTGAGTTTGA CCTGTCTCGTGAAAGGCTTTTATC CCAGTGATATAGCCGTGGAATGG GAAAGTAACGGGCAGCCCGAGAA CAACTATAAGACCACACCACCCAT GCTGGACTCCGACGGTTCTTTCTT CCTTTATAGCAAGCTGACAGTGGA TAAATCCAGGTGGCAGCAGGGTAA CGTATTCAGTTGCAGTGTCATGCA CGAGGCACTCCACAACCACTATAC

			TCAGAAAAGTCTTTCCCTGAGTCC AGGCAAG

SEQ ID 2354	EVQLVQSGGGLVQPGR SLRLSCTASGFTFGDYA MSWFRQAPGKGLEWV GFIRSKAYGGTTEYAAS VKGRFTISRDDSKSIAYL QMNSLKTEDTAVYYCT RDDKIAAAGFTYWYFDL WGRGTLVTVSSASTKG PSVFPLAPCSRSTSEST AALGCLVKDYFPEPVTV SWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVP SSNFGTQTYTCNVDHK PSNTKVDKTVERKCCVE CPPCPAPPVAGPSVFLF PPKPKDTLMISRTPEVT CVVVDVSHEDPEVQFN WYVDGVEVHNAKTKPR EEQFNSTFRVVSVLTVV HQDWLNGKEYKCKVSN KGLPAPIEKTISKTKGQP REPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDI AVEWESNGQPENNYKT TPPMLDSDGSFFLYSKL TVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSL SPGK	SEQ ID 2462	GAGGTCCAGCTGGTACAGTCTGG GGGAGGCTTGGTACAGCCAGGGC GGTCCCTGAGACTCTCCTGTACAG CTTCTGGATTCACCTTTGGTGATTA TGCTATGAGCTGGTTCCGCCAGG CTCCAGGGAAGGGGCTGGAGTGG GTAGGTTTCATTAGAAGCAAAGCT TATGGTGGGACAACAGAATACGCC GCGTCTGTGAAAGGCAGATTCACC ATCTCAAGAGATGATTCCAAAAGC ATCGCCTATCTGCAAATGAACAGC CTGAAAACCGAGGACACAGCCGT GTATTACTGTACTAGAGACGACAA AATAGCAGCAGCTGGATTCACATA CTGGTACTTCGATCTCTGGGGCCG TGGCACCCTGGTCACCGTCTCCTC AGCAAGCACAAAAGGTCCTTCAGT GTTCCCTCTGGCACCTTGCTCACG CAGCACCTCTGAGAGTACAGCCG CCCTGGGCTGCCTGGTAAAGGAC TACTTTCCCGAACCAGTCACTGTG TCCTGGAATAGCGGGGCCTTGAC CTCTGGAGTGCACACATTTCCAGC TGTACTGCAGTCATCTGGACTCTA CAGCCTGTCCAGTGTGGTCACCGT ACCTTCCTCCAACTTTGGCACTCA AACATATACATGTAACGTGGATCA TAAGCCCTCTAACACCAAAGTGGA TAAAACTGTGGAGCGTAAGTGTTG TGTCGAGTGTCCTCCTTGTCCTGC TCCTCCTGTGGCAGGCCCATCTGT GTTTCTCTTTCCCCCAAAGCCAAA GGACACTTTGATGATATCCCGGAC CCCTGAGGTGACTTGCGTCGTCGT AGATGTTTCACACGAAGATCCAGA GGTGCAGTTCAACTGGTACGTGGA TGGCGTGGAAGTGCATAATGCCAA GACAAAGCCCCGCGAAGAGCAGT TTAATTCCACCTTCCGCGTGGTGT CTGTGCTGACCGTGGTACATCAGG ATTGGCTTAACGGTAAGGAGTACA AGTGCAAGGTGAGTAACAAGGGG CTGCCCGCCCCTATCGAGAAGACT ATCAGTAAAACCAAGGGCCAGCCA AGGGAGCCACAGGTGTACACACTT CCACCATCTAGGGAGGAAATGACA AAGAACCAGGTGAGTTTGACCTGT CTCGTGAAAGGCTTTTATCCCAGT GATATAGCCGTGGAATGGGAAAGT AACGGGCAGCCCGAGAACAACTA TAAGACCACACCACCCATGCTGGA CTCCGACGGTTCTTTCTTCCTTTAT AGCAAGCTGACAGTGGATAAATCC AGGTGGCAGCAGGGTAACGTATT CAGTTGCAGTGTCATGCACGAGG CACTCCACAACCACTATACTCAGA

			AAAGTCTTTCCCTGAGTCCAGGCAAG

SEQ ID 2355	QVQLVQSGAEVKKPGA SVKVSCKASGYTFAAYY LHWVRQAPGQGLEWM GRISPGNGVTSYAQKFQ GRVTMTGDTSINTVYM QLNNLISGDTAVYYCAR EAADDPFDHWGQGALV TVSSASTKGPSVFPLAP CSRSTSESTAALGCLVK DYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLY SLSSVVTVPSSNFGTQT YTCNVDHKPSNTKVDKT VERKCCVECPPCPAPP VAGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSH EDPEVQFNWYVDGVEV HNAKTKPREEQFNSTFR VVSVLTVVHQDWLNGK EYKCKVSNKGLPAPIEK TISKTKGQPREPQVYTL PPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNG QPENNYKTTPPMLDSD GSFFLYSKLTVDKSRW QQGNVFSCSVMHEALH NHYTQKSLSLSPGK	SEQ ID 2463	CAGGTGCAGCTGGTGCAGTCTGG GGCTGAGGTGAAGAAGCCTGGGG CCTCAGTGAAGGTCTCCTGCAAGG CTTCTGGATACACCTTCGCCGCCT ATTATTTACACTGGGTGCGACAGG CCCCTGGACAAGGCCTTGAGTGG ATGGGGCGGATCAGCCCTGGTAA CGGTGTCACAAGTTATGCACAGAA ATTTCAGGGCAGAGTCACCATGAC CGGGGACACGTCCATTAACACAGT CTACATGCAACTGAACAATTTGATT TCTGGCGACACGGCCGTATATTAC TGTGCGAGAGAGGCTGCCGACGA CCCGTTTGACCATTGGGGCCAGG GAGCCCTGGTCACCGTCTCCTCA GCAAGCACAAAAGGTCCTTCAGTG TTCCCTCTGGCACCTTGCTCACGC AGCACCTCTGAGAGTACAGCCGC CCTGGGCTGCCTGGTAAAGGACT ACTTTCCCGAACCAGTCACTGTGT CCTGGAATAGCGGGGCCTTGACC TCTGGAGTGCACACATTTCCAGCT GTACTGCAGTCATCTGGACTCTAC AGCCTGTCCAGTGTGGTCACCGTA CCTTCCTCCAACTTTGGCACTCAA ACATATACATGTAACGTGGATCAT AAGCCCTCTAACACCAAAGTGGAT AAAACTGTGGAGCGTAAGTGTTGT GTCGAGTGTCCTCCTTGTCCTGCT CCTCCTGTGGCAGGCCCATCTGT GTTTCTCTTTCCCCCAAAGCCAAA GGACACTTTGATGATATCCCGGAC CCCTGAGGTGACTTGCGTCGTCGT AGATGTTTCACACGAAGATCCAGA GGTGCAGTTCAACTGGTACGTGGA TGGCGTGGAAGTGCATAATGCCAA GACAAAGCCCCGCGAAGAGCAGT TTAATTCCACCTTCCGCGTGGTGT CTGTGCTGACCGTGGTACATCAGG ATTGGCTTAACGGTAAGGAGTACA AGTGCAAGGTGAGTAACAAGGGG CTGCCCGCCCCTATCGAGAAGACT ATCAGTAAAACCAAGGGCCAGCCA AGGGAGCCACAGGTGTACACACTT CCACCATCTAGGGAGGAAATGACA AAGAACCAGGTGAGTTTGACCTGT CTCGTGAAAGGCTTTTATCCCAGT GATATAGCCGTGGAATGGGAAAGT AACGGGCAGCCCGAGAACAACTA TAAGACCACACCACCCATGCTGGA CTCCGACGGTTCTTTCTTCCTTTAT AGCAAGCTGACAGTGGATAAATCC AGGTGGCAGCAGGGTAACGTATT CAGTTGCAGTGTCATGCACGAGG CACTCCACAACCACTATACTCAGA

			AAAGTCTTTCCCTGAGTCCAGGCAAG

SEQ ID 2356	EVQLVQSGGGVVQPGR SLTLSCAASGFTFSSHL MHWVRQAPGKGLEWV AVISYDGTSKYYGDSVK GRFTISRDNSKNTLYLQ MNSLRAEDTAIYYCAKA DYKYDWGQGTLVTVSS ASTKGPSVFPLAPCSRS TSESTAALGCLVKDYFP EPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSS VVTVPSSNFGTQTYTCN VDHKPSNTKVDKTVERK CCVECPPCPAPPVAGP SVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEV QFNWYVDGVEVHNAKT KPREEQFNSTFRVVSVL TVVHQDWLNGKEYKCK VSNKGLPAPIEKTISKTK GQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFY PSDIAVEWESNGQPEN NYKTTPPMLDSDGSFFL YSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQ KSLSLSPGK	SEQ ID 2464	GAAGTGCAGCTGGTGCAGTCTGG GGGAGGCGTGGTCCAGCCTGGGA GGTCCCTGACACTCTCCTGTGCAG CCTCTGGATTCACCTTCAGTTCCC ATCTTATGCACTGGGTCCGCCAGG CTCCAGGCAAGGGGCTGGAGTGG GTGGCAGTTATATCATATGATGGA ACTAGTAAATATTACGGAGACTCC GTGAAGGGCCGCTTCACCATCTCC AGAGACAATTCCAAGAACACGTTG TATCTGCAAATGAACAGCCTGCGA GCTGAAGACACGGCTATATATTAC TGTGCGAAAGCAGATTATAAATAT GACTGGGGCCAGGGAACCCTGGT CACCGTCTCCTCAGCAAGCACAAA AGGTCCTTCAGTGTTCCCTCTGGC ACCTTGCTCACGCAGCACCTCTGA GAGTACAGCCGCCCTGGGCTGCC TGGTAAAGGACTACTTTCCCGAAC CAGTCACTGTGTCCTGGAATAGCG GGGCCTTGACCTCTGGAGTGCAC ACATTTCCAGCTGTACTGCAGTCA TCTGGACTCTACAGCCTGTCCAGT GTGGTCACCGTACCTTCCTCCAAC TTTGGCACTCAAACATATACATGTA ACGTGGATCATAAGCCCTCTAACA CCAAAGTGGATAAAACTGTGGAGC GTAAGTGTTGTGTCGAGTGTCCTC CTTGTCCTGCTCCTCCTGTGGCAG GCCCATCTGTGTTTCTCTTTCCCC CAAAGCCAAAGGACACTTTGATGA TATCCCGGACCCCTGAGGTGACTT GCGTCGTCGTAGATGTTTCACACG AAGATCCAGAGGTGCAGTTCAACT GGTACGTGGATGGCGTGGAAGTG CATAATGCCAAGACAAAGCCCCGC GAAGAGCAGTTTAATTCCACCTTC CGCGTGGTGTCTGTGCTGACCGT GGTACATCAGGATTGGCTTAACGG TAAGGAGTACAAGTGCAAGGTGAG TAACAAGGGGCTGCCCGCCCCTA TCGAGAAGACTATCAGTAAAACCA AGGGCCAGCCAAGGGAGCCACAG GTGTACACACTTCCACCATCTAGG GAGGAAATGACAAAGAACCAGGT GAGTTTGACCTGTCTCGTGAAAGG CTTTTATCCCAGTGATATAGCCGT GGAATGGGAAAGTAACGGGCAGC CCGAGAACAACTATAAGACCACAC CACCCATGCTGGACTCCGACGGTT CTTTCTTCCTTTATAGCAAGCTGAC AGTGGATAAATCCAGGTGGCAGCA GGGTAACGTATTCAGTTGCAGTGT CATGCACGAGGCACTCCACAACCA CTATACTCAGAAAAGTCTTTCCCT GAGTCCAGGCAAG

SEQ ID 2357	EVQLVQSGGGLVKPGG SLRLSCTASGFTFGDYA MSWVRQAPGKGLEWV GFIRSKAYGGTTEYAAS VKGRFTISRDDSKSIAYL QMNSLKTEDTAVYYCTT HRRPIYDILTGFDYWGQ GTLVTVSSASTKGPSVF PLAPCSRSTSESTAALG CLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSNF GTQTYTCNVDHKPSNT KVDKTVERKCCVECPP CPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVV VDVSHEDPEVQFNWYV DGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQD WLNGKEYKCKVSNKGL PAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPP MLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVM HEALHNHYTQKSLSLSP GK	SEQ ID 2465	GAGGTGCAGCTGGTGCAGTCTGG GGGAGGCTTGGTCAAGCCTGGAG GGTCCCTGAGACTCTCCTGTACAG CTTCTGGATTCACCTTTGGTGATTA TGCTATGAGCTGGGTCCGCCAGG CTCCAGGGAAGGGGCTGGAGTGG GTAGGTTTCATTAGAAGCAAAGCT TATGGTGGGACAACAGAATACGCC GCGTCTGTGAAAGGCAGATTCACC ATCTCAAGAGATGATTCCAAAAGC ATCGCCTATCTGCAAATGAACAGC CTGAAAACCGAGGACACAGCCGT GTATTACTGTACTACTCATAGACG CCCAATTTACGATATTTTGACTGGT TTTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTCTCCTCAGCAAG CACAAAAGGTCCTTCAGTGTTCCC TCTGGCACCTTGCTCACGCAGCAC CTCTGAGAGTACAGCCGCCCTGG GCTGCCTGGTAAAGGACTACTTTC CCGAACCAGTCACTGTGTCCTGGA ATAGCGGGGCCTTGACCTCTGGA GTGCACACATTTCCAGCTGTACTG CAGTCATCTGGACTCTACAGCCTG TCCAGTGTGGTCACCGTACCTTCC TCCAACTTTGGCACTCAAACATATA CATGTAACGTGGATCATAAGCCCT CTAACACCAAAGTGGATAAAACTG TGGAGCGTAAGTGTTGTGTCGAGT GTCCTCCTTGTCCTGCTCCTCCTG TGGCAGGCCCATCTGTGTTTCTCT TTCCCCCAAAGCCAAAGGACACTT TGATGATATCCCGGACCCCTGAGG TGACTTGCGTCGTCGTAGATGTTT CACACGAAGATCCAGAGGTGCAG TTCAACTGGTACGTGGATGGCGTG GAAGTGCATAATGCCAAGACAAAG CCCCGCGAAGAGCAGTTTAATTCC ACCTTCCGCGTGGTGTCTGTGCTG ACCGTGGTACATCAGGATTGGCTT AACGGTAAGGAGTACAAGTGCAAG GTGAGTAACAAGGGGCTGCCCGC CCCTATCGAGAAGACTATCAGTAA AACCAAGGGCCAGCCAAGGGAGC CACAGGTGTACACACTTCCACCAT CTAGGGAGGAAATGACAAAGAACC AGGTGAGTTTGACCTGTCTCGTGA AAGGCTTTTATCCCAGTGATATAG CCGTGGAATGGGAAAGTAACGGG CAGCCCGAGAACAACTATAAGACC ACACCACCCATGCTGGACTCCGAC GGTTCTTTCTTCCTTTATAGCAAGC TGACAGTGGATAAATCCAGGTGGC AGCAGGGTAACGTATTCAGTTGCA GTGTCATGCACGAGGCACTCCACA

			ACCACTATACTCAGAAAAGTCTTTC CCTGAGTCCAGGCAAG

SEQ ID 2358	QLQLQESGGGLVQPGR SLRLSCTASGFTFGDYA MSWVRQAPGKGLEWV GFIRSKAYGGTTEYAAS VKGRFTISRDDSKSIAYL QMNSLKTEDTAVYYCT REDTMVRGVIPWGQGT LVTVSSASTKGPSVFPL APCSRSTSESTAALGCL VKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSG LYSLSSVVTVPSSNFGT QTYTCNVDHKPSNTKV DKTVERKCCVECPPCP APPVAGPSVFLFPPKPK DTLMISRTPEVTCVVVD VSHEDPEVQFNWYVDG VEVHNAKTKPREEQFN STFRVVSVLTVVHQDWL NGKEYKCKVSNKGLPA PIEKTISKTKGQPREPQV YTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWE SNGQPENNYKTTPPML DSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK	SEQ ID 2466	CAGCTGCAGCTGCAGGAGTCCGG GGGAGGCTTGGTACAGCCAGGGC GGTCCCTGAGACTCTCCTGTACAG CTTCTGGATTCACCTTTGGTGATTA TGCTATGAGCTGGGTCCGCCAGG CTCCAGGGAAGGGGCTGGAGTGG GTAGGTTTCATTAGAAGCAAAGCT TATGGTGGGACAACAGAATACGCC GCGTCTGTGAAAGGCAGATTCACC ATCTCAAGAGATGATTCCAAAAGC ATCGCCTATCTGCAAATGAACAGC CTGAAAACCGAGGACACAGCCGT GTATTACTGTACTAGAGAGGATAC TATGGTTCGGGGAGTTATTCCCTG GGGCCAGGGAACCCTGGTCACCG TCTCCTCAGCAAGCACAAAAGGTC CTTCAGTGTTCCCTCTGGCACCTT GCTCACGCAGCACCTCTGAGAGTA CAGCCGCCCTGGGCTGCCTGGTA AAGGACTACTTTCCCGAACCAGTC ACTGTGTCCTGGAATAGCGGGGC CTTGACCTCTGGAGTGCACACATT TCCAGCTGTACTGCAGTCATCTGG ACTCTACAGCCTGTCCAGTGTGGT CACCGTACCTTCCTCCAACTTTGG CACTCAAACATATACATGTAACGT GGATCATAAGCCCTCTAACACCAA AGTGGATAAAACTGTGGAGCGTAA GTGTTGTGTCGAGTGTCCTCCTTG TCCTGCTCCTCCTGTGGCAGGCC CATCTGTGTTTCTCTTTCCCCCAAA GCCAAAGGACACTTTGATGATATC CCGGACCCCTGAGGTGACTTGCG TCGTCGTAGATGTTTCACACGAAG ATCCAGAGGTGCAGTTCAACTGGT ACGTGGATGGCGTGGAAGTGCAT AATGCCAAGACAAAGCCCCGCGA AGAGCAGTTTAATTCCACCTTCCG CGTGGTGTCTGTGCTGACCGTGG TACATCAGGATTGGCTTAACGGTA AGGAGTACAAGTGCAAGGTGAGTA ACAAGGGGCTGCCCGCCCCTATC GAGAAGACTATCAGTAAAACCAAG GGCCAGCCAAGGGAGCCACAGGT GTACACACTTCCACCATCTAGGGA GGAAATGACAAAGAACCAGGTGA GTTTGACCTGTCTCGTGAAAGGCT TTTATCCCAGTGATATAGCCGTGG AATGGGAAAGTAACGGGCAGCCC GAGAACAACTATAAGACCACACCA CCCATGCTGGACTCCGACGGTTCT TTCTTCCTTTATAGCAAGCTGACA GTGGATAAATCCAGGTGGCAGCA GGGTAACGTATTCAGTTGCAGTGT CATGCACGAGGCACTCCACAACCA

			CTATACTCAGAAAAGTCTTTCCCT GAGTCCAGGCAAG

SEQ ID 2359	QLQLQESGSGLVKPSQ TLSLTCAVSGGSISSGG YSWSWIRQPPGKGLEW IGYIYHSGSTYYNPSLKS RVTISVDRSKNQFSLKL SSVTAADTAVYYCARDR RYYDSSGYYPAYYFDY WGQGTLVTVSSASTKG PSVFPLAPCSRSTSEST AALGCLVKDYFPEPVTV SWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVP SSNFGTQTYTCNVDHK PSNTKVDKTVERKCCVE CPPCPAPPVAGPSVFLF PPKPKDTLMISRTPEVT CVVVDVSHEDPEVQFN WYVDGVEVHNAKTKPR EEQFNSTFRVVSVLTVV HQDWLNGKEYKCKVSN KGLPAPIEKTISKTKGQP REPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDI AVEWESNGQPENNYKT TPPMLDSDGSFFLYSKL TVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSL SPGK	SEQ ID 2467	CAGCTGCAGCTGCAGGAGTCCGG CTCAGGACTGGTGAAGCCTTCACA GACCCTGTCCCTCACCTGCGCTGT CTCTGGTGGCTCCATCAGCAGTG GTGGTTACTCCTGGAGCTGGATCC GGCAGCCACCAGGGAAGGGCCTG GAGTGGATTGGGTACATCTATCAT AGTGGGAGCACCTACTACAACCC GTCCCTCAAGAGTCGAGTCACCAT ATCAGTAGACAGGTCCAAGAACCA GTTCTCCCTGAAGCTGAGCTCTGT GACCGCCGCGGACACGGCTGTGT ATTACTGTGCGAGAGATCGGCGTT ACTATGATAGTAGTGGTTATTATCC CGCCTACTACTTTGACTACTGGGG CCAGGGAACCCTGGTCACCGTCT CCTCAGCAAGCACAAAAGGTCCTT CAGTGTTCCCTCTGGCACCTTGCT CACGCAGCACCTCTGAGAGTACA GCCGCCCTGGGCTGCCTGGTAAA GGACTACTTTCCCGAACCAGTCAC TGTGTCCTGGAATAGCGGGGCCTT GACCTCTGGAGTGCACACATTTCC AGCTGTACTGCAGTCATCTGGACT CTACAGCCTGTCCAGTGTGGTCAC CGTACCTTCCTCCAACTTTGGCAC TCAAACATATACATGTAACGTGGA TCATAAGCCCTCTAACACCAAAGT GGATAAAACTGTGGAGCGTAAGTG TTGTGTCGAGTGTCCTCCTTGTCC TGCTCCTCCTGTGGCAGGCCCATC TGTGTTTCTCTTTCCCCCAAAGCC AAAGGACACTTTGATGATATCCCG GACCCCTGAGGTGACTTGCGTCG TCGTAGATGTTTCACACGAAGATC CAGAGGTGCAGTTCAACTGGTACG TGGATGGCGTGGAAGTGCATAATG CCAAGACAAAGCCCCGCGAAGAG CAGTTTAATTCCACCTTCCGCGTG GTGTCTGTGCTGACCGTGGTACAT CAGGATTGGCTTAACGGTAAGGAG TACAAGTGCAAGGTGAGTAACAAG GGGCTGCCCGCCCCTATCGAGAA GACTATCAGTAAAACCAAGGGCCA GCCAAGGGAGCCACAGGTGTACA CACTTCCACCATCTAGGGAGGAAA TGACAAAGAACCAGGTGAGTTTGA CCTGTCTCGTGAAAGGCTTTTATC CCAGTGATATAGCCGTGGAATGG GAAAGTAACGGGCAGCCCGAGAA CAACTATAAGACCACACCACCCAT GCTGGACTCCGACGGTTCTTTCTT CCTTTATAGCAAGCTGACAGTGGA TAAATCCAGGTGGCAGCAGGGTAA CGTATTCAGTTGCAGTGTCATGCA CGAGGCACTCCACAACCACTATAC

			TCAGAAAAGTCTTTCCCTGAGTCC AGGCAAG

SEQ ID 2360	EVQLVQSGGGLVKPGG SLRLSCAASGFTFSSYS MNWVRQAPGKGLEWV SYISSSGSYTNYADSVK GRFTISRDNAKNSLYLQI NSLRAEDTAIYYCARDG GYDSSGFHFDYWGQGT LVTVSSASTKGPSVFPL APCSRSTSESTAALGCL VKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSG LYSLSSVVTVPSSNFGT QTYTCNVDHKPSNTKV DKTVERKCCVECPPCP APPVAGPSVFLFPPKPK DTLMISRTPEVTCVVVD VSHEDPEVQFNWYVDG VEVHNAKTKPREEQFN STFRVVSVLTVVHQDWL NGKEYKCKVSNKGLPA PIEKTISKTKGQPREPQV YTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWE SNGQPENNYKTTPPML DSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK	SEQ ID 2468	GAAGTGCAGCTGGTGCAGTCTGG GGGAGGCCTGGTCAAGCCTGGGG GGTCCCTGAGACTCTCCTGTGCAG CCTCTGGATTCACCTTCAGTAGCT ATAGCATGAACTGGGTCCGCCAG GCTCCAGGGAAGGGGCTGGAGTG GGTTTCATACATTAGTAGTAGTGG TAGTTACACAAACTACGCAGACTC TGTGAAGGGCCGATTCACCATCTC CAGAGACAACGCCAAGAACTCACT GTATCTGCAAATAAACAGCCTGAG AGCCGAGGACACGGCCATTTATTA CTGTGCGAGAGACGGGGGCTATG ATAGTAGTGGTTTTCACTTTGACTA CTGGGGCCAGGGAACCCTGGTCA CCGTCTCCTCAGCAAGCACAAAAG GTCCTTCAGTGTTCCCTCTGGCAC CTTGCTCACGCAGCACCTCTGAGA GTACAGCCGCCCTGGGCTGCCTG GTAAAGGACTACTTTCCCGAACCA GTCACTGTGTCCTGGAATAGCGG GGCCTTGACCTCTGGAGTGCACA CATTTCCAGCTGTACTGCAGTCAT CTGGACTCTACAGCCTGTCCAGTG TGGTCACCGTACCTTCCTCCAACT TTGGCACTCAAACATATACATGTAA CGTGGATCATAAGCCCTCTAACAC CAAAGTGGATAAAACTGTGGAGCG TAAGTGTTGTGTCGAGTGTCCTCC TTGTCCTGCTCCTCCTGTGGCAGG CCCATCTGTGTTTCTCTTTCCCCC AAAGCCAAAGGACACTTTGATGAT ATCCCGGACCCCTGAGGTGACTT GCGTCGTCGTAGATGTTTCACACG AAGATCCAGAGGTGCAGTTCAACT GGTACGTGGATGGCGTGGAAGTG CATAATGCCAAGACAAAGCCCCGC GAAGAGCAGTTTAATTCCACCTTC CGCGTGGTGTCTGTGCTGACCGT GGTACATCAGGATTGGCTTAACGG TAAGGAGTACAAGTGCAAGGTGAG TAACAAGGGGCTGCCCGCCCCTA TCGAGAAGACTATCAGTAAAACCA AGGGCCAGCCAAGGGAGCCACAG GTGTACACACTTCCACCATCTAGG GAGGAAATGACAAAGAACCAGGT GAGTTTGACCTGTCTCGTGAAAGG CTTTTATCCCAGTGATATAGCCGT GGAATGGGAAAGTAACGGGCAGC CCGAGAACAACTATAAGACCACAC CACCCATGCTGGACTCCGACGGTT CTTTCTTCCTTTATAGCAAGCTGAC AGTGGATAAATCCAGGTGGCAGCA GGGTAACGTATTCAGTTGCAGTGT CATGCACGAGGCACTCCACAACCA

			CTATACTCAGAAAAGTCTTTCCCT GAGTCCAGGCAAG

SEQ ID 2361	QVQLQQSGPGLVKPSQ TLSLTCAISGDSVSNNR AAWNWIRQSPSRGLEW LGRTYYRSKWYNEYAV SVKSRITINPDTSKNQFS LQLNSMTPEDSAVYYCA ILPSSGYLQDHHYYGMD VWGQGTTVTVSSASTK GPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVT VSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTV PSSNFGTQTYTCNVDH KPSNTKVDKTVERKCCV ECPPCPAPPVAGPSVFL FPPKPKDTLMISRTPEV TCVVVDVSHEDPEVQF NWYVDGVEVHNAKTKP REEQFNSTFRVVSVLTV VHQDWLNGKEYKCKVS NKGLPAPIEKTISKTKGQ PREPQVYTLPPSREEMT KNQVSLTCLVKGFYPSD IAVEWESNGQPENNYK TTPPMLDSDGSFFLYSK LTVDKSRWQQGNVFSC SVMHEALHNHYTQKSL SLSPGK	SEQ ID 2469	CAGGTACAGCTGCAGCAGTCAGG TCCAGGACTGGTGAAGCCCTCGC AGACCCTCTCACTCACCTGTGCCA TCTCCGGGGACAGTGTCTCTAACA ACAGGGCTGCTTGGAACTGGATCA GGCAGTCGCCATCGAGAGGCCTT GAGTGGCTGGGAAGGACATACTA CAGGTCCAAGTGGTATAATGAATA TGCAGTCTCTGTGAAAAGTCGAAT AACCATCAACCCAGACACATCCAA GAACCAGTTCTCCCTGCAGCTGAA CTCTATGACTCCCGAGGACTCGGC TGTGTATTACTGTGCAATTTTGCCT AGTAGTGGTTATCTACAGGACCAC CACTACTACGGTATGGACGTCTGG GGCCAAGGGACCACGGTCACCGT CTCCTCAGCAAGCACAAAAGGTCC TTCAGTGTTCCCTCTGGCACCTTG CTCACGCAGCACCTCTGAGAGTAC AGCCGCCCTGGGCTGCCTGGTAA AGGACTACTTTCCCGAACCAGTCA CTGTGTCCTGGAATAGCGGGGCC TTGACCTCTGGAGTGCACACATTT CCAGCTGTACTGCAGTCATCTGGA CTCTACAGCCTGTCCAGTGTGGTC ACCGTACCTTCCTCCAACTTTGGC ACTCAAACATATACATGTAACGTG GATCATAAGCCCTCTAACACCAAA GTGGATAAAACTGTGGAGCGTAAG TGTTGTGTCGAGTGTCCTCCTTGT CCTGCTCCTCCTGTGGCAGGCCC ATCTGTGTTTCTCTTTCCCCCAAAG CCAAAGGACACTTTGATGATATCC CGGACCCCTGAGGTGACTTGCGT CGTCGTAGATGTTTCACACGAAGA TCCAGAGGTGCAGTTCAACTGGTA CGTGGATGGCGTGGAAGTGCATA ATGCCAAGACAAAGCCCCGCGAA GAGCAGTTTAATTCCACCTTCCGC GTGGTGTCTGTGCTGACCGTGGTA CATCAGGATTGGCTTAACGGTAAG GAGTACAAGTGCAAGGTGAGTAAC AAGGGGCTGCCCGCCCCTATCGA GAAGACTATCAGTAAAACCAAGGG CCAGCCAAGGGAGCCACAGGTGT ACACACTTCCACCATCTAGGGAGG AAATGACAAAGAACCAGGTGAGTT TGACCTGTCTCGTGAAAGGCTTTT ATCCCAGTGATATAGCCGTGGAAT GGGAAAGTAACGGGCAGCCCGAG AACAACTATAAGACCACACCACCC ATGCTGGACTCCGACGGTTCTTTC TTCCTTTATAGCAAGCTGACAGTG GATAAATCCAGGTGGCAGCAGGG TAACGTATTCAGTTGCAGTGTCAT GCACGAGGCACTCCACAACCACTA

			TACTCAGAAAAGTCTTTCCCTGAG TCCAGGCAAG

SEQ ID 2362	EVQLVQSGAEVKKPGA SVKVSCKASGYTFTSYG ISWVRQAPGQGLEWMG WISAYNGNTNYAQKLQ GRVTMTTDTSTSTAYM ELSSLRSEDTAVYYCAR AAVGDGYSYGRLDWG QGTLVTVSSASTKGPSV FPLAPCSRSTSESTAAL GCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSN FGTQTYTCNVDHKPSN TKVDKTVERKCCVECPP CPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVV VDVSHEDPEVQFNWYV DGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQD WLNGKEYKCKVSNKGL PAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPP MLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVM HEALHNHYTQKSLSLSP GK	SEQ ID 2470	GAGGTGCAGCTGGTGCAGTCTGG AGCTGAGGTGAAGAAGCCTGGGG CCTCAGTGAAGGTCTCCTGCAAGG CTTCTGGTTACACCTTTACCAGCT ACGGTATCAGCTGGGTGCGACAG GCCCCTGGACAAGGGCTTGAGTG GATGGGATGGATCAGCGCTTACAA TGGTAACACAAACTATGCACAGAA GCTCCAGGGCAGAGTCACCATGA CCACAGACACATCCACGAGCACA GCCTACATGGAGCTGAGCAGCCT GAGATCTGAGGACACGGCCGTGT ATTACTGTGCGAGAGCCGCGGTG GGGGATGGATACAGCTATGGTCG GCTCGATTGGGGCCAGGGAACCC TGGTCACCGTCTCCTCAGCAAGCA CAAAAGGTCCTTCAGTGTTCCCTC TGGCACCTTGCTCACGCAGCACCT CTGAGAGTACAGCCGCCCTGGGC TGCCTGGTAAAGGACTACTTTCCC GAACCAGTCACTGTGTCCTGGAAT AGCGGGGCCTTGACCTCTGGAGT GCACACATTTCCAGCTGTACTGCA GTCATCTGGACTCTACAGCCTGTC CAGTGTGGTCACCGTACCTTCCTC CAACTTTGGCACTCAAACATATAC ATGTAACGTGGATCATAAGCCCTC TAACACCAAAGTGGATAAAACTGT GGAGCGTAAGTGTTGTGTCGAGT GTCCTCCTTGTCCTGCTCCTCCTG TGGCAGGCCCATCTGTGTTTCTCT TTCCCCCAAAGCCAAAGGACACTT TGATGATATCCCGGACCCCTGAGG TGACTTGCGTCGTCGTAGATGTTT CACACGAAGATCCAGAGGTGCAG TTCAACTGGTACGTGGATGGCGTG GAAGTGCATAATGCCAAGACAAAG CCCCGCGAAGAGCAGTTTAATTCC ACCTTCCGCGTGGTGTCTGTGCTG ACCGTGGTACATCAGGATTGGCTT AACGGTAAGGAGTACAAGTGCAAG GTGAGTAACAAGGGGCTGCCCGC CCCTATCGAGAAGACTATCAGTAA AACCAAGGGCCAGCCAAGGGAGC CACAGGTGTACACACTTCCACCAT CTAGGGAGGAAATGACAAAGAACC AGGTGAGTTTGACCTGTCTCGTGA AAGGCTTTTATCCCAGTGATATAG CCGTGGAATGGGAAAGTAACGGG CAGCCCGAGAACAACTATAAGACC ACACCACCCATGCTGGACTCCGAC GGTTCTTTCTTCCTTTATAGCAAGC TGACAGTGGATAAATCCAGGTGGC AGCAGGGTAACGTATTCAGTTGCA GTGTCATGCACGAGGCACTCCACA

			ACCACTATACTCAGAAAAGTCTTTC CCTGAGTCCAGGCAAG

SEQ ID 2363	EVQLVQSGAEVKKPGE SLKISCKGSGYSFTSYW IGWVRQMPGKGLEWM GIIYPGDSDTRYSPSFQ GQVTISADKSISTAYLQ WSSLKASDTAMYYCAR LPSYYYDSSGYFTWYF DLWGRGTLVTVSSAST KGPSVFPLAPCSRSTSE STAALGCLVKDYFPEPV TVSWNSGALTSGVHTF PAVLQSSGLYSLSSVVT VPSSNFGTQTYTCNVD HKPSNTKVDKTVERKC CVECPPCPAPPVAGPS VFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEV QFNWYVDGVEVHNAKT KPREEQFNSTFRVVSVL TVVHQDWLNGKEYKCK VSNKGLPAPIEKTISKTK GQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFY PSDIAVEWESNGQPEN NYKTTPPMLDSDGSFFL YSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQ KSLSLSPGK	SEQ ID 2471	GAGGTCCAGCTGGTACAGTCTGG AGCAGAGGTGAAAAAGCCCGGGG AGTCTCTGAAGATCTCCTGTAAGG GTTCTGGATACAGCTTTACCAGCT ACTGGATCGGCTGGGTGCGCCAG ATGCCCGGGAAAGGCCTGGAGTG GATGGGGATCATCTATCCTGGTGA CTCTGATACCAGATACAGCCCGTC CTTCCAAGGCCAGGTCACCATCTC AGCCGACAAGTCCATCAGCACCG CCTACCTGCAGTGGAGCAGCCTG AAGGCCTCGGACACCGCCATGTAT TACTGTGCGAGACTCCCCTCGTAT TACTATGATAGTAGTGGTTACTTTA CCTGGTACTTCGATCTCTGGGGCC GTGGCACCCTGGTGACCGTCTCTT CAGCAAGCACAAAAGGTCCTTCAG TGTTCCCTCTGGCACCTTGCTCAC GCAGCACCTCTGAGAGTACAGCC GCCCTGGGCTGCCTGGTAAAGGA CTACTTTCCCGAACCAGTCACTGT GTCCTGGAATAGCGGGGCCTTGA CCTCTGGAGTGCACACATTTCCAG CTGTACTGCAGTCATCTGGACTCT ACAGCCTGTCCAGTGTGGTCACC GTACCTTCCTCCAACTTTGGCACT CAAACATATACATGTAACGTGGAT CATAAGCCCTCTAACACCAAAGTG GATAAAACTGTGGAGCGTAAGTGT TGTGTCGAGTGTCCTCCTTGTCCT GCTCCTCCTGTGGCAGGCCCATCT GTGTTTCTCTTTCCCCCAAAGCCA AAGGACACTTTGATGATATCCCGG ACCCCTGAGGTGACTTGCGTCGTC GTAGATGTTTCACACGAAGATCCA GAGGTGCAGTTCAACTGGTACGTG GATGGCGTGGAAGTGCATAATGC CAAGACAAAGCCCCGCGAAGAGC AGTTTAATTCCACCTTCCGCGTGG TGTCTGTGCTGACCGTGGTACATC AGGATTGGCTTAACGGTAAGGAGT ACAAGTGCAAGGTGAGTAACAAGG GGCTGCCCGCCCCTATCGAGAAG ACTATCAGTAAAACCAAGGGCCAG CCAAGGGAGCCACAGGTGTACAC ACTTCCACCATCTAGGGAGGAAAT GACAAAGAACCAGGTGAGTTTGAC CTGTCTCGTGAAAGGCTTTTATCC CAGTGATATAGCCGTGGAATGGGA AAGTAACGGGCAGCCCGAGAACA ACTATAAGACCACACCACCCATGC TGGACTCCGACGGTTCTTTCTTCC TTTATAGCAAGCTGACAGTGGATA AATCCAGGTGGCAGCAGGGTAAC GTATTCAGTTGCAGTGTCATGCAC GAGGCACTCCACAACCACTATACT

			CAGAAAAGTCTTTCCCTGAGTCCA GGCAAG

SEQ ID 2364	EVQLVQSGAEVKKPGA SVKVSCKASGYTFTSYG ISWVRQAPGQGLEWMG WIIPIFGIANYAQKFQGR VTITADKSTSTAYMELSS LRSEDTAVYYCARELYN YGSKDYFDYWGQGTLV TVSSASTKGPSVFPLAP CSRSTSESTAALGCLVK DYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLY SLSSVVTVPSSNFGTQT YTCNVDHKPSNTKVDKT VERKCCVECPPCPAPP VAGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSH EDPEVQFNWYVDGVEV HNAKTKPREEQFNSTFR VVSVLTVVHQDWLNGK EYKCKVSNKGLPAPIEK TISKTKGQPREPQVYTL PPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNG QPENNYKTTPPMLDSD GSFFLYSKLTVDKSRW QQGNVFSCSVMHEALH NHYTQKSLSLSPGK	SEQ ID 2472	GAGGTCCAGCTGGTACAGTCTGG AGCTGAGGTGAAGAAGCCTGGGG CCTCAGTGAAGGTCTCCTGCAAGG CTTCTGGTTACACCTTTACCAGCT ATGGTATCAGCTGGGTGCGACAG GCCCCTGGACAAGGGCTTGAGTG GATGGGATGGATCATCCCTATCTT TGGTATAGCAAACTACGCACAGAA GTTCCAGGGCAGAGTCACGATTAC CGCGGACAAATCCACGAGCACAG CCTACATGGAGCTGAGCAGCCTG AGATCTGAGGACACGGCCGTGTAT TACTGTGCGAGAGAACTATACAAC TATGGTTCAAAGGACTACTTTGAC TACTGGGGCCAGGGAACCCTGGT CACCGTCTCCTCAGCAAGCACAAA AGGTCCTTCAGTGTTCCCTCTGGC ACCTTGCTCACGCAGCACCTCTGA GAGTACAGCCGCCCTGGGCTGCC TGGTAAAGGACTACTTTCCCGAAC CAGTCACTGTGTCCTGGAATAGCG GGGCCTTGACCTCTGGAGTGCAC ACATTTCCAGCTGTACTGCAGTCA TCTGGACTCTACAGCCTGTCCAGT GTGGTCACCGTACCTTCCTCCAAC TTTGGCACTCAAACATATACATGTA ACGTGGATCATAAGCCCTCTAACA CCAAAGTGGATAAAACTGTGGAGC GTAAGTGTTGTGTCGAGTGTCCTC CTTGTCCTGCTCCTCCTGTGGCAG GCCCATCTGTGTTTCTCTTTCCCC CAAAGCCAAAGGACACTTTGATGA TATCCCGGACCCCTGAGGTGACTT GCGTCGTCGTAGATGTTTCACACG AAGATCCAGAGGTGCAGTTCAACT GGTACGTGGATGGCGTGGAAGTG CATAATGCCAAGACAAAGCCCCGC GAAGAGCAGTTTAATTCCACCTTC CGCGTGGTGTCTGTGCTGACCGT GGTACATCAGGATTGGCTTAACGG TAAGGAGTACAAGTGCAAGGTGAG TAACAAGGGGCTGCCCGCCCCTA TCGAGAAGACTATCAGTAAAACCA AGGGCCAGCCAAGGGAGCCACAG GTGTACACACTTCCACCATCTAGG GAGGAAATGACAAAGAACCAGGT GAGTTTGACCTGTCTCGTGAAAGG CTTTTATCCCAGTGATATAGCCGT GGAATGGGAAAGTAACGGGCAGC CCGAGAACAACTATAAGACCACAC CACCCATGCTGGACTCCGACGGTT CTTTCTTCCTTTATAGCAAGCTGAC AGTGGATAAATCCAGGTGGCAGCA GGGTAACGTATTCAGTTGCAGTGT CATGCACGAGGCACTCCACAACCA

			CTATACTCAGAAAAGTCTTTCCCT GAGTCCAGGCAAG

SEQ ID 2365	EVQLVQSGAEVKKPGE SLKISCKGSGYSFTSYW IGWVRQMPGKGLEWM GIIYPGDSDTRYSPSFQ GQVTISADKSISTAYLQ WSSLKASDTAMYYCAR GGTWDTAMVTGFDYW GQGTLVTVSSASTKGPS VFPLAPCSRSTSESTAA LGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSN FGTQTYTCNVDHKPSN TKVDKTVERKCCVECPP CPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVV VDVSHEDPEVQFNWYV DGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQD WLNGKEYKCKVSNKGL PAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPP MLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVM HEALHNHYTQKSLSLSP GK	SEQ ID 2473	GAAGTGCAGCTGGTGCAGTCTGG AGCAGAGGTGAAAAAGCCCGGGG AGTCTCTGAAGATCTCCTGTAAGG GTTCTGGATACAGCTTTACCAGCT ACTGGATCGGCTGGGTGCGCCAG ATGCCCGGGAAAGGCCTGGAGTG GATGGGGATCATCTATCCTGGTGA CTCTGATACCAGATACAGCCCGTC CTTCCAAGGCCAGGTCACCATCTC AGCCGACAAGTCCATCAGCACCG CCTACCTGCAGTGGAGCAGCCTG AAGGCCTCGGACACCGCCATGTAT TACTGTGCGAGGGGCGGTACTTG GGATACAGCTATGGTTACGGGCTT TGACTACTGGGGCCAGGGAACCC TGGTCACCGTCTCCTCAGCAAGCA CAAAAGGTCCTTCAGTGTTCCCTC TGGCACCTTGCTCACGCAGCACCT CTGAGAGTACAGCCGCCCTGGGC TGCCTGGTAAAGGACTACTTTCCC GAACCAGTCACTGTGTCCTGGAAT AGCGGGGCCTTGACCTCTGGAGT GCACACATTTCCAGCTGTACTGCA GTCATCTGGACTCTACAGCCTGTC CAGTGTGGTCACCGTACCTTCCTC CAACTTTGGCACTCAAACATATAC ATGTAACGTGGATCATAAGCCCTC TAACACCAAAGTGGATAAAACTGT GGAGCGTAAGTGTTGTGTCGAGT GTCCTCCTTGTCCTGCTCCTCCTG TGGCAGGCCCATCTGTGTTTCTCT TTCCCCCAAAGCCAAAGGACACTT TGATGATATCCCGGACCCCTGAGG TGACTTGCGTCGTCGTAGATGTTT CACACGAAGATCCAGAGGTGCAG TTCAACTGGTACGTGGATGGCGTG GAAGTGCATAATGCCAAGACAAAG CCCCGCGAAGAGCAGTTTAATTCC ACCTTCCGCGTGGTGTCTGTGCTG ACCGTGGTACATCAGGATTGGCTT AACGGTAAGGAGTACAAGTGCAAG GTGAGTAACAAGGGGCTGCCCGC CCCTATCGAGAAGACTATCAGTAA AACCAAGGGCCAGCCAAGGGAGC CACAGGTGTACACACTTCCACCAT CTAGGGAGGAAATGACAAAGAACC AGGTGAGTTTGACCTGTCTCGTGA AAGGCTTTTATCCCAGTGATATAG CCGTGGAATGGGAAAGTAACGGG CAGCCCGAGAACAACTATAAGACC ACACCACCCATGCTGGACTCCGAC GGTTCTTTCTTCCTTTATAGCAAGC TGACAGTGGATAAATCCAGGTGGC AGCAGGGTAACGTATTCAGTTGCA GTGTCATGCACGAGGCACTCCACA

			ACCACTATACTCAGAAAAGTCTTTC CCTGAGTCCAGGCAAG

SEQ ID 2366	EVQLVQSGAEVKKPGE SLKISCKGSGYSFTSYW IAWVRQMPGKGLEWM GVIYPGDSDTRYSPSFQ GQVTISADKSINTAYLQ WSSLKASDTAMYYCAR PHYDILTGSRAPFDYWG QGTLVTVSSASTKGPSV FPLAPCSRSTSESTAAL GCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSN FGTQTYTCNVDHKPSN TKVDKTVERKCCVECPP CPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVV VDVSHEDPEVQFNWYV DGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQD WLNGKEYKCKVSNKGL PAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPP MLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVM HEALHNHYTQKSLSLSP GK	SEQ ID 2474	GAAGTGCAGCTGGTGCAGTCTGG AGCAGAGGTGAAAAAGCCCGGGG AGTCTCTGAAGATCTCCTGTAAGG GTTCTGGATACAGCTTTACCAGCT ACTGGATCGCCTGGGTGCGCCAG ATGCCCGGGAAAGGCCTGGAGTG GATGGGGGTCATCTATCCTGGTGA CTCTGATACCAGATACAGCCCGTC CTTCCAAGGCCAGGTCACCATCTC AGCCGACAAGTCCATCAATACCGC CTACCTGCAGTGGAGCAGCCTGA AGGCCTCGGACACCGCCATGTATT ACTGTGCGAGACCCCATTACGATA TTTTGACTGGTTCCCGGGCGCCCT TTGACTACTGGGGCCAGGGAACC CTGGTCACCGTCTCCTCAGCAAGC ACAAAAGGTCCTTCAGTGTTCCCT CTGGCACCTTGCTCACGCAGCAC CTCTGAGAGTACAGCCGCCCTGG GCTGCCTGGTAAAGGACTACTTTC CCGAACCAGTCACTGTGTCCTGGA ATAGCGGGGCCTTGACCTCTGGA GTGCACACATTTCCAGCTGTACTG CAGTCATCTGGACTCTACAGCCTG TCCAGTGTGGTCACCGTACCTTCC TCCAACTTTGGCACTCAAACATATA CATGTAACGTGGATCATAAGCCCT CTAACACCAAAGTGGATAAAACTG TGGAGCGTAAGTGTTGTGTCGAGT GTCCTCCTTGTCCTGCTCCTCCTG TGGCAGGCCCATCTGTGTTTCTCT TTCCCCCAAAGCCAAAGGACACTT TGATGATATCCCGGACCCCTGAGG TGACTTGCGTCGTCGTAGATGTTT CACACGAAGATCCAGAGGTGCAG TTCAACTGGTACGTGGATGGCGTG GAAGTGCATAATGCCAAGACAAAG CCCCGCGAAGAGCAGTTTAATTCC ACCTTCCGCGTGGTGTCTGTGCTG ACCGTGGTACATCAGGATTGGCTT AACGGTAAGGAGTACAAGTGCAAG GTGAGTAACAAGGGGCTGCCCGC CCCTATCGAGAAGACTATCAGTAA AACCAAGGGCCAGCCAAGGGAGC CACAGGTGTACACACTTCCACCAT CTAGGGAGGAAATGACAAAGAACC AGGTGAGTTTGACCTGTCTCGTGA AAGGCTTTTATCCCAGTGATATAG CCGTGGAATGGGAAAGTAACGGG CAGCCCGAGAACAACTATAAGACC ACACCACCCATGCTGGACTCCGAC GGTTCTTTCTTCCTTTATAGCAAGC TGACAGTGGATAAATCCAGGTGGC AGCAGGGTAACGTATTCAGTTGCA GTGTCATGCACGAGGCACTCCACA

			ACCACTATACTCAGAAAAGTCTTTC CCTGAGTCCAGGCAAG

SEQ ID 2367	QVQLQQWGAGLLKPSE TLSLTCAVYGGSFSGYY WSWIRQPPGKGLEWIG EINHSGSTNYNPSLKSR VTISVDTSKNQFSLKLSS VTAADTAVYYCARARVE SKDGYFDYWGQGTLVT VSSASTKGPSVFPLAPC SRSTSESTAALGCLVKD YFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSL SSVVTVPSSNFGTQTYT CNVDHKPSNTKVDKTV ERKCCVECPPCPAPPV AGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHE DPEVQFNWYVDGVEVH NAKTKPREEQFNSTFRV VSVLTVVHQDWLNGKE YKCKVSNKGLPAPIEKTI SKTKGQPREPQVYTLPP SREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQ PENNYKTTPPMLDSDG SFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHN HYTQKSLSLSPGK	SEQ ID 2475	CAGGTGCAGCTACAGCAGTGGGG CGCAGGACTGTTGAAGCCTTCGG AGACCCTGTCCCTCACCTGCGCTG TCTATGGTGGGTCCTTCAGTGGTT ACTACTGGAGCTGGATCCGCCAG CCCCCAGGGAAGGGGCTGGAGTG GATTGGGGAAATCAATCATAGTGG AAGCACCAACTACAACCCGTCCCT CAAGAGTCGAGTCACCATATCAGT AGACACGTCCAAGAACCAGTTCTC CCTGAAGCTGAGCTCTGTGACCG CCGCGGACACGGCTGTGTATTACT GTGCGAGAGCCCGAGTGGAATCC AAGGATGGGTACTTTGACTACTGG GGCCAGGGAACCCTGGTCACCGT CTCCTCAGCAAGCACAAAAGGTCC TTCAGTGTTCCCTCTGGCACCTTG CTCACGCAGCACCTCTGAGAGTAC AGCCGCCCTGGGCTGCCTGGTAA AGGACTACTTTCCCGAACCAGTCA CTGTGTCCTGGAATAGCGGGGCC TTGACCTCTGGAGTGCACACATTT CCAGCTGTACTGCAGTCATCTGGA CTCTACAGCCTGTCCAGTGTGGTC ACCGTACCTTCCTCCAACTTTGGC ACTCAAACATATACATGTAACGTG GATCATAAGCCCTCTAACACCAAA GTGGATAAAACTGTGGAGCGTAAG TGTTGTGTCGAGTGTCCTCCTTGT CCTGCTCCTCCTGTGGCAGGCCC ATCTGTGTTTCTCTTTCCCCCAAAG CCAAAGGACACTTTGATGATATCC CGGACCCCTGAGGTGACTTGCGT CGTCGTAGATGTTTCACACGAAGA TCCAGAGGTGCAGTTCAACTGGTA CGTGGATGGCGTGGAAGTGCATA ATGCCAAGACAAAGCCCCGCGAA GAGCAGTTTAATTCCACCTTCCGC GTGGTGTCTGTGCTGACCGTGGTA CATCAGGATTGGCTTAACGGTAAG GAGTACAAGTGCAAGGTGAGTAAC AAGGGGCTGCCCGCCCCTATCGA GAAGACTATCAGTAAAACCAAGGG CCAGCCAAGGGAGCCACAGGTGT ACACACTTCCACCATCTAGGGAGG AAATGACAAAGAACCAGGTGAGTT TGACCTGTCTCGTGAAAGGCTTTT ATCCCAGTGATATAGCCGTGGAAT GGGAAAGTAACGGGCAGCCCGAG AACAACTATAAGACCACACCACCC ATGCTGGACTCCGACGGTTCTTTC TTCCTTTATAGCAAGCTGACAGTG GATAAATCCAGGTGGCAGCAGGG TAACGTATTCAGTTGCAGTGTCAT GCACGAGGCACTCCACAACCACTA

			TACTCAGAAAAGTCTTTCCCTGAG TCCAGGCAAG

SEQ ID 2368	EVQLVESGGGVVQPGR SLRLSCAASGFTFTDAW MNWVRQAPGKGLEWIG RVKNKADGETTDYAAP VKGRITISRDDAKNTLYV QMNSLKTEDTAVYYCTA DLRLSTWDAYDFWGQG TMVTVSSASTKGPSVFP LAPCSRSTSESTAALGC LVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSS GLYSLSSVVTVPSSNFG TQTYTCNVDHKPSNTKV DKTVERKCCVECPPCP APPVAGPSVFLFPPKPK DTLMISRTPEVTCVVVD VSHEDPEVQFNWYVDG VEVHNAKTKPREEQFN STFRVVSVLTVVHQDWL NGKEYKCKVSNKGLPA PIEKTISKTKGQPREPQV YTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWE SNGQPENNYKTTPPML DSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK	SEQ ID 2476	GAGGTGCAGCTGGTGGAGTCTGG GGGAGGCGTGGTCCAGCCTGGGA GGTCCCTGAGACTCTCCTGTGCAG CCTCTGGATTCACTTTCACTGATG CCTGGATGAACTGGGTCCGCCAG GCTCCAGGGAAGGGGCTGGAGTG GATTGGCCGTGTTAAAAACAAAGC TGATGGTGAGACAACGGACTACG CTGCACCCGTCAAAGGCAGAATCA CCATCTCAAGAGATGATGCAAAGA ACACTCTGTATGTGCAAATGAACA GCCTGAAAACCGAGGACACAGCC GTGTATTATTGTACCGCTGACCTG CGACTTTCTACGTGGGATGCTTAT GATTTCTGGGGCCAAGGGACAAT GGTCACCGTCTCTTCAGCAAGCAC AAAAGGTCCTTCAGTGTTCCCTCT GGCACCTTGCTCACGCAGCACCT CTGAGAGTACAGCCGCCCTGGGC TGCCTGGTAAAGGACTACTTTCCC GAACCAGTCACTGTGTCCTGGAAT AGCGGGGCCTTGACCTCTGGAGT GCACACATTTCCAGCTGTACTGCA GTCATCTGGACTCTACAGCCTGTC CAGTGTGGTCACCGTACCTTCCTC CAACTTTGGCACTCAAACATATAC ATGTAACGTGGATCATAAGCCCTC TAACACCAAAGTGGATAAAACTGT GGAGCGTAAGTGTTGTGTCGAGT GTCCTCCTTGTCCTGCTCCTCCTG TGGCAGGCCCATCTGTGTTTCTCT TTCCCCCAAAGCCAAAGGACACTT TGATGATATCCCGGACCCCTGAGG TGACTTGCGTCGTCGTAGATGTTT CACACGAAGATCCAGAGGTGCAG TTCAACTGGTACGTGGATGGCGTG GAAGTGCATAATGCCAAGACAAAG CCCCGCGAAGAGCAGTTTAATTCC ACCTTCCGCGTGGTGTCTGTGCTG ACCGTGGTACATCAGGATTGGCTT AACGGTAAGGAGTACAAGTGCAAG GTGAGTAACAAGGGGCTGCCCGC CCCTATCGAGAAGACTATCAGTAA AACCAAGGGCCAGCCAAGGGAGC CACAGGTGTACACACTTCCACCAT CTAGGGAGGAAATGACAAAGAACC AGGTGAGTTTGACCTGTCTCGTGA AAGGCTTTTATCCCAGTGATATAG CCGTGGAATGGGAAAGTAACGGG CAGCCCGAGAACAACTATAAGACC ACACCACCCATGCTGGACTCCGAC GGTTCTTTCTTCCTTTATAGCAAGC TGACAGTGGATAAATCCAGGTGGC AGCAGGGTAACGTATTCAGTTGCA GTGTCATGCACGAGGCACTCCACA

			ACCACTATACTCAGAAAAGTCTTTC CCTGAGTCCAGGCAAG

SEQ ID 2369	QITLKESGGGLVQPGGS LRLSCTVSGFTFSNNW MTWVRQTPGKGLEWV ANIKQDGTEKHYVDSVK GRFTISRDNAENSLYLQ MNSLRGEDTAVYYCAR NSQRSFDYWGQGTLVT VSSASTKGPSVFPLAPC SRSTSESTAALGCLVKD YFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSL SSVVTVPSSNFGTQTYT CNVDHKPSNTKVDKTV ERKCCVECPPCPAPPV AGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHE DPEVQFNWYVDGVEVH NAKTKPREEQFNSTFRV VSVLTVVHQDWLNGKE YKCKVSNKGLPAPIEKTI SKTKGQPREPQVYTLPP SREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQ PENNYKTTPPMLDSDG SFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHN HYTQKSLSLSPGK	SEQ ID 2477	CAGATCACCTTGAAGGAGTCTGGG GGAGGCTTGGTCCAGCCTGGGGG GTCCCTAAGACTCTCTTGTACAGT CTCAGGATTCACCTTTAGTAACAAT TGGATGACCTGGGTCCGCCAGAC TCCAGGGAAGGGGCTGGAGTGGG TGGCCAACATAAAGCAAGATGGAA CTGAGAAACACTATGTGGACTCTG TGAAGGGCCGATTCACCATCTCCA GAGACAACGCCGAGAACTCACTGT ATCTGCAGATGAACAGCCTGAGAG GTGAGGACACGGCCGTGTATTATT GTGCGAGAAACAGTCAACGTTCGT TTGACTACTGGGGCCAGGGCACC CTGGTGACCGTCTCCTCAGCAAGC ACAAAAGGTCCTTCAGTGTTCCCT CTGGCACCTTGCTCACGCAGCAC CTCTGAGAGTACAGCCGCCCTGG GCTGCCTGGTAAAGGACTACTTTC CCGAACCAGTCACTGTGTCCTGGA ATAGCGGGGCCTTGACCTCTGGA GTGCACACATTTCCAGCTGTACTG CAGTCATCTGGACTCTACAGCCTG TCCAGTGTGGTCACCGTACCTTCC TCCAACTTTGGCACTCAAACATATA CATGTAACGTGGATCATAAGCCCT CTAACACCAAAGTGGATAAAACTG TGGAGCGTAAGTGTTGTGTCGAGT GTCCTCCTTGTCCTGCTCCTCCTG TGGCAGGCCCATCTGTGTTTCTCT TTCCCCCAAAGCCAAAGGACACTT TGATGATATCCCGGACCCCTGAGG TGACTTGCGTCGTCGTAGATGTTT CACACGAAGATCCAGAGGTGCAG TTCAACTGGTACGTGGATGGCGTG GAAGTGCATAATGCCAAGACAAAG CCCCGCGAAGAGCAGTTTAATTCC ACCTTCCGCGTGGTGTCTGTGCTG ACCGTGGTACATCAGGATTGGCTT AACGGTAAGGAGTACAAGTGCAAG GTGAGTAACAAGGGGCTGCCCGC CCCTATCGAGAAGACTATCAGTAA AACCAAGGGCCAGCCAAGGGAGC CACAGGTGTACACACTTCCACCAT CTAGGGAGGAAATGACAAAGAACC AGGTGAGTTTGACCTGTCTCGTGA AAGGCTTTTATCCCAGTGATATAG CCGTGGAATGGGAAAGTAACGGG CAGCCCGAGAACAACTATAAGACC ACACCACCCATGCTGGACTCCGAC GGTTCTTTCTTCCTTTATAGCAAGC TGACAGTGGATAAATCCAGGTGGC AGCAGGGTAACGTATTCAGTTGCA GTGTCATGCACGAGGCACTCCACA ACCACTATACTCAGAAAAGTCTTTC CCTGAGTCCAGGCAAG

SEQ ID 2370	QVTLKESGGGVVQPGR SLRLSCAASGFTFSSYG MHWVRQAPGKGLEWV AVISYDGSNKYYADSVK GRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCAK DLGDPRGGILNYWGQG TLVTVSSASTKGPSVFP LAPCSRSTSESTAALGC LVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSS GLYSLSSVVTVPSSNFG TQTYTCNVDHKPSNTKV DKTVERKCCVECPPCP APPVAGPSVFLFPPKPK DTLMISRTPEVTCVVVD VSHEDPEVQFNWYVDG VEVHNAKTKPREEQFN STFRVVSVLTVVHQDWL NGKEYKCKVSNKGLPA PIEKTISKTKGQPREPQV YTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWE SNGQPENNYKTTPPML DSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK	SEQ ID 2478	CAGGTCACCTTGAAGGAGTCTGG GGGAGGCGTGGTCCAGCCTGGGA GGTCCCTGAGACTCTCCTGTGCAG CCTCTGGATTCACCTTCAGTAGCT ATGGCATGCACTGGGTCCGCCAG GCTCCAGGCAAGGGGCTGGAGTG GGTGGCAGTTATATCATATGATGG AAGTAATAAATACTATGCAGACTC CGTGAAGGGCCGATTCACCATCTC CAGAGACAATTCCAAGAACACGCT GTATCTGCAAATGAACAGCCTGAG AGCTGAGGACACGGCTGTGTATTA CTGTGCGAAAGATTTAGGGGATCC CCGGGGTGGTATTTTGAACTACTG GGGCCAGGGCACCCTGGTCACCG TCTCCTCAGCAAGCACAAAAGGTC CTTCAGTGTTCCCTCTGGCACCTT GCTCACGCAGCACCTCTGAGAGTA CAGCCGCCCTGGGCTGCCTGGTA AAGGACTACTTTCCCGAACCAGTC ACTGTGTCCTGGAATAGCGGGGC CTTGACCTCTGGAGTGCACACATT TCCAGCTGTACTGCAGTCATCTGG ACTCTACAGCCTGTCCAGTGTGGT CACCGTACCTTCCTCCAACTTTGG CACTCAAACATATACATGTAACGT GGATCATAAGCCCTCTAACACCAA AGTGGATAAAACTGTGGAGCGTAA GTGTTGTGTCGAGTGTCCTCCTTG TCCTGCTCCTCCTGTGGCAGGCC CATCTGTGTTTCTCTTTCCCCCAAA GCCAAAGGACACTTTGATGATATC CCGGACCCCTGAGGTGACTTGCG TCGTCGTAGATGTTTCACACGAAG ATCCAGAGGTGCAGTTCAACTGGT ACGTGGATGGCGTGGAAGTGCAT AATGCCAAGACAAAGCCCCGCGA AGAGCAGTTTAATTCCACCTTCCG CGTGGTGTCTGTGCTGACCGTGG TACATCAGGATTGGCTTAACGGTA AGGAGTACAAGTGCAAGGTGAGTA ACAAGGGGCTGCCCGCCCCTATC GAGAAGACTATCAGTAAAACCAAG GGCCAGCCAAGGGAGCCACAGGT GTACACACTTCCACCATCTAGGGA GGAAATGACAAAGAACCAGGTGA GTTTGACCTGTCTCGTGAAAGGCT TTTATCCCAGTGATATAGCCGTGG AATGGGAAAGTAACGGGCAGCCC GAGAACAACTATAAGACCACACCA CCCATGCTGGACTCCGACGGTTCT TTCTTCCTTTATAGCAAGCTGACA GTGGATAAATCCAGGTGGCAGCA GGGTAACGTATTCAGTTGCAGTGT CATGCACGAGGCACTCCACAACCA

			CTATACTCAGAAAAGTCTTTCCCT GAGTCCAGGCAAG

SEQ ID 2371	EVQLVESGGGVVQPGR SLRLSCAASGFTFSSYA MHWVRQAPGKGLEWV AVISYDGSNKYYADSVK GRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCAR SSPWGELSLYQGAFDI WGQGTMVTVSSASTKG PSVFPLAPCSRSTSEST AALGCLVKDYFPEPVTV SWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVP SSNFGTQTYTCNVDHK PSNTKVDKTVERKCCVE CPPCPAPPVAGPSVFLF PPKPKDTLMISRTPEVT CVVVDVSHEDPEVQFN WYVDGVEVHNAKTKPR EEQFNSTFRVVSVLTVV HQDWLNGKEYKCKVSN KGLPAPIEKTISKTKGQP REPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDI AVEWESNGQPENNYKT TPPMLDSDGSFFLYSKL TVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSL SPGK	SEQ ID 2479	GAGGTGCAGCTGGTGGAGTCTGG GGGAGGCGTGGTCCAGCCTGGGA GGTCCCTGAGACTCTCCTGTGCAG CCTCTGGATTCACCTTCAGTAGCT ATGCTATGCACTGGGTCCGCCAG GCTCCAGGCAAGGGGCTGGAGTG GGTGGCAGTTATATCATATGATGG AAGTAATAAATACTACGCAGACTC CGTGAAGGGCCGATTCACCATCTC CAGAGACAATTCCAAGAACACGCT GTATCTGCAAATGAACAGCCTGAG AGCTGAGGACACGGCTGTGTATTA CTGTGCCCGGTCGAGCCCCTGGG GGGAGTTATCGTTATACCAGGGG GCTTTTGATATCTGGGGCCAAGGG ACAATGGTCACCGTCTCTTCAGCA AGCACAAAAGGTCCTTCAGTGTTC CCTCTGGCACCTTGCTCACGCAGC ACCTCTGAGAGTACAGCCGCCCT GGGCTGCCTGGTAAAGGACTACTT TCCCGAACCAGTCACTGTGTCCTG GAATAGCGGGGCCTTGACCTCTG GAGTGCACACATTTCCAGCTGTAC TGCAGTCATCTGGACTCTACAGCC TGTCCAGTGTGGTCACCGTACCTT CCTCCAACTTTGGCACTCAAACAT ATACATGTAACGTGGATCATAAGC CCTCTAACACCAAAGTGGATAAAA CTGTGGAGCGTAAGTGTTGTGTCG AGTGTCCTCCTTGTCCTGCTCCTC CTGTGGCAGGCCCATCTGTGTTTC TCTTTCCCCCAAAGCCAAAGGACA CTTTGATGATATCCCGGACCCCTG AGGTGACTTGCGTCGTCGTAGATG TTTCACACGAAGATCCAGAGGTGC AGTTCAACTGGTACGTGGATGGCG TGGAAGTGCATAATGCCAAGACAA AGCCCCGCGAAGAGCAGTTTAATT CCACCTTCCGCGTGGTGTCTGTGC TGACCGTGGTACATCAGGATTGGC TTAACGGTAAGGAGTACAAGTGCA AGGTGAGTAACAAGGGGCTGCCC GCCCCTATCGAGAAGACTATCAGT AAAACCAAGGGCCAGCCAAGGGA GCCACAGGTGTACACACTTCCACC ATCTAGGGAGGAAATGACAAAGAA CCAGGTGAGTTTGACCTGTCTCGT GAAAGGCTTTTATCCCAGTGATAT AGCCGTGGAATGGGAAAGTAACG GGCAGCCCGAGAACAACTATAAGA CCACACCACCCATGCTGGACTCC GACGGTTCTTTCTTCCTTTATAGCA AGCTGACAGTGGATAAATCCAGGT GGCAGCAGGGTAACGTATTCAGTT GCAGTGTCATGCACGAGGCACTC

			CACAACCACTATACTCAGAAAAGT CTTTCCCTGAGTCCAGGCAAG

SEQ ID 2372	QITLKESGGGLVQPGRS LRLSCAASGFTFDDYAM HWVRQAPGKGLEWVS AISGSGGSTYYADSVKG RFTISRDNSKNTLYLQM NSLRAEDTAVYYCAKDN DFWSGKVFDYWGQGTL VTVSSASTKGPSVFPLA PCSRSTSESTAALGCLV KDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGL YSLSSVVTVPSSNFGTQ TYTCNVDHKPSNTKVDK TVERKCCVECPPCPAP PVAGPSVFLFPPKPKDT LMISRTPEVTCVVVDVS HEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTF RVVSVLTVVHQDWLNG KEYKCKVSNKGLPAPIE KTISKTKGQPREPQVYT LPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESN GQPENNYKTTPPMLDS DGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALH NHYTQKSLSLSPGK	SEQ ID 2480	CAGATCACCTTGAAGGAGTCTGGG GGAGGCTTGGTACAGCCTGGCAG GTCCCTGAGACTCTCCTGTGCAGC CTCTGGATTCACCTTTGATGATTAT GCCATGCACTGGGTCCGGCAAGC TCCAGGGAAGGGGCTGGAGTGGG TCTCAGCTATTAGTGGTAGTGGTG GTAGCACATACTACGCAGACTCCG TGAAGGGCCGGTTCACCATCTCCA GAGACAATTCCAAGAACACGCTGT ATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCCGTATATTACT GTGCGAAAGATAACGATTTTTGGA GTGGGAAAGTCTTTGACTACTGGG GCCAGGGCACCCTGGTCACCGTC TCCTCAGCAAGCACAAAAGGTCCT TCAGTGTTCCCTCTGGCACCTTGC TCACGCAGCACCTCTGAGAGTACA GCCGCCCTGGGCTGCCTGGTAAA GGACTACTTTCCCGAACCAGTCAC TGTGTCCTGGAATAGCGGGGCCTT GACCTCTGGAGTGCACACATTTCC AGCTGTACTGCAGTCATCTGGACT CTACAGCCTGTCCAGTGTGGTCAC CGTACCTTCCTCCAACTTTGGCAC TCAAACATATACATGTAACGTGGA TCATAAGCCCTCTAACACCAAAGT GGATAAAACTGTGGAGCGTAAGTG TTGTGTCGAGTGTCCTCCTTGTCC TGCTCCTCCTGTGGCAGGCCCATC TGTGTTTCTCTTTCCCCCAAAGCC AAAGGACACTTTGATGATATCCCG GACCCCTGAGGTGACTTGCGTCG TCGTAGATGTTTCACACGAAGATC CAGAGGTGCAGTTCAACTGGTACG TGGATGGCGTGGAAGTGCATAATG CCAAGACAAAGCCCCGCGAAGAG CAGTTTAATTCCACCTTCCGCGTG GTGTCTGTGCTGACCGTGGTACAT CAGGATTGGCTTAACGGTAAGGAG TACAAGTGCAAGGTGAGTAACAAG GGGCTGCCCGCCCCTATCGAGAA GACTATCAGTAAAACCAAGGGCCA GCCAAGGGAGCCACAGGTGTACA CACTTCCACCATCTAGGGAGGAAA TGACAAAGAACCAGGTGAGTTTGA CCTGTCTCGTGAAAGGCTTTTATC CCAGTGATATAGCCGTGGAATGG GAAAGTAACGGGCAGCCCGAGAA CAACTATAAGACCACACCACCCAT GCTGGACTCCGACGGTTCTTTCTT CCTTTATAGCAAGCTGACAGTGGA TAAATCCAGGTGGCAGCAGGGTAA CGTATTCAGTTGCAGTGTCATGCA CGAGGCACTCCACAACCACTATAC

			TCAGAAAAGTCTTTCCCTGAGTCC AGGCAAG

SEQ ID 2373	EVQLVQSGGGLVQPGG SLRLSCAASGFTFSSYS MNWVRQAPGKGLEWV SYISSTSSTIYYADSVKG RFTISRDNSKNMLFLQM NSLRAEDTAVYYCAKEG GSGWRHYFDYWGQGT LVTVSSASTKGPSVFPL APCSRSTSESTAALGCL VKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSG LYSLSSVVTVPSSNFGT QTYTCNVDHKPSNTKV DKTVERKCCVECPPCP APPVAGPSVFLFPPKPK DTLMISRTPEVTCVVVD VSHEDPEVQFNWYVDG VEVHNAKTKPREEQFN STFRVVSVLTVVHQDWL NGKEYKCKVSNKGLPA PIEKTISKTKGQPREPQV YTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWE SNGQPENNYKTTPPML DSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK	SEQ ID 2481	GAAGTGCAGCTGGTGCAGTCTGG GGGAGGCTTGGTACAGCCTGGGG GGTCCCTGAGACTCTCCTGTGCAG CCTCTGGATTCACCTTCAGTAGTT ATAGCATGAACTGGGTCCGCCAG GCTCCAGGGAAGGGGCTGGAGTG GGTTTCATACATCAGTAGTACTAG TAGTACCATATACTACGCAGACTC CGTGAAGGGCCGATTCACCATCTC CAGAGACAATTCCAAGAATATGCT GTTTCTACAAATGAACAGCCTGAG AGCTGAGGACACGGCTGTGTATTA CTGTGCGAAAGAAGGGGGCAGTG GCTGGCGCCACTACTTTGACTACT GGGGCCAGGGAACCCTGGTCACC GTCTCCTCAGCAAGCACAAAAGGT CCTTCAGTGTTCCCTCTGGCACCT TGCTCACGCAGCACCTCTGAGAGT ACAGCCGCCCTGGGCTGCCTGGT AAAGGACTACTTTCCCGAACCAGT CACTGTGTCCTGGAATAGCGGGG CCTTGACCTCTGGAGTGCACACAT TTCCAGCTGTACTGCAGTCATCTG GACTCTACAGCCTGTCCAGTGTGG TCACCGTACCTTCCTCCAACTTTG GCACTCAAACATATACATGTAACG TGGATCATAAGCCCTCTAACACCA AAGTGGATAAAACTGTGGAGCGTA AGTGTTGTGTCGAGTGTCCTCCTT GTCCTGCTCCTCCTGTGGCAGGC CCATCTGTGTTTCTCTTTCCCCCAA AGCCAAAGGACACTTTGATGATAT CCCGGACCCCTGAGGTGACTTGC GTCGTCGTAGATGTTTCACACGAA GATCCAGAGGTGCAGTTCAACTGG TACGTGGATGGCGTGGAAGTGCA TAATGCCAAGACAAAGCCCCGCGA AGAGCAGTTTAATTCCACCTTCCG CGTGGTGTCTGTGCTGACCGTGG TACATCAGGATTGGCTTAACGGTA AGGAGTACAAGTGCAAGGTGAGTA ACAAGGGGCTGCCCGCCCCTATC GAGAAGACTATCAGTAAAACCAAG GGCCAGCCAAGGGAGCCACAGGT GTACACACTTCCACCATCTAGGGA GGAAATGACAAAGAACCAGGTGA GTTTGACCTGTCTCGTGAAAGGCT TTTATCCCAGTGATATAGCCGTGG AATGGGAAAGTAACGGGCAGCCC GAGAACAACTATAAGACCACACCA CCCATGCTGGACTCCGACGGTTCT TTCTTCCTTTATAGCAAGCTGACA GTGGATAAATCCAGGTGGCAGCA GGGTAACGTATTCAGTTGCAGTGT CATGCACGAGGCACTCCACAACCA

			CTATACTCAGAAAAGTCTTTCCCT GAGTCCAGGCAAG

SEQ ID 2374	QVTLKESGGGVVQPGR SLRLSCAASGFTFSSYA MHWVRQAPGKGLEWV AVISYDGSNKYYADSVK GRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCAR DYCSSTSCQNWFDPW GQGTLVTVSSASTKGPS VFPLAPCSRSTSESTAA LGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSN FGTQTYTCNVDHKPSN TKVDKTVERKCCVECPP CPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVV VDVSHEDPEVQFNWYV DGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQD WLNGKEYKCKVSNKGL PAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPP MLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVM HEALHNHYTQKSLSLSP GK	SEQ ID 2482	CAGGTCACCTTGAAGGAGTCTGG GGGAGGCGTGGTCCAGCCTGGGA GGTCCCTGAGACTGTCCTGTGCA GCCTCTGGATTCACCTTCAGCAGC TATGCTATGCACTGGGTCCGCCAG GCTCCAGGCAAGGGGCTGGAGTG GGTGGCAGTTATATCATATGATGG AAGTAATAAATACTACGCAGACTC CGTGAAGGGCCGATTCACCATCTC CAGAGACAATTCCAAGAACACGCT GTATCTGCAAATGAACAGCCTGAG AGCTGAGGACACGGCTGTGTATTA CTGTGCGAGAGATTATTGTAGTAG TACCAGCTGCCAGAACTGGTTCGA CCCCTGGGGCCAGGGCACCCTGG TCACCGTCTCCTCAGCAAGCACAA AAGGTCCTTCAGTGTTCCCTCTGG CACCTTGCTCACGCAGCACCTCTG AGAGTACAGCCGCCCTGGGCTGC CTGGTAAAGGACTACTTTCCCGAA CCAGTCACTGTGTCCTGGAATAGC GGGGCCTTGACCTCTGGAGTGCA CACATTTCCAGCTGTACTGCAGTC ATCTGGACTCTACAGCCTGTCCAG TGTGGTCACCGTACCTTCCTCCAA CTTTGGCACTCAAACATATACATGT AACGTGGATCATAAGCCCTCTAAC ACCAAAGTGGATAAAACTGTGGAG CGTAAGTGTTGTGTCGAGTGTCCT CCTTGTCCTGCTCCTCCTGTGGCA GGCCCATCTGTGTTTCTCTTTCCC CCAAAGCCAAAGGACACTTTGATG ATATCCCGGACCCCTGAGGTGACT TGCGTCGTCGTAGATGTTTCACAC GAAGATCCAGAGGTGCAGTTCAAC TGGTACGTGGATGGCGTGGAAGT GCATAATGCCAAGACAAAGCCCCG CGAAGAGCAGTTTAATTCCACCTT CCGCGTGGTGTCTGTGCTGACCG TGGTACATCAGGATTGGCTTAACG GTAAGGAGTACAAGTGCAAGGTGA GTAACAAGGGGCTGCCCGCCCCT ATCGAGAAGACTATCAGTAAAACC AAGGGCCAGCCAAGGGAGCCACA GGTGTACACACTTCCACCATCTAG GGAGGAAATGACAAAGAACCAGG TGAGTTTGACCTGTCTCGTGAAAG GCTTTTATCCCAGTGATATAGCCG TGGAATGGGAAAGTAACGGGCAG CCCGAGAACAACTATAAGACCACA CCACCCATGCTGGACTCCGACGG TTCTTTCTTCCTTTATAGCAAGCTG ACAGTGGATAAATCCAGGTGGCAG CAGGGTAACGTATTCAGTTGCAGT GTCATGCACGAGGCACTCCACAAC

			CACTATACTCAGAAAAGTCTTTCC CTGAGTCCAGGCAAG

SEQ ID 2375	QVQLVQSGGGLVQPGG SLRLSCAASGFTFSNYV MSWVRQAPGKGLEWV SAISGIGDTTYYADSVK GRFTISRDNAKNTLYLQ MNSLRAEDTAVYYCAR GRVAGDAFDIWGQGTM VTVSSASTKGPSVFPLA PCSRSTSESTAALGCLV KDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGL YSLSSVVTVPSSNFGTQ TYTCNVDHKPSNTKVDK TVERKCCVECPPCPAP PVAGPSVFLFPPKPKDT LMISRTPEVTCVVVDVS HEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTF RVVSVLTVVHQDWLNG KEYKCKVSNKGLPAPIE KTISKTKGQPREPQVYT LPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESN GQPENNYKTTPPMLDS DGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALH NHYTQKSLSLSPGK	SEQ ID 2483	CAGGTCCAGCTGGTGCAGTCTGG GGGAGGCTTGGTACAGCCTGGGG GGTCCCTGAGACTCTCCTGTGCAG CCTCTGGATTCACCTTTAGCAACT ATGTCATGAGCTGGGTCCGCCAG GCTCCAGGGAAGGGGCTGGAGTG GGTCTCAGCTATTAGTGGTATTGG TGATACTACATACTACGCGGACTC CGTGAAGGGCCGATTCACCATCTC CAGAGACAACGCCAAGAACACGC TGTATCTGCAAATGAACAGTCTGA GAGCCGAGGACACGGCTGTGTAT TACTGTGCAAGAGGGCGCGTGGC GGGGGATGCTTTTGATATCTGGGG CCAAGGGACAATGGTGACCGTCT CTTCAGCAAGCACAAAAGGTCCTT CAGTGTTCCCTCTGGCACCTTGCT CACGCAGCACCTCTGAGAGTACA GCCGCCCTGGGCTGCCTGGTAAA GGACTACTTTCCCGAACCAGTCAC TGTGTCCTGGAATAGCGGGGCCTT GACCTCTGGAGTGCACACATTTCC AGCTGTACTGCAGTCATCTGGACT CTACAGCCTGTCCAGTGTGGTCAC CGTACCTTCCTCCAACTTTGGCAC TCAAACATATACATGTAACGTGGA TCATAAGCCCTCTAACACCAAAGT GGATAAAACTGTGGAGCGTAAGTG TTGTGTCGAGTGTCCTCCTTGTCC TGCTCCTCCTGTGGCAGGCCCATC TGTGTTTCTCTTTCCCCCAAAGCC AAAGGACACTTTGATGATATCCCG GACCCCTGAGGTGACTTGCGTCG TCGTAGATGTTTCACACGAAGATC CAGAGGTGCAGTTCAACTGGTACG TGGATGGCGTGGAAGTGCATAATG CCAAGACAAAGCCCCGCGAAGAG CAGTTTAATTCCACCTTCCGCGTG GTGTCTGTGCTGACCGTGGTACAT CAGGATTGGCTTAACGGTAAGGAG TACAAGTGCAAGGTGAGTAACAAG GGGCTGCCCGCCCCTATCGAGAA GACTATCAGTAAAACCAAGGGCCA GCCAAGGGAGCCACAGGTGTACA CACTTCCACCATCTAGGGAGGAAA TGACAAAGAACCAGGTGAGTTTGA CCTGTCTCGTGAAAGGCTTTTATC CCAGTGATATAGCCGTGGAATGG GAAAGTAACGGGCAGCCCGAGAA CAACTATAAGACCACACCACCCAT GCTGGACTCCGACGGTTCTTTCTT CCTTTATAGCAAGCTGACAGTGGA TAAATCCAGGTGGCAGCAGGGTAA CGTATTCAGTTGCAGTGTCATGCA CGAGGCACTCCACAACCACTATAC

			TCAGAAAAGTCTTTCCCTGAGTCC AGGCAAG

SEQ ID 2376	QLQLQESGGGLVQPGG SLRLSCAASGFTFSSYA MSWVRQAPGKGLEWV SAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCAK DQGAAAGTLGYFDYWG QGTLVTVSSASTKGPSV FPLAPCSRSTSESTAAL GCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSN FGTQTYTCNVDHKPSN TKVDKTVERKCCVECPP CPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVV VDVSHEDPEVQFNWYV DGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQD WLNGKEYKCKVSNKGL PAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPP MLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVM HEALHNHYTQKSLSLSP GK	SEQ ID 2484	CAGCTGCAGCTGCAGGAGTCGGG GGGAGGCTTGGTACAGCCTGGGG GGTCCCTGAGACTCTCCTGTGCAG CCTCTGGATTCACCTTTAGCAGCT ATGCCATGAGCTGGGTCCGCCAG GCTCCAGGGAAGGGGCTGGAGTG GGTCTCAGCTATTAGTGGTAGTGG TGGTAGCACATACTACGCAGACTC CGTGAAGGGCCGGTTCACCATCT CCAGAGACAATTCCAAGAACACGC TGTATCTGCAAATGAACAGCCTGA GAGCCGAGGACACGGCCGTATAT TACTGTGCGAAAGATCAAGGGGCA GCAGCTGGTACCCTGGGGTACTTT GACTACTGGGGCCAGGGAACCCT GGTGACCGTCTCCTCAGCAAGCA CAAAAGGTCCTTCAGTGTTCCCTC TGGCACCTTGCTCACGCAGCACCT CTGAGAGTACAGCCGCCCTGGGC TGCCTGGTAAAGGACTACTTTCCC GAACCAGTCACTGTGTCCTGGAAT AGCGGGGCCTTGACCTCTGGAGT GCACACATTTCCAGCTGTACTGCA GTCATCTGGACTCTACAGCCTGTC CAGTGTGGTCACCGTACCTTCCTC CAACTTTGGCACTCAAACATATAC ATGTAACGTGGATCATAAGCCCTC TAACACCAAAGTGGATAAAACTGT GGAGCGTAAGTGTTGTGTCGAGT GTCCTCCTTGTCCTGCTCCTCCTG TGGCAGGCCCATCTGTGTTTCTCT TTCCCCCAAAGCCAAAGGACACTT TGATGATATCCCGGACCCCTGAGG TGACTTGCGTCGTCGTAGATGTTT CACACGAAGATCCAGAGGTGCAG TTCAACTGGTACGTGGATGGCGTG GAAGTGCATAATGCCAAGACAAAG CCCCGCGAAGAGCAGTTTAATTCC ACCTTCCGCGTGGTGTCTGTGCTG ACCGTGGTACATCAGGATTGGCTT AACGGTAAGGAGTACAAGTGCAAG GTGAGTAACAAGGGGCTGCCCGC CCCTATCGAGAAGACTATCAGTAA AACCAAGGGCCAGCCAAGGGAGC CACAGGTGTACACACTTCCACCAT CTAGGGAGGAAATGACAAAGAACC AGGTGAGTTTGACCTGTCTCGTGA AAGGCTTTTATCCCAGTGATATAG CCGTGGAATGGGAAAGTAACGGG CAGCCCGAGAACAACTATAAGACC ACACCACCCATGCTGGACTCCGAC GGTTCTTTCTTCCTTTATAGCAAGC TGACAGTGGATAAATCCAGGTGGC AGCAGGGTAACGTATTCAGTTGCA GTGTCATGCACGAGGCACTCCACA

			ACCACTATACTCAGAAAAGTCTTTC CCTGAGTCCAGGCAAG

SEQ ID 2377	QVQLVQSGAEVKKPGA SVKVSCKASGYTFTSYD INWVRQATGQGLEWMG WMNPNSGNTGYAQKF QGRVTMTRNTSISTAYM ELSSLRSEDTAVYYCTR GIYDSSGSSNPFDSWG QGTLVTVSSASTKGPSV FPLAPCSRSTSESTAAL GCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSN FGTQTYTCNVDHKPSN TKVDKTVERKCCVECPP CPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVV VDVSHEDPEVQFNWYV DGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQD WLNGKEYKCKVSNKGL PAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPP MLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVM HEALHNHYTQKSLSLSP GK	SEQ ID 2485	CAGGTGCAGCTGGTGCAGTCTGG GGCTGAGGTGAAGAAGCCTGGGG CCTCAGTGAAGGTCTCCTGCAAGG CTTCTGGATACACCTTCACCAGTT ATGATATCAACTGGGTGCGACAGG CCACTGGACAAGGGCTTGAGTGG ATGGGATGGATGAACCCTAACAGT GGTAACACAGGCTATGCACAGAAG TTCCAGGGCAGAGTCACCATGACC AGGAACACCTCCATAAGCACAGCC TACATGGAGCTGAGCAGCCTGAG ATCTGAGGACACGGCCGTGTATTA CTGTACGAGAGGAATCTATGATAG TAGTGGTTCTTCCAATCCCTTTGA CTCCTGGGGCCAGGGAACCCTGG TGACCGTCTCCTCAGCAAGCACAA AAGGTCCTTCAGTGTTCCCTCTGG CACCTTGCTCACGCAGCACCTCTG AGAGTACAGCCGCCCTGGGCTGC CTGGTAAAGGACTACTTTCCCGAA CCAGTCACTGTGTCCTGGAATAGC GGGGCCTTGACCTCTGGAGTGCA CACATTTCCAGCTGTACTGCAGTC ATCTGGACTCTACAGCCTGTCCAG TGTGGTCACCGTACCTTCCTCCAA CTTTGGCACTCAAACATATACATGT AACGTGGATCATAAGCCCTCTAAC ACCAAAGTGGATAAAACTGTGGAG CGTAAGTGTTGTGTCGAGTGTCCT CCTTGTCCTGCTCCTCCTGTGGCA GGCCCATCTGTGTTTCTCTTTCCC CCAAAGCCAAAGGACACTTTGATG ATATCCCGGACCCCTGAGGTGACT TGCGTCGTCGTAGATGTTTCACAC GAAGATCCAGAGGTGCAGTTCAAC TGGTACGTGGATGGCGTGGAAGT GCATAATGCCAAGACAAAGCCCCG CGAAGAGCAGTTTAATTCCACCTT CCGCGTGGTGTCTGTGCTGACCG TGGTACATCAGGATTGGCTTAACG GTAAGGAGTACAAGTGCAAGGTGA GTAACAAGGGGCTGCCCGCCCCT ATCGAGAAGACTATCAGTAAAACC AAGGGCCAGCCAAGGGAGCCACA GGTGTACACACTTCCACCATCTAG GGAGGAAATGACAAAGAACCAGG TGAGTTTGACCTGTCTCGTGAAAG GCTTTTATCCCAGTGATATAGCCG TGGAATGGGAAAGTAACGGGCAG CCCGAGAACAACTATAAGACCACA CCACCCATGCTGGACTCCGACGG TTCTTTCTTCCTTTATAGCAAGCTG ACAGTGGATAAATCCAGGTGGCAG CAGGGTAACGTATTCAGTTGCAGT GTCATGCACGAGGCACTCCACAAC

			CACTATACTCAGAAAAGTCTTTCC CTGAGTCCAGGCAAG

SEQ ID 2378	EVQLVQSGAEVKKPGA SVKISCEASGYTFTDYAI HWVRQAPGQRLEWMG WINAGDGGTKSSREFQ GRVTITRDTSATTAYME VSSLRSEDTAVYYCARG YCSGGSCPGTDFDYWG QGTLVTVSSASTKGPSV FPLAPCSRSTSESTAAL GCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSN FGTQTYTCNVDHKPSN TKVDKTVERKCCVECPP CPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVV VDVSHEDPEVQFNWYV DGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQD WLNGKEYKCKVSNKGL PAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPP MLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVM HEALHNHYTQKSLSLSP GK	SEQ ID 2486	GAGGTGCAGCTGGTGCAGTCTGG GGCTGAGGTGAAGAAGCCTGGGG CCTCAGTGAAGATTTCCTGCGAGG CTTCTGGATACACCTTCACTGATTA TGCTATACATTGGGTGCGCCAGGC CCCCGGACAAAGACTTGAGTGGAT GGGATGGATCAACGCTGGCGATG GTGGCACAAAAAGTTCACGGGAGT TCCAGGGCAGAGTCACCATTACCA GGGACACATCCGCGACCACAGCC TACATGGAGGTGAGCAGTCTGAGA TCTGAAGACACGGCTGTCTATTAC TGTGCGAGAGGATATTGTAGTGGT GGTAGCTGCCCAGGAACGGATTTT GACTACTGGGGCCAGGGAACCCT GGTCACCGTCTCCTCAGCAAGCAC AAAAGGTCCTTCAGTGTTCCCTCT GGCACCTTGCTCACGCAGCACCT CTGAGAGTACAGCCGCCCTGGGC TGCCTGGTAAAGGACTACTTTCCC GAACCAGTCACTGTGTCCTGGAAT AGCGGGGCCTTGACCTCTGGAGT GCACACATTTCCAGCTGTACTGCA GTCATCTGGACTCTACAGCCTGTC CAGTGTGGTCACCGTACCTTCCTC CAACTTTGGCACTCAAACATATAC ATGTAACGTGGATCATAAGCCCTC TAACACCAAAGTGGATAAAACTGT GGAGCGTAAGTGTTGTGTCGAGT GTCCTCCTTGTCCTGCTCCTCCTG TGGCAGGCCCATCTGTGTTTCTCT TTCCCCCAAAGCCAAAGGACACTT TGATGATATCCCGGACCCCTGAGG TGACTTGCGTCGTCGTAGATGTTT CACACGAAGATCCAGAGGTGCAG TTCAACTGGTACGTGGATGGCGTG GAAGTGCATAATGCCAAGACAAAG CCCCGCGAAGAGCAGTTTAATTCC ACCTTCCGCGTGGTGTCTGTGCTG ACCGTGGTACATCAGGATTGGCTT AACGGTAAGGAGTACAAGTGCAAG GTGAGTAACAAGGGGCTGCCCGC CCCTATCGAGAAGACTATCAGTAA AACCAAGGGCCAGCCAAGGGAGC CACAGGTGTACACACTTCCACCAT CTAGGGAGGAAATGACAAAGAACC AGGTGAGTTTGACCTGTCTCGTGA AAGGCTTTTATCCCAGTGATATAG CCGTGGAATGGGAAAGTAACGGG CAGCCCGAGAACAACTATAAGACC ACACCACCCATGCTGGACTCCGAC GGTTCTTTCTTCCTTTATAGCAAGC TGACAGTGGATAAATCCAGGTGGC AGCAGGGTAACGTATTCAGTTGCA GTGTCATGCACGAGGCACTCCACA

			ACCACTATACTCAGAAAAGTCTTTC CCTGAGTCCAGGCAAG

SEQ ID 2379	QVQLVQSGAEVKKPGA SVKVSCKASGYTFTSYY MHWVRQAPGQGLEWM GIINPSGGSTSYAQKFQ GRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCAR DGVGGRDGYNFDYWG QGTLVTVSSASTKGPSV FPLAPCSRSTSESTAAL GCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSN FGTQTYTCNVDHKPSN TKVDKTVERKCCVECPP CPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVV VDVSHEDPEVQFNWYV DGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQD WLNGKEYKCKVSNKGL PAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPP MLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVM HEALHNHYTQKSLSLSP GK	SEQ ID 2487	CAGGTGCAGCTGGTGCAGTCTGG GGCTGAGGTGAAGAAGCCTGGGG CCTCAGTGAAGGTTTCCTGCAAGG CATCTGGATACACCTTCACCAGCT ACTATATGCACTGGGTGCGACAGG CCCCTGGACAAGGGCTTGAGTGG ATGGGAATAATCAACCCTAGTGGT GGTAGCACAAGCTACGCACAGAA GTTCCAGGGCAGAGTCACCATGA CCAGGGACACGTCCACGAGCACA GTCTACATGGAGCTGAGCAGCCT GAGATCTGAGGACACGGCCGTGT ATTACTGTGCGAGAGATGGTGTAG GAGGGAGAGATGGCTACAATTTTG ACTACTGGGGCCAGGGAACCCTG GTCACCGTCTCCTCAGCAAGCACA AAAGGTCCTTCAGTGTTCCCTCTG GCACCTTGCTCACGCAGCACCTCT GAGAGTACAGCCGCCCTGGGCTG CCTGGTAAAGGACTACTTTCCCGA ACCAGTCACTGTGTCCTGGAATAG CGGGGCCTTGACCTCTGGAGTGC ACACATTTCCAGCTGTACTGCAGT CATCTGGACTCTACAGCCTGTCCA GTGTGGTCACCGTACCTTCCTCCA ACTTTGGCACTCAAACATATACAT GTAACGTGGATCATAAGCCCTCTA ACACCAAAGTGGATAAAACTGTGG AGCGTAAGTGTTGTGTCGAGTGTC CTCCTTGTCCTGCTCCTCCTGTGG CAGGCCCATCTGTGTTTCTCTTTC CCCCAAAGCCAAAGGACACTTTGA TGATATCCCGGACCCCTGAGGTGA CTTGCGTCGTCGTAGATGTTTCAC ACGAAGATCCAGAGGTGCAGTTCA ACTGGTACGTGGATGGCGTGGAA GTGCATAATGCCAAGACAAAGCCC CGCGAAGAGCAGTTTAATTCCACC TTCCGCGTGGTGTCTGTGCTGACC GTGGTACATCAGGATTGGCTTAAC GGTAAGGAGTACAAGTGCAAGGT GAGTAACAAGGGGCTGCCCGCCC CTATCGAGAAGACTATCAGTAAAA CCAAGGGCCAGCCAAGGGAGCCA CAGGTGTACACACTTCCACCATCT AGGGAGGAAATGACAAAGAACCA GGTGAGTTTGACCTGTCTCGTGAA AGGCTTTTATCCCAGTGATATAGC CGTGGAATGGGAAAGTAACGGGC AGCCCGAGAACAACTATAAGACCA CACCACCCATGCTGGACTCCGAC GGTTCTTTCTTCCTTTATAGCAAGC TGACAGTGGATAAATCCAGGTGGC AGCAGGGTAACGTATTCAGTTGCA GTGTCATGCACGAGGCACTCCACA

			ACCACTATACTCAGAAAAGTCTTTC CCTGAGTCCAGGCAAG

SEQ ID 2380	EVQLVQSGGGLVQPGG SLRLSCAASGFTVSSNY MSWVRQAPGKGLEWV SVIYSGGSTYYADSVKG RFTISRDNSKNTLYLQM NSLRAEDTAVYYCARAP LAADGYFDYWGQGTLV TVSSASTKGPSVFPLAP CSRSTSESTAALGCLVK DYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLY SLSSVVTVPSSNFGTQT YTCNVDHKPSNTKVDKT VERKCCVECPPCPAPP VAGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSH EDPEVQFNWYVDGVEV HNAKTKPREEQFNSTFR VVSVLTVVHQDWLNGK EYKCKVSNKGLPAPIEK TISKTKGQPREPQVYTL PPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNG QPENNYKTTPPMLDSD GSFFLYSKLTVDKSRW QQGNVFSCSVMHEALH NHYTQKSLSLSPGK	SEQ ID 2488	GAAGTGCAGCTGGTGCAGTCTGG GGGAGGCTTGGTCCAGCCTGGGG GGTCCCTGAGACTCTCCTGTGCAG CCTCTGGATTCACCGTCAGTAGCA ACTACATGAGCTGGGTCCGCCAG GCTCCAGGGAAGGGGCTGGAGTG GGTCTCAGTTATTTATAGCGGTGG TAGCACATACTACGCAGACTCCGT GAAGGGCCGATTCACCATCTCCAG AGACAATTCCAAGAACACGCTGTA TCTTCAAATGAACAGCCTGAGAGC TGAGGACACGGCTGTGTATTACTG TGCGAGAGCCCCCCTAGCAGCAG ATGGCTACTTTGACTACTGGGGCC AGGGAACCCTGGTCACCGTCTCCT CAGCAAGCACAAAAGGTCCTTCAG TGTTCCCTCTGGCACCTTGCTCAC GCAGCACCTCTGAGAGTACAGCC GCCCTGGGCTGCCTGGTAAAGGA CTACTTTCCCGAACCAGTCACTGT GTCCTGGAATAGCGGGGCCTTGA CCTCTGGAGTGCACACATTTCCAG CTGTACTGCAGTCATCTGGACTCT ACAGCCTGTCCAGTGTGGTCACC GTACCTTCCTCCAACTTTGGCACT CAAACATATACATGTAACGTGGAT CATAAGCCCTCTAACACCAAAGTG GATAAAACTGTGGAGCGTAAGTGT TGTGTCGAGTGTCCTCCTTGTCCT GCTCCTCCTGTGGCAGGCCCATCT GTGTTTCTCTTTCCCCCAAAGCCA AAGGACACTTTGATGATATCCCGG ACCCCTGAGGTGACTTGCGTCGTC GTAGATGTTTCACACGAAGATCCA GAGGTGCAGTTCAACTGGTACGTG GATGGCGTGGAAGTGCATAATGC CAAGACAAAGCCCCGCGAAGAGC AGTTTAATTCCACCTTCCGCGTGG TGTCTGTGCTGACCGTGGTACATC AGGATTGGCTTAACGGTAAGGAGT ACAAGTGCAAGGTGAGTAACAAGG GGCTGCCCGCCCCTATCGAGAAG ACTATCAGTAAAACCAAGGGCCAG CCAAGGGAGCCACAGGTGTACAC ACTTCCACCATCTAGGGAGGAAAT GACAAAGAACCAGGTGAGTTTGAC CTGTCTCGTGAAAGGCTTTTATCC CAGTGATATAGCCGTGGAATGGGA AAGTAACGGGCAGCCCGAGAACA ACTATAAGACCACACCACCCATGC TGGACTCCGACGGTTCTTTCTTCC TTTATAGCAAGCTGACAGTGGATA AATCCAGGTGGCAGCAGGGTAAC GTATTCAGTTGCAGTGTCATGCAC GAGGCACTCCACAACCACTATACT

			CAGAAAAGTCTTTCCCTGAGTCCA GGCAAG

SEQ ID 2381	EVQLVQSGAEVKKPGS SVKVSCKASGGTFSSYA ISWVRQAPGQGLEWMG GIIPIFGTANYAQKFQGR VTITADESTSTAYMELSS LRSEDTAVYYCARARGL QYLIWYFDLWGRGTLVT VSSASTKGPSVFPLAPC SRSTSESTAALGCLVKD YFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSL SSVVTVPSSNFGTQTYT CNVDHKPSNTKVDKTV ERKCCVECPPCPAPPV AGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHE DPEVQFNWYVDGVEVH NAKTKPREEQFNSTFRV VSVLTVVHQDWLNGKE YKCKVSNKGLPAPIEKTI SKTKGQPREPQVYTLPP SREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQ PENNYKTTPPMLDSDG SFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHN HYTQKSLSLSPGK	SEQ ID 2489	GAGGTCCAGCTGGTGCAGTCTGG GGCTGAGGTGAAGAAGCCTGGGT CCTCGGTGAAGGTCTCCTGCAAG GCTTCTGGAGGCACCTTCAGCAG CTATGCTATCAGCTGGGTGCGACA GGCCCCTGGACAAGGGCTTGAGT GGATGGGAGGGATCATCCCTATCT TTGGTACAGCAAACTACGCACAGA AGTTCCAGGGCAGAGTCACGATTA CCGCGGACGAATCCACGAGCACA GCCTACATGGAGCTGAGCAGCCT GAGATCTGAGGACACGGCCGTGT ATTACTGTGCGAGAGCCCGGGGG CTACAGTACCTAATCTGGTACTTC GATCTCTGGGGCCGTGGCACCCT GGTGACCGTCTCCTCAGCAAGCA CAAAAGGTCCTTCAGTGTTCCCTC TGGCACCTTGCTCACGCAGCACCT CTGAGAGTACAGCCGCCCTGGGC TGCCTGGTAAAGGACTACTTTCCC GAACCAGTCACTGTGTCCTGGAAT AGCGGGGCCTTGACCTCTGGAGT GCACACATTTCCAGCTGTACTGCA GTCATCTGGACTCTACAGCCTGTC CAGTGTGGTCACCGTACCTTCCTC CAACTTTGGCACTCAAACATATAC ATGTAACGTGGATCATAAGCCCTC TAACACCAAAGTGGATAAAACTGT GGAGCGTAAGTGTTGTGTCGAGT GTCCTCCTTGTCCTGCTCCTCCTG TGGCAGGCCCATCTGTGTTTCTCT TTCCCCCAAAGCCAAAGGACACTT TGATGATATCCCGGACCCCTGAGG TGACTTGCGTCGTCGTAGATGTTT CACACGAAGATCCAGAGGTGCAG TTCAACTGGTACGTGGATGGCGTG GAAGTGCATAATGCCAAGACAAAG CCCCGCGAAGAGCAGTTTAATTCC ACCTTCCGCGTGGTGTCTGTGCTG ACCGTGGTACATCAGGATTGGCTT AACGGTAAGGAGTACAAGTGCAAG GTGAGTAACAAGGGGCTGCCCGC CCCTATCGAGAAGACTATCAGTAA AACCAAGGGCCAGCCAAGGGAGC CACAGGTGTACACACTTCCACCAT CTAGGGAGGAAATGACAAAGAACC AGGTGAGTTTGACCTGTCTCGTGA AAGGCTTTTATCCCAGTGATATAG CCGTGGAATGGGAAAGTAACGGG CAGCCCGAGAACAACTATAAGACC ACACCACCCATGCTGGACTCCGAC GGTTCTTTCTTCCTTTATAGCAAGC TGACAGTGGATAAATCCAGGTGGC AGCAGGGTAACGTATTCAGTTGCA GTGTCATGCACGAGGCACTCCACA

			ACCACTATACTCAGAAAAGTCTTTC CCTGAGTCCAGGCAAG

SEQ ID 2382	QVQLVQSGAEVKKPGA SVKVSCKASGYTFTSYY MHWVRQAPGQGLEWM GIINPSGGSTSYAQKFQ GRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCAS PGMVRGVITAPLDYWG QGTLVTVSSASTKGPSV FPLAPCSRSTSESTAAL GCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSN FGTQTYTCNVDHKPSN TKVDKTVERKCCVECPP CPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVV VDVSHEDPEVQFNWYV DGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQD WLNGKEYKCKVSNKGL PAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPP MLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVM HEALHNHYTQKSLSLSP GK	SEQ ID 2490	CAGGTCCAGCTGGTACAGTCTGG GGCTGAGGTGAAGAAGCCTGGGG CCTCAGTGAAGGTTTCCTGCAAGG CATCTGGATACACCTTCACCAGCT ACTATATGCACTGGGTGCGACAGG CCCCTGGACAAGGGCTTGAGTGG ATGGGAATAATCAACCCTAGTGGT GGTAGCACAAGCTACGCACAGAA GTTCCAGGGCAGAGTCACCATGA CCAGGGACACGTCCACGAGCACA GTCTACATGGAGCTGAGCAGCCT GAGATCTGAGGACACGGCCGTGT ATTACTGTGCGAGCCCGGGTATG GTTCGGGGAGTTATTACTGCCCCG CTTGACTACTGGGGCCAGGGCAC CCTGGTCACCGTCTCCTCAGCAAG CACAAAAGGTCCTTCAGTGTTCCC TCTGGCACCTTGCTCACGCAGCAC CTCTGAGAGTACAGCCGCCCTGG GCTGCCTGGTAAAGGACTACTTTC CCGAACCAGTCACTGTGTCCTGGA ATAGCGGGGCCTTGACCTCTGGA GTGCACACATTTCCAGCTGTACTG CAGTCATCTGGACTCTACAGCCTG TCCAGTGTGGTCACCGTACCTTCC TCCAACTTTGGCACTCAAACATATA CATGTAACGTGGATCATAAGCCCT CTAACACCAAAGTGGATAAAACTG TGGAGCGTAAGTGTTGTGTCGAGT GTCCTCCTTGTCCTGCTCCTCCTG TGGCAGGCCCATCTGTGTTTCTCT TTCCCCCAAAGCCAAAGGACACTT TGATGATATCCCGGACCCCTGAGG TGACTTGCGTCGTCGTAGATGTTT CACACGAAGATCCAGAGGTGCAG TTCAACTGGTACGTGGATGGCGTG GAAGTGCATAATGCCAAGACAAAG CCCCGCGAAGAGCAGTTTAATTCC ACCTTCCGCGTGGTGTCTGTGCTG ACCGTGGTACATCAGGATTGGCTT AACGGTAAGGAGTACAAGTGCAAG GTGAGTAACAAGGGGCTGCCCGC CCCTATCGAGAAGACTATCAGTAA AACCAAGGGCCAGCCAAGGGAGC CACAGGTGTACACACTTCCACCAT CTAGGGAGGAAATGACAAAGAACC AGGTGAGTTTGACCTGTCTCGTGA AAGGCTTTTATCCCAGTGATATAG CCGTGGAATGGGAAAGTAACGGG CAGCCCGAGAACAACTATAAGACC ACACCACCCATGCTGGACTCCGAC GGTTCTTTCTTCCTTTATAGCAAGC TGACAGTGGATAAATCCAGGTGGC AGCAGGGTAACGTATTCAGTTGCA GTGTCATGCACGAGGCACTCCACA

			ACCACTATACTCAGAAAAGTCTTTC CCTGAGTCCAGGCAAG

SEQ ID 2383	EVQLVQSGGGLVKPGG SLRLSCAASGFTFSSYAI SWVRQAPGQGLEWMG GIIPMYGTANYAQKFQG RVTITADESTSTAYMEL SSLRSEDTALYYCAREA KWGMYYFDYWGQGTL VTVSSASTKGPSVFPLA PCSRSTSESTAALGCLV KDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGL YSLSSVVTVPSSNFGTQ TYTCNVDHKPSNTKVDK TVERKCCVECPPCPAP PVAGPSVFLFPPKPKDT LMISRTPEVTCVVVDVS HEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTF RVVSVLTVVHQDWLNG KEYKCKVSNKGLPAPIE KTISKTKGQPREPQVYT LPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESN GQPENNYKTTPPMLDS DGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALH NHYTQKSLSLSPGK	SEQ ID 2491	GAGGTCCAGCTGGTACAGTCTGG GGGAGGCCTGGTCAAGCCTGGGG GGTCCCTGAGACTCTCCTGTGCAG CCTCTGGATTCACCTTCAGCAGCT ATGCTATCAGCTGGGTGCGACAG GCCCCTGGACAAGGGCTTGAGTG GATGGGAGGGATCATCCCTATGTA TGGTACAGCAAACTACGCACAGAA GTTCCAGGGCAGAGTCACGATTAC CGCGGACGAATCCACGAGCACAG CCTACATGGAACTGAGCAGCCTGA GATCTGAGGACACGGCCCTCTATT ACTGTGCGAGAGAAGCTAAGTGG GGAATGTACTACTTTGACTACTGG GGCCAGGGCACCCTGGTCACCGT CTCCTCAGCAAGCACAAAAGGTCC TTCAGTGTTCCCTCTGGCACCTTG CTCACGCAGCACCTCTGAGAGTAC AGCCGCCCTGGGCTGCCTGGTAA AGGACTACTTTCCCGAACCAGTCA CTGTGTCCTGGAATAGCGGGGCC TTGACCTCTGGAGTGCACACATTT CCAGCTGTACTGCAGTCATCTGGA CTCTACAGCCTGTCCAGTGTGGTC ACCGTACCTTCCTCCAACTTTGGC ACTCAAACATATACATGTAACGTG GATCATAAGCCCTCTAACACCAAA GTGGATAAAACTGTGGAGCGTAAG TGTTGTGTCGAGTGTCCTCCTTGT CCTGCTCCTCCTGTGGCAGGCCC ATCTGTGTTTCTCTTTCCCCCAAAG CCAAAGGACACTTTGATGATATCC CGGACCCCTGAGGTGACTTGCGT CGTCGTAGATGTTTCACACGAAGA TCCAGAGGTGCAGTTCAACTGGTA CGTGGATGGCGTGGAAGTGCATA ATGCCAAGACAAAGCCCCGCGAA GAGCAGTTTAATTCCACCTTCCGC GTGGTGTCTGTGCTGACCGTGGTA CATCAGGATTGGCTTAACGGTAAG GAGTACAAGTGCAAGGTGAGTAAC AAGGGGCTGCCCGCCCCTATCGA GAAGACTATCAGTAAAACCAAGGG CCAGCCAAGGGAGCCACAGGTGT ACACACTTCCACCATCTAGGGAGG AAATGACAAAGAACCAGGTGAGTT TGACCTGTCTCGTGAAAGGCTTTT ATCCCAGTGATATAGCCGTGGAAT GGGAAAGTAACGGGCAGCCCGAG AACAACTATAAGACCACACCACCC ATGCTGGACTCCGACGGTTCTTTC TTCCTTTATAGCAAGCTGACAGTG GATAAATCCAGGTGGCAGCAGGG TAACGTATTCAGTTGCAGTGTCAT GCACGAGGCACTCCACAACCACTA

			TACTCAGAAAAGTCTTTCCCTGAG TCCAGGCAAG

SEQ ID 2384	EVQLVESGGGVVQPGR SLRLSCAASGFTFSSYAI HWVRQAPGKGLEWVAII SDDGSKSYYADSVQGR FTISRDNSRNTVYLQMN SLRAEDTAMYYCARDR GTKWNQLNDVFDMWG QGTMVTVSSASTKGPS VFPLAPCSRSTSESTAA LGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSN FGTQTYTCNVDHKPSN TKVDKTVERKCCVECPP CPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVV VDVSHEDPEVQFNWYV DGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQD WLNGKEYKCKVSNKGL PAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPP MLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVM HEALHNHYTQKSLSLSP GK	SEQ ID 2492	GAGGTGCAGCTGGTGGAGTCCGG GGGAGGCGTGGTCCAGCCTGGGA GGTCCCTGAGACTCTCCTGTGCAG CCTCTGGATTCACCTTCAGTAGCT ATGCTATACACTGGGTCCGCCAGG CTCCAGGCAAGGGGCTGGAGTGG GTGGCAATTATATCAGATGATGGA AGTAAGAGTTACTACGCAGACTCC GTGCAGGGCCGATTCACCATCTCC AGAGACAATTCGAGGAACACAGTA TATCTGCAAATGAACAGCCTGAGA GCTGAGGACACGGCTATGTATTAC TGTGCGAGAGACAGGGGAACTAA ATGGAACCAATTGAATGATGTTTTT GATATGTGGGGCCAAGGGACAAT GGTCACCGTCTCTTCAGCAAGCAC AAAAGGTCCTTCAGTGTTCCCTCT GGCACCTTGCTCACGCAGCACCT CTGAGAGTACAGCCGCCCTGGGC TGCCTGGTAAAGGACTACTTTCCC GAACCAGTCACTGTGTCCTGGAAT AGCGGGGCCTTGACCTCTGGAGT GCACACATTTCCAGCTGTACTGCA GTCATCTGGACTCTACAGCCTGTC CAGTGTGGTCACCGTACCTTCCTC CAACTTTGGCACTCAAACATATAC ATGTAACGTGGATCATAAGCCCTC TAACACCAAAGTGGATAAAACTGT GGAGCGTAAGTGTTGTGTCGAGT GTCCTCCTTGTCCTGCTCCTCCTG TGGCAGGCCCATCTGTGTTTCTCT TTCCCCCAAAGCCAAAGGACACTT TGATGATATCCCGGACCCCTGAGG TGACTTGCGTCGTCGTAGATGTTT CACACGAAGATCCAGAGGTGCAG TTCAACTGGTACGTGGATGGCGTG GAAGTGCATAATGCCAAGACAAAG CCCCGCGAAGAGCAGTTTAATTCC ACCTTCCGCGTGGTGTCTGTGCTG ACCGTGGTACATCAGGATTGGCTT AACGGTAAGGAGTACAAGTGCAAG GTGAGTAACAAGGGGCTGCCCGC CCCTATCGAGAAGACTATCAGTAA AACCAAGGGCCAGCCAAGGGAGC CACAGGTGTACACACTTCCACCAT CTAGGGAGGAAATGACAAAGAACC AGGTGAGTTTGACCTGTCTCGTGA AAGGCTTTTATCCCAGTGATATAG CCGTGGAATGGGAAAGTAACGGG CAGCCCGAGAACAACTATAAGACC ACACCACCCATGCTGGACTCCGAC GGTTCTTTCTTCCTTTATAGCAAGC TGACAGTGGATAAATCCAGGTGGC AGCAGGGTAACGTATTCAGTTGCA GTGTCATGCACGAGGCACTCCACA

			ACCACTATACTCAGAAAAGTCTTTC CCTGAGTCCAGGCAAG

SEQ ID 2385	QMQLVQSGAEVKKPGA SVKVSCTASGYTFTSSD INWVRQATGQGLEWMG WMNPNSGNTGYAEKFQ GRVTMTSDSSISTAYME LRSLTTEDTAVYYCARG GGASYTDSWGQGTLVT VSSASTKGPSVFPLAPC SRSTSESTAALGCLVKD YFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSL SSVVTVPSSNFGTQTYT CNVDHKPSNTKVDKTV ERKCCVECPPCPAPPV AGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHE DPEVQFNWYVDGVEVH NAKTKPREEQFNSTFRV VSVLTVVHQDWLNGKE YKCKVSNKGLPAPIEKTI SKTKGQPREPQVYTLPP SREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQ PENNYKTTPPMLDSDG SFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHN HYTQKSLSLSPGK	SEQ ID 2493	CAGATGCAGCTGGTGCAATCTGG GGCTGAGGTGAAGAAGCCTGGGG CCTCAGTGAAGGTCTCCTGCACG GCTTCTGGATACACCTTCACCAGT TCTGATATCAACTGGGTGCGACAG GCCACTGGACAAGGGCTTGAGTG GATGGGATGGATGAACCCTAACAG TGGTAACACCGGCTATGCAGAGAA GTTCCAGGGCAGGGTCACCATGA CCAGCGACTCCTCCATAAGCACCG CCTACATGGAGTTGAGAAGCCTGA CCACTGAGGACACGGCCGTATATT ACTGTGCGAGAGGTGGGGGTGCG AGCTATACTGACTCCTGGGGCCAG GGCACCCTGGTCACCGTCTCCTCA GCAAGCACAAAAGGTCCTTCAGTG TTCCCTCTGGCACCTTGCTCACGC AGCACCTCTGAGAGTACAGCCGC CCTGGGCTGCCTGGTAAAGGACT ACTTTCCCGAACCAGTCACTGTGT CCTGGAATAGCGGGGCCTTGACC TCTGGAGTGCACACATTTCCAGCT GTACTGCAGTCATCTGGACTCTAC AGCCTGTCCAGTGTGGTCACCGTA CCTTCCTCCAACTTTGGCACTCAA ACATATACATGTAACGTGGATCAT AAGCCCTCTAACACCAAAGTGGAT AAAACTGTGGAGCGTAAGTGTTGT GTCGAGTGTCCTCCTTGTCCTGCT CCTCCTGTGGCAGGCCCATCTGT GTTTCTCTTTCCCCCAAAGCCAAA GGACACTTTGATGATATCCCGGAC CCCTGAGGTGACTTGCGTCGTCGT AGATGTTTCACACGAAGATCCAGA GGTGCAGTTCAACTGGTACGTGGA TGGCGTGGAAGTGCATAATGCCAA GACAAAGCCCCGCGAAGAGCAGT TTAATTCCACCTTCCGCGTGGTGT CTGTGCTGACCGTGGTACATCAGG ATTGGCTTAACGGTAAGGAGTACA AGTGCAAGGTGAGTAACAAGGGG CTGCCCGCCCCTATCGAGAAGACT ATCAGTAAAACCAAGGGCCAGCCA AGGGAGCCACAGGTGTACACACTT CCACCATCTAGGGAGGAAATGACA AAGAACCAGGTGAGTTTGACCTGT CTCGTGAAAGGCTTTTATCCCAGT GATATAGCCGTGGAATGGGAAAGT AACGGGCAGCCCGAGAACAACTA TAAGACCACACCACCCATGCTGGA CTCCGACGGTTCTTTCTTCCTTTAT AGCAAGCTGACAGTGGATAAATCC AGGTGGCAGCAGGGTAACGTATT CAGTTGCAGTGTCATGCACGAGG CACTCCACAACCACTATACTCAGA

			AAAGTCTTTCCCTGAGTCCAGGCAAG

SEQ ID 2386	QVQLVQSGGGLVQPGR SLRLSCTASGFTFGDYA MSWFRQAPGKGLEWV GFIRSKAYGGTTEYAAS VKGRFTISRDDSKSIAYL QMNSLKTEDTAVYYCTA KGGYVGYSYGPFGGY WGQGTLVTVSSASTKG PSVFPLAPCSRSTSEST AALGCLVKDYFPEPVTV SWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVP SSNFGTQTYTCNVDHK PSNTKVDKTVERKCCVE CPPCPAPPVAGPSVFLF PPKPKDTLMISRTPEVT CVVVDVSHEDPEVQFN WYVDGVEVHNAKTKPR EEQFNSTFRVVSVLTVV HQDWLNGKEYKCKVSN KGLPAPIEKTISKTKGQP REPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDI AVEWESNGQPENNYKT TPPMLDSDGSFFLYSKL TVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSL SPGK	SEQ ID 2494	CAGGTCCAGCTGGTGCAGTCTGG GGGAGGCTTGGTACAGCCAGGGC GGTCCCTGAGACTCTCCTGTACAG CTTCTGGATTCACCTTTGGTGATTA TGCTATGAGCTGGTTCCGCCAGG CTCCAGGGAAGGGGCTGGAGTGG GTAGGTTTCATTAGAAGCAAAGCT TATGGTGGGACAACAGAATACGCC GCGTCTGTGAAAGGCAGATTCACC ATCTCAAGAGATGATTCCAAAAGC ATCGCCTATCTGCAAATGAACAGC CTGAAAACCGAGGACACAGCCGT GTATTACTGTACCGCTAAGGGGGG CTACGTCGGATACAGCTATGGACC TTTTGGGGGCTACTGGGGCCAGG GAACCCTGGTCACCGTCTCCTCAG CAAGCACAAAAGGTCCTTCAGTGT TCCCTCTGGCACCTTGCTCACGCA GCACCTCTGAGAGTACAGCCGCC CTGGGCTGCCTGGTAAAGGACTA CTTTCCCGAACCAGTCACTGTGTC CTGGAATAGCGGGGCCTTGACCT CTGGAGTGCACACATTTCCAGCTG TACTGCAGTCATCTGGACTCTACA GCCTGTCCAGTGTGGTCACCGTAC CTTCCTCCAACTTTGGCACTCAAA CATATACATGTAACGTGGATCATA AGCCCTCTAACACCAAAGTGGATA AAACTGTGGAGCGTAAGTGTTGTG TCGAGTGTCCTCCTTGTCCTGCTC CTCCTGTGGCAGGCCCATCTGTGT TTCTCTTTCCCCCAAAGCCAAAGG ACACTTTGATGATATCCCGGACCC CTGAGGTGACTTGCGTCGTCGTAG ATGTTTCACACGAAGATCCAGAGG TGCAGTTCAACTGGTACGTGGATG GCGTGGAAGTGCATAATGCCAAGA CAAAGCCCCGCGAAGAGCAGTTTA ATTCCACCTTCCGCGTGGTGTCTG TGCTGACCGTGGTACATCAGGATT GGCTTAACGGTAAGGAGTACAAGT GCAAGGTGAGTAACAAGGGGCTG CCCGCCCCTATCGAGAAGACTATC AGTAAAACCAAGGGCCAGCCAAG GGAGCCACAGGTGTACACACTTCC ACCATCTAGGGAGGAAATGACAAA GAACCAGGTGAGTTTGACCTGTCT CGTGAAAGGCTTTTATCCCAGTGA TATAGCCGTGGAATGGGAAAGTAA CGGGCAGCCCGAGAACAACTATA AGACCACACCACCCATGCTGGACT CCGACGGTTCTTTCTTCCTTTATAG CAAGCTGACAGTGGATAAATCCAG GTGGCAGCAGGGTAACGTATTCA GTTGCAGTGTCATGCACGAGGCA

			CTCCACAACCACTATACTCAGAAA AGTCTTTCCCTGAGTCCAGGCAAG

SEQ ID 2387	QVQLVQSGGGLVQPGR SLRLSCTASGFTFGDYA MSWFRQAPGKGLEWV GFIRSKAYGGTTEYAAS VKGRFTISRDDSKSIAYL QMNSLKTEDTAVYYCT RGGTMVRGFGFNYWG QGTLVTVSSASTKGPSV FPLAPCSRSTSESTAAL GCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSN FGTQTYTCNVDHKPSN TKVDKTVERKCCVECPP CPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVV VDVSHEDPEVQFNWYV DGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQD WLNGKEYKCKVSNKGL PAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPP MLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVM HEALHNHYTQKSLSLSP GK	SEQ ID 2495	CAGGTGCAGCTGGTGCAGTCTGG GGGAGGCTTGGTACAGCCAGGGC GGTCCCTGAGACTCTCCTGTACAG CTTCTGGATTCACCTTTGGTGATTA TGCTATGAGCTGGTTCCGCCAGG CTCCAGGGAAGGGGCTGGAGTGG GTAGGTTTCATTAGAAGCAAAGCT TATGGTGGGACAACAGAATACGCC GCGTCTGTGAAAGGCAGATTCACC ATCTCAAGAGATGATTCCAAAAGC ATCGCCTATCTGCAAATGAACAGC CTGAAAACCGAGGACACAGCCGT GTATTACTGTACTAGAGGGGGGAC TATGGTTCGGGGTTTCGGATTTAA CTACTGGGGCCAGGGAACCCTGG TCACCGTCTCCTCAGCAAGCACAA AAGGTCCTTCAGTGTTCCCTCTGG CACCTTGCTCACGCAGCACCTCTG AGAGTACAGCCGCCCTGGGCTGC CTGGTAAAGGACTACTTTCCCGAA CCAGTCACTGTGTCCTGGAATAGC GGGGCCTTGACCTCTGGAGTGCA CACATTTCCAGCTGTACTGCAGTC ATCTGGACTCTACAGCCTGTCCAG TGTGGTCACCGTACCTTCCTCCAA CTTTGGCACTCAAACATATACATGT AACGTGGATCATAAGCCCTCTAAC ACCAAAGTGGATAAAACTGTGGAG CGTAAGTGTTGTGTCGAGTGTCCT CCTTGTCCTGCTCCTCCTGTGGCA GGCCCATCTGTGTTTCTCTTTCCC CCAAAGCCAAAGGACACTTTGATG ATATCCCGGACCCCTGAGGTGACT TGCGTCGTCGTAGATGTTTCACAC GAAGATCCAGAGGTGCAGTTCAAC TGGTACGTGGATGGCGTGGAAGT GCATAATGCCAAGACAAAGCCCCG CGAAGAGCAGTTTAATTCCACCTT CCGCGTGGTGTCTGTGCTGACCG TGGTACATCAGGATTGGCTTAACG GTAAGGAGTACAAGTGCAAGGTGA GTAACAAGGGGCTGCCCGCCCCT ATCGAGAAGACTATCAGTAAAACC AAGGGCCAGCCAAGGGAGCCACA GGTGTACACACTTCCACCATCTAG GGAGGAAATGACAAAGAACCAGG TGAGTTTGACCTGTCTCGTGAAAG GCTTTTATCCCAGTGATATAGCCG TGGAATGGGAAAGTAACGGGCAG CCCGAGAACAACTATAAGACCACA CCACCCATGCTGGACTCCGACGG TTCTTTCTTCCTTTATAGCAAGCTG ACAGTGGATAAATCCAGGTGGCAG CAGGGTAACGTATTCAGTTGCAGT GTCATGCACGAGGCACTCCACAAC

			CACTATACTCAGAAAAGTCTTTCC CTGAGTCCAGGCAAG

SEQ ID 2388	QVQLQQWGAGLLKPSE TLSLTCAVYGGSFSGYY WSWIRQPPGKGLEWIG EINHSGSTNYNPSLKSR VTISVDTSKNQFSLKLSS VTAADTAVYYCARARRA MIGPLPRLVGYFDLWGR GTLVTVSSASTKGPSVF PLAPCSRSTSESTAALG CLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSNF GTQTYTCNVDHKPSNT KVDKTVERKCCVECPP CPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVV VDVSHEDPEVQFNWYV DGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQD WLNGKEYKCKVSNKGL PAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPP MLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVM HEALHNHYTQKSLSLSP GK	SEQ ID 2496	CAGGTGCAGCTACAGCAGTGGGG CGCAGGACTGTTGAAGCCTTCGG AGACCCTGTCCCTCACCTGCGCTG TCTATGGTGGGTCCTTCAGTGGTT ACTACTGGAGCTGGATCCGCCAG CCCCCAGGGAAGGGGCTGGAGTG GATTGGGGAAATCAATCATAGTGG AAGCACCAACTACAACCCGTCCCT CAAGAGTCGAGTCACCATATCAGT AGACACGTCCAAGAACCAGTTCTC CCTGAAGCTGAGCTCTGTGACCG CCGCGGACACGGCTGTGTATTACT GTGCGAGAGCCCGGCGGGCTATG ATAGGGCCGCTTCCGCGACTTGTC GGGTACTTCGATCTCTGGGGCCG TGGAACCCTGGTCACCGTCTCCTC AGCAAGCACAAAAGGTCCTTCAGT GTTCCCTCTGGCACCTTGCTCACG CAGCACCTCTGAGAGTACAGCCG CCCTGGGCTGCCTGGTAAAGGAC TACTTTCCCGAACCAGTCACTGTG TCCTGGAATAGCGGGGCCTTGAC CTCTGGAGTGCACACATTTCCAGC TGTACTGCAGTCATCTGGACTCTA CAGCCTGTCCAGTGTGGTCACCGT ACCTTCCTCCAACTTTGGCACTCA AACATATACATGTAACGTGGATCA TAAGCCCTCTAACACCAAAGTGGA TAAAACTGTGGAGCGTAAGTGTTG TGTCGAGTGTCCTCCTTGTCCTGC TCCTCCTGTGGCAGGCCCATCTGT GTTTCTCTTTCCCCCAAAGCCAAA GGACACTTTGATGATATCCCGGAC CCCTGAGGTGACTTGCGTCGTCGT AGATGTTTCACACGAAGATCCAGA GGTGCAGTTCAACTGGTACGTGGA TGGCGTGGAAGTGCATAATGCCAA GACAAAGCCCCGCGAAGAGCAGT TTAATTCCACCTTCCGCGTGGTGT CTGTGCTGACCGTGGTACATCAGG ATTGGCTTAACGGTAAGGAGTACA AGTGCAAGGTGAGTAACAAGGGG CTGCCCGCCCCTATCGAGAAGACT ATCAGTAAAACCAAGGGCCAGCCA AGGGAGCCACAGGTGTACACACTT CCACCATCTAGGGAGGAAATGACA AAGAACCAGGTGAGTTTGACCTGT CTCGTGAAAGGCTTTTATCCCAGT GATATAGCCGTGGAATGGGAAAGT AACGGGCAGCCCGAGAACAACTA TAAGACCACACCACCCATGCTGGA CTCCGACGGTTCTTTCTTCCTTTAT AGCAAGCTGACAGTGGATAAATCC AGGTGGCAGCAGGGTAACGTATT CAGTTGCAGTGTCATGCACGAGG CACTCCACAACCACTATACTCAGA

			AAAGTCTTTCCCTGAGTCCAGGCAAG

SEQ ID 2389	QVQLQQWGAGLLKPSE TLSLTCAVYGGSFSGYY WSWIRQPPGKGLEWIG EINHSGSTNYNPSLKSR VTISVDTSKNQFSLKLSS VTAADTAVYYCARGRP APSWVKTRNWFDPWG QGTLVTVSSASTKGPSV FPLAPCSRSTSESTAAL GCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSN FGTQTYTCNVDHKPSN TKVDKTVERKCCVECPP CPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVV VDVSHEDPEVQFNWYV DGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQD WLNGKEYKCKVSNKGL PAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPP MLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVM HEALHNHYTQKSLSLSP GK	SEQ ID 2497	CAGGTGCAGCTACAGCAGTGGGG CGCAGGACTGTTGAAGCCTTCGG AGACCCTGTCCCTCACCTGCGCTG TCTATGGTGGGTCCTTCAGTGGTT ACTACTGGAGCTGGATCCGCCAG CCCCCAGGGAAGGGGCTGGAGTG GATTGGGGAAATCAATCATAGTGG AAGCACCAACTACAACCCGTCCCT CAAGAGTCGAGTCACCATATCAGT AGACACGTCCAAGAACCAGTTCTC CCTGAAGCTGAGCTCTGTGACCG CCGCGGACACGGCTGTGTATTACT GTGCGAGAGGCCGCCCCGCCCCA TCCTGGGTTAAAACCCGTAACTGG TTCGACCCCTGGGGCCAGGGAAC CCTGGTCACCGTCTCCTCAGCAAG CACAAAAGGTCCTTCAGTGTTCCC TCTGGCACCTTGCTCACGCAGCAC CTCTGAGAGTACAGCCGCCCTGG GCTGCCTGGTAAAGGACTACTTTC CCGAACCAGTCACTGTGTCCTGGA ATAGCGGGGCCTTGACCTCTGGA GTGCACACATTTCCAGCTGTACTG CAGTCATCTGGACTCTACAGCCTG TCCAGTGTGGTCACCGTACCTTCC TCCAACTTTGGCACTCAAACATATA CATGTAACGTGGATCATAAGCCCT CTAACACCAAAGTGGATAAAACTG TGGAGCGTAAGTGTTGTGTCGAGT GTCCTCCTTGTCCTGCTCCTCCTG TGGCAGGCCCATCTGTGTTTCTCT TTCCCCCAAAGCCAAAGGACACTT TGATGATATCCCGGACCCCTGAGG TGACTTGCGTCGTCGTAGATGTTT CACACGAAGATCCAGAGGTGCAG TTCAACTGGTACGTGGATGGCGTG GAAGTGCATAATGCCAAGACAAAG CCCCGCGAAGAGCAGTTTAATTCC ACCTTCCGCGTGGTGTCTGTGCTG ACCGTGGTACATCAGGATTGGCTT AACGGTAAGGAGTACAAGTGCAAG GTGAGTAACAAGGGGCTGCCCGC CCCTATCGAGAAGACTATCAGTAA AACCAAGGGCCAGCCAAGGGAGC CACAGGTGTACACACTTCCACCAT CTAGGGAGGAAATGACAAAGAACC AGGTGAGTTTGACCTGTCTCGTGA AAGGCTTTTATCCCAGTGATATAG CCGTGGAATGGGAAAGTAACGGG CAGCCCGAGAACAACTATAAGACC ACACCACCCATGCTGGACTCCGAC GGTTCTTTCTTCCTTTATAGCAAGC TGACAGTGGATAAATCCAGGTGGC AGCAGGGTAACGTATTCAGTTGCA GTGTCATGCACGAGGCACTCCACA

			ACCACTATACTCAGAAAAGTCTTTC CCTGAGTCCAGGCAAG

SEQ ID 2390	QVQLQQSGPGLVKPSQ TLSLTCAISGDSVSSNS AAWNWIRQSPSRGLEW LGRTYYRSKWYNDYAV SVKSRITINPDTSKNQFS LQLNSVTPEDTAVYYCA REASSGWNWGQGTLV TVSSASTKGPSVFPLAP CSRSTSESTAALGCLVK DYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLY SLSSVVTVPSSNFGTQT YTCNVDHKPSNTKVDKT VERKCCVECPPCPAPP VAGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSH EDPEVQFNWYVDGVEV HNAKTKPREEQFNSTFR VVSVLTVVHQDWLNGK EYKCKVSNKGLPAPIEK TISKTKGQPREPQVYTL PPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNG QPENNYKTTPPMLDSD GSFFLYSKLTVDKSRW QQGNVFSCSVMHEALH NHYTQKSLSLSPGK	SEQ ID 2498	CAGGTACAGCTGCAGCAGTCAGG TCCAGGACTGGTGAAGCCCTCGC AGACCCTCTCACTCACCTGTGCCA TCTCCGGGGACAGTGTCTCTAGCA ACAGTGCTGCTTGGAACTGGATCA GGCAGTCCCCATCGAGAGGCCTT GAGTGGCTGGGAAGGACATACTA CAGGTCCAAGTGGTATAATGATTA TGCAGTATCTGTGAAAAGTCGAAT AACCATCAACCCAGACACATCCAA GAACCAGTTCTCCCTGCAGCTGAA CTCTGTGACTCCCGAGGACACGG CTGTGTATTACTGTGCAAGAGAGG CTAGCAGTGGCTGGAACTGGGGC CAGGGAACCCTGGTCACCGTCTC CTCAGCAAGCACAAAAGGTCCTTC AGTGTTCCCTCTGGCACCTTGCTC ACGCAGCACCTCTGAGAGTACAG CCGCCCTGGGCTGCCTGGTAAAG GACTACTTTCCCGAACCAGTCACT GTGTCCTGGAATAGCGGGGCCTT GACCTCTGGAGTGCACACATTTCC AGCTGTACTGCAGTCATCTGGACT CTACAGCCTGTCCAGTGTGGTCAC CGTACCTTCCTCCAACTTTGGCAC TCAAACATATACATGTAACGTGGA TCATAAGCCCTCTAACACCAAAGT GGATAAAACTGTGGAGCGTAAGTG TTGTGTCGAGTGTCCTCCTTGTCC TGCTCCTCCTGTGGCAGGCCCATC TGTGTTTCTCTTTCCCCCAAAGCC AAAGGACACTTTGATGATATCCCG GACCCCTGAGGTGACTTGCGTCG TCGTAGATGTTTCACACGAAGATC CAGAGGTGCAGTTCAACTGGTACG TGGATGGCGTGGAAGTGCATAATG CCAAGACAAAGCCCCGCGAAGAG CAGTTTAATTCCACCTTCCGCGTG GTGTCTGTGCTGACCGTGGTACAT CAGGATTGGCTTAACGGTAAGGAG TACAAGTGCAAGGTGAGTAACAAG GGGCTGCCCGCCCCTATCGAGAA GACTATCAGTAAAACCAAGGGCCA GCCAAGGGAGCCACAGGTGTACA CACTTCCACCATCTAGGGAGGAAA TGACAAAGAACCAGGTGAGTTTGA CCTGTCTCGTGAAAGGCTTTTATC CCAGTGATATAGCCGTGGAATGG GAAAGTAACGGGCAGCCCGAGAA CAACTATAAGACCACACCACCCAT GCTGGACTCCGACGGTTCTTTCTT CCTTTATAGCAAGCTGACAGTGGA TAAATCCAGGTGGCAGCAGGGTAA CGTATTCAGTTGCAGTGTCATGCA CGAGGCACTCCACAACCACTATAC

			TCAGAAAAGTCTTTCCCTGAGTCC AGGCAAG

SEQ ID 2391	QVQLQESGPGLVKPSQ TLSLTCAISGDSVSSNN AAWNWIRQSPSRGLEW LGRTFYRSKWYNDYAV SVKSRLTVNPDTSKNQF SLRLNSVSPEDTAVYYC ARGGRYTKGGYFDDW GQGTLVTVSSASTKGPS VFPLAPCSRSTSESTAA LGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSN FGTQTYTCNVDHKPSN TKVDKTVERKCCVECPP CPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVV VDVSHEDPEVQFNWYV DGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQD WLNGKEYKCKVSNKGL PAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPP MLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVM HEALHNHYTQKSLSLSP GK	SEQ ID 2499	CAGGTGCAGCTGCAGGAGTCCGG TCCAGGACTGGTGAAGCCCTCGC AGACCCTCTCACTCACCTGTGCCA TCTCCGGGGACAGTGTCTCTAGCA ACAATGCTGCTTGGAACTGGATCA GGCAGTCCCCATCGAGAGGCCTT GAGTGGCTGGGAAGGACATTCTA CAGGTCCAAGTGGTATAATGACTA TGCAGTTTCTGTGAAAAGTCGACT AACCGTCAACCCAGACACATCCAA GAACCAGTTCTCCCTGCGGTTGAA CTCTGTGAGTCCCGAGGACACGG CTGTGTATTACTGTGCAAGAGGGG GAAGATATACCAAGGGAGGGTACT TTGACGACTGGGGCCAGGGAACC CTGGTGACCGTCTCCTCAGCAAGC ACAAAAGGTCCTTCAGTGTTCCCT CTGGCACCTTGCTCACGCAGCAC CTCTGAGAGTACAGCCGCCCTGG GCTGCCTGGTAAAGGACTACTTTC CCGAACCAGTCACTGTGTCCTGGA ATAGCGGGGCCTTGACCTCTGGA GTGCACACATTTCCAGCTGTACTG CAGTCATCTGGACTCTACAGCCTG TCCAGTGTGGTCACCGTACCTTCC TCCAACTTTGGCACTCAAACATATA CATGTAACGTGGATCATAAGCCCT CTAACACCAAAGTGGATAAAACTG TGGAGCGTAAGTGTTGTGTCGAGT GTCCTCCTTGTCCTGCTCCTCCTG TGGCAGGCCCATCTGTGTTTCTCT TTCCCCCAAAGCCAAAGGACACTT TGATGATATCCCGGACCCCTGAGG TGACTTGCGTCGTCGTAGATGTTT CACACGAAGATCCAGAGGTGCAG TTCAACTGGTACGTGGATGGCGTG GAAGTGCATAATGCCAAGACAAAG CCCCGCGAAGAGCAGTTTAATTCC ACCTTCCGCGTGGTGTCTGTGCTG ACCGTGGTACATCAGGATTGGCTT AACGGTAAGGAGTACAAGTGCAAG GTGAGTAACAAGGGGCTGCCCGC CCCTATCGAGAAGACTATCAGTAA AACCAAGGGCCAGCCAAGGGAGC CACAGGTGTACACACTTCCACCAT CTAGGGAGGAAATGACAAAGAACC AGGTGAGTTTGACCTGTCTCGTGA AAGGCTTTTATCCCAGTGATATAG CCGTGGAATGGGAAAGTAACGGG CAGCCCGAGAACAACTATAAGACC ACACCACCCATGCTGGACTCCGAC GGTTCTTTCTTCCTTTATAGCAAGC TGACAGTGGATAAATCCAGGTGGC AGCAGGGTAACGTATTCAGTTGCA GTGTCATGCACGAGGCACTCCACA

			ACCACTATACTCAGAAAAGTCTTTC CCTGAGTCCAGGCAAG

SEQ ID 2392	QVTLKESGPTLVKPTQT LTLTCTFSGFSLSTSGV GVGWIRQPPGKALEWL ALIYWDDDKRYSPSLKS RLTITKDTSKNQVVLTM TNMDPVDTATYYCAHR LDSSGRGGYFDYWGQ GTLVTVSSASTKGPSVF PLAPCSRSTSESTAALG CLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSNF GTQTYTCNVDHKPSNT KVDKTVERKCCVECPP CPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVV VDVSHEDPEVQFNWYV DGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQD WLNGKEYKCKVSNKGL PAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPP MLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVM HEALHNHYTQKSLSLSP GK	SEQ ID 2500	CAGGTCACCTTGAAGGAGTCTGGT CCTACGCTGGTGAAACCCACACAG ACCCTCACGCTGACCTGCACCTTC TCTGGGTTCTCACTCAGCACTAGT GGAGTGGGTGTGGGCTGGATCCG TCAGCCCCCAGGAAAGGCCCTGG AGTGGCTTGCACTCATTTATTGGG ATGATGATAAGCGCTACAGCCCAT CTCTGAAGAGCAGGCTCACCATCA CCAAGGACACCTCCAAAAACCAGG TGGTCCTTACAATGACCAACATGG ACCCTGTGGACACAGCCACATATT ACTGTGCACACAGATTGGATAGCA GTGGCCGTGGTGGTTACTTTGACT ACTGGGGCCAGGGCACCCTGGTC ACCGTCTCCTCAGCAAGCACAAAA GGTCCTTCAGTGTTCCCTCTGGCA CCTTGCTCACGCAGCACCTCTGAG AGTACAGCCGCCCTGGGCTGCCT GGTAAAGGACTACTTTCCCGAACC AGTCACTGTGTCCTGGAATAGCGG GGCCTTGACCTCTGGAGTGCACA CATTTCCAGCTGTACTGCAGTCAT CTGGACTCTACAGCCTGTCCAGTG TGGTCACCGTACCTTCCTCCAACT TTGGCACTCAAACATATACATGTAA CGTGGATCATAAGCCCTCTAACAC CAAAGTGGATAAAACTGTGGAGCG TAAGTGTTGTGTCGAGTGTCCTCC TTGTCCTGCTCCTCCTGTGGCAGG CCCATCTGTGTTTCTCTTTCCCCC AAAGCCAAAGGACACTTTGATGAT ATCCCGGACCCCTGAGGTGACTT GCGTCGTCGTAGATGTTTCACACG AAGATCCAGAGGTGCAGTTCAACT GGTACGTGGATGGCGTGGAAGTG CATAATGCCAAGACAAAGCCCCGC GAAGAGCAGTTTAATTCCACCTTC CGCGTGGTGTCTGTGCTGACCGT GGTACATCAGGATTGGCTTAACGG TAAGGAGTACAAGTGCAAGGTGAG TAACAAGGGGCTGCCCGCCCCTA TCGAGAAGACTATCAGTAAAACCA AGGGCCAGCCAAGGGAGCCACAG GTGTACACACTTCCACCATCTAGG GAGGAAATGACAAAGAACCAGGT GAGTTTGACCTGTCTCGTGAAAGG CTTTTATCCCAGTGATATAGCCGT GGAATGGGAAAGTAACGGGCAGC CCGAGAACAACTATAAGACCACAC CACCCATGCTGGACTCCGACGGTT CTTTCTTCCTTTATAGCAAGCTGAC AGTGGATAAATCCAGGTGGCAGCA GGGTAACGTATTCAGTTGCAGTGT CATGCACGAGGCACTCCACAACCA

			CTATACTCAGAAAAGTCTTTCCCT GAGTCCAGGCAAG

SEQ ID 2393	EVQLVESGGGVVQPGR SLRLSCTASGFTFSSYG MHWVRQAPGKGLEWV AVISYDGSNKYYADSVK GRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCAK ELVGTSSPYYYYYYGM DVWGQGTMVTVSSAST KGPSVFPLAPCSRSTSE STAALGCLVKDYFPEPV TVSWNSGALTSGVHTF PAVLQSSGLYSLSSVVT VPSSNFGTQTYTCNVD HKPSNTKVDKTVERKC CVECPPCPAPPVAGPS VFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEV QFNWYVDGVEVHNAKT KPREEQFNSTFRVVSVL TVVHQDWLNGKEYKCK VSNKGLPAPIEKTISKTK GQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFY PSDIAVEWESNGQPEN NYKTTPPMLDSDGSFFL YSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQ KSLSLSPGK	SEQ ID 2501	GAGGTGCAGCTGGTGGAGTCTGG GGGAGGCGTGGTCCAGCCTGGGA GGTCCCTGAGACTCTCCTGTACAG CCTCTGGATTCACCTTCAGTAGCT ATGGCATGCACTGGGTCCGCCAG GCTCCAGGCAAGGGGCTGGAGTG GGTGGCAGTTATATCATATGATGG AAGTAATAAATACTATGCAGACTC CGTGAAGGGCCGATTCACCATCTC CAGAGACAATTCCAAGAACACGCT GTATCTGCAAATGAACAGCCTGAG AGCTGAGGACACGGCTGTGTATTA CTGTGCGAAAGAGTTGGTGGGTA CCAGCTCTCCTTATTACTACTACTA CTACGGTATGGACGTCTGGGGCC AAGGGACAATGGTCACCGTCTCTT CAGCAAGCACAAAAGGTCCTTCAG TGTTCCCTCTGGCACCTTGCTCAC GCAGCACCTCTGAGAGTACAGCC GCCCTGGGCTGCCTGGTAAAGGA CTACTTTCCCGAACCAGTCACTGT GTCCTGGAATAGCGGGGCCTTGA CCTCTGGAGTGCACACATTTCCAG CTGTACTGCAGTCATCTGGACTCT ACAGCCTGTCCAGTGTGGTCACC GTACCTTCCTCCAACTTTGGCACT CAAACATATACATGTAACGTGGAT CATAAGCCCTCTAACACCAAAGTG GATAAAACTGTGGAGCGTAAGTGT TGTGTCGAGTGTCCTCCTTGTCCT GCTCCTCCTGTGGCAGGCCCATCT GTGTTTCTCTTTCCCCCAAAGCCA AAGGACACTTTGATGATATCCCGG ACCCCTGAGGTGACTTGCGTCGTC GTAGATGTTTCACACGAAGATCCA GAGGTGCAGTTCAACTGGTACGTG GATGGCGTGGAAGTGCATAATGC CAAGACAAAGCCCCGCGAAGAGC AGTTTAATTCCACCTTCCGCGTGG TGTCTGTGCTGACCGTGGTACATC AGGATTGGCTTAACGGTAAGGAGT ACAAGTGCAAGGTGAGTAACAAGG GGCTGCCCGCCCCTATCGAGAAG ACTATCAGTAAAACCAAGGGCCAG CCAAGGGAGCCACAGGTGTACAC ACTTCCACCATCTAGGGAGGAAAT GACAAAGAACCAGGTGAGTTTGAC CTGTCTCGTGAAAGGCTTTTATCC CAGTGATATAGCCGTGGAATGGGA AAGTAACGGGCAGCCCGAGAACA ACTATAAGACCACACCACCCATGC TGGACTCCGACGGTTCTTTCTTCC TTTATAGCAAGCTGACAGTGGATA AATCCAGGTGGCAGCAGGGTAAC GTATTCAGTTGCAGTGTCATGCAC GAGGCACTCCACAACCACTATACT

			CAGAAAAGTCTTTCCCTGAGTCCA GGCAAG

SEQ ID 2394	QLQLQESGGGLVQPGG SLRLSCAASGFTVSSNY MSWVRQAPGKGLEWV SVIYSGGSTYYADSVKG RFTISRDNSKNTLYLQM NSLRAEDTAVYYCARDY YYGSGSSPWGQGTLVT VSSASTKGPSVFPLAPC SRSTSESTAALGCLVKD YFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSL SSVVTVPSSNFGTQTYT CNVDHKPSNTKVDKTV ERKCCVECPPCPAPPV AGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHE DPEVQFNWYVDGVEVH NAKTKPREEQFNSTFRV VSVLTVVHQDWLNGKE YKCKVSNKGLPAPIEKTI SKTKGQPREPQVYTLPP SREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQ PENNYKTTPPMLDSDG SFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHN HYTQKSLSLSPGK	SEQ ID 2502	CAGCTGCAGCTGCAGGAGTCGGG GGGAGGCTTGGTCCAGCCTGGGG GGTCCCTGAGACTCTCCTGTGCAG CCTCTGGATTCACCGTCAGTAGCA ACTACATGAGCTGGGTCCGCCAG GCTCCAGGGAAGGGGCTGGAGTG GGTCTCAGTTATTTATAGCGGTGG TAGCACATACTACGCAGACTCCGT GAAGGGCAGATTCACCATCTCCAG AGACAATTCCAAGAACACGCTGTA TCTTCAAATGAACAGCCTGAGAGC CGAGGACACGGCTGTGTATTACTG TGCGAGAGACTATTACTATGGTTC GGGGAGTTCTCCCTGGGGCCAGG GAACCCTGGTCACCGTCTCCTCAG CAAGCACAAAAGGTCCTTCAGTGT TCCCTCTGGCACCTTGCTCACGCA GCACCTCTGAGAGTACAGCCGCC CTGGGCTGCCTGGTAAAGGACTA CTTTCCCGAACCAGTCACTGTGTC CTGGAATAGCGGGGCCTTGACCT CTGGAGTGCACACATTTCCAGCTG TACTGCAGTCATCTGGACTCTACA GCCTGTCCAGTGTGGTCACCGTAC CTTCCTCCAACTTTGGCACTCAAA CATATACATGTAACGTGGATCATA AGCCCTCTAACACCAAAGTGGATA AAACTGTGGAGCGTAAGTGTTGTG TCGAGTGTCCTCCTTGTCCTGCTC CTCCTGTGGCAGGCCCATCTGTGT TTCTCTTTCCCCCAAAGCCAAAGG ACACTTTGATGATATCCCGGACCC CTGAGGTGACTTGCGTCGTCGTAG ATGTTTCACACGAAGATCCAGAGG TGCAGTTCAACTGGTACGTGGATG GCGTGGAAGTGCATAATGCCAAGA CAAAGCCCCGCGAAGAGCAGTTTA ATTCCACCTTCCGCGTGGTGTCTG TGCTGACCGTGGTACATCAGGATT GGCTTAACGGTAAGGAGTACAAGT GCAAGGTGAGTAACAAGGGGCTG CCCGCCCCTATCGAGAAGACTATC AGTAAAACCAAGGGCCAGCCAAG GGAGCCACAGGTGTACACACTTCC ACCATCTAGGGAGGAAATGACAAA GAACCAGGTGAGTTTGACCTGTCT CGTGAAAGGCTTTTATCCCAGTGA TATAGCCGTGGAATGGGAAAGTAA CGGGCAGCCCGAGAACAACTATA AGACCACACCACCCATGCTGGACT CCGACGGTTCTTTCTTCCTTTATAG CAAGCTGACAGTGGATAAATCCAG GTGGCAGCAGGGTAACGTATTCA GTTGCAGTGTCATGCACGAGGCA CTCCACAACCACTATACTCAGAAA AGTCTTTCCCTGAGTCCAGGCAAG

SEQ ID 2395	QVQLQQWGAGLLKPSE TLSLTCAVYGGSFSGYY WSWIRQPPGKGLEWIG EINHSGSTNYNPSLKSR VTISVDTSKNQFSLKLSS VTAADTAVYYCARGRP YCSSTSCYPEWFDPWG QGTLVTVSSASTKGPSV FPLAPCSRSTSESTAAL GCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSN FGTQTYTCNVDHKPSN TKVDKTVERKCCVECPP CPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVV VDVSHEDPEVQFNWYV DGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQD WLNGKEYKCKVSNKGL PAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPP MLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVM HEALHNHYTQKSLSLSP GK	SEQ ID 2503	CAGGTGCAGCTACAGCAGTGGGG CGCAGGACTGTTGAAGCCTTCGG AGACCCTGTCCCTCACCTGCGCTG TCTATGGTGGGTCCTTCAGTGGTT ACTACTGGAGCTGGATCCGCCAG CCCCCAGGGAAGGGGCTGGAGTG GATTGGGGAAATCAATCATAGTGG AAGCACCAACTACAACCCGTCCCT CAAGAGTCGAGTCACCATATCAGT AGACACGTCCAAGAACCAGTTCTC CCTGAAGCTGAGCTCTGTGACCG CCGCGGACACGGCTGTGTATTACT GTGCGAGAGGCCGGCCATATTGT AGTAGTACCAGCTGCTACCCAGAG TGGTTCGACCCCTGGGGCCAGGG AACCCTGGTCACCGTCTCCTCAGC AAGCACAAAAGGTCCTTCAGTGTT CCCTCTGGCACCTTGCTCACGCAG CACCTCTGAGAGTACAGCCGCCCT GGGCTGCCTGGTAAAGGACTACTT TCCCGAACCAGTCACTGTGTCCTG GAATAGCGGGGCCTTGACCTCTG GAGTGCACACATTTCCAGCTGTAC TGCAGTCATCTGGACTCTACAGCC TGTCCAGTGTGGTCACCGTACCTT CCTCCAACTTTGGCACTCAAACAT ATACATGTAACGTGGATCATAAGC CCTCTAACACCAAAGTGGATAAAA CTGTGGAGCGTAAGTGTTGTGTCG AGTGTCCTCCTTGTCCTGCTCCTC CTGTGGCAGGCCCATCTGTGTTTC TCTTTCCCCCAAAGCCAAAGGACA CTTTGATGATATCCCGGACCCCTG AGGTGACTTGCGTCGTCGTAGATG TTTCACACGAAGATCCAGAGGTGC AGTTCAACTGGTACGTGGATGGCG TGGAAGTGCATAATGCCAAGACAA AGCCCCGCGAAGAGCAGTTTAATT CCACCTTCCGCGTGGTGTCTGTGC TGACCGTGGTACATCAGGATTGGC TTAACGGTAAGGAGTACAAGTGCA AGGTGAGTAACAAGGGGCTGCCC GCCCCTATCGAGAAGACTATCAGT AAAACCAAGGGCCAGCCAAGGGA GCCACAGGTGTACACACTTCCACC ATCTAGGGAGGAAATGACAAAGAA CCAGGTGAGTTTGACCTGTCTCGT GAAAGGCTTTTATCCCAGTGATAT AGCCGTGGAATGGGAAAGTAACG GGCAGCCCGAGAACAACTATAAGA CCACACCACCCATGCTGGACTCC GACGGTTCTTTCTTCCTTTATAGCA AGCTGACAGTGGATAAATCCAGGT GGCAGCAGGGTAACGTATTCAGTT GCAGTGTCATGCACGAGGCACTC

			CACAACCACTATACTCAGAAAAGT CTTTCCCTGAGTCCAGGCAAG

SEQ ID 2396	QVTLKESGGGVVQPGR SLRLSCAASGFTFSSYG MHWVRQAPGKGLEWV AVISYDGSNKYYADSVK GRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCAKL RGIDYYDSSGYQRGFD YWGQGTLVTVSSASTK GPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVT VSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTV PSSNFGTQTYTCNVDH KPSNTKVDKTVERKCCV ECPPCPAPPVAGPSVFL FPPKPKDTLMISRTPEV TCVVVDVSHEDPEVQF NWYVDGVEVHNAKTKP REEQFNSTFRVVSVLTV VHQDWLNGKEYKCKVS NKGLPAPIEKTISKTKGQ PREPQVYTLPPSREEMT KNQVSLTCLVKGFYPSD IAVEWESNGQPENNYK TTPPMLDSDGSFFLYSK LTVDKSRWQQGNVFSC SVMHEALHNHYTQKSL SLSPGK	SEQ ID 2504	CAGGTCACCTTGAAGGAGTCTGG GGGAGGCGTGGTCCAGCCTGGGA GGTCCCTGAGACTCTCCTGTGCAG CCTCTGGATTCACCTTCAGTAGCT ATGGCATGCACTGGGTCCGCCAG GCTCCAGGCAAGGGGCTGGAGTG GGTGGCAGTTATATCATATGATGG AAGTAATAAATACTATGCAGACTC CGTGAAGGGCCGATTCACCATCTC CAGAGACAATTCCAAGAACACGCT GTATCTGCAAATGAACAGCCTGAG AGCTGAGGACACGGCTGTGTATTA CTGTGCGAAATTAAGGGGTATAGA TTACTATGATAGTAGTGGTTACCAA CGGGGGTTTGACTACTGGGGCCA GGGAACCCTGGTCACCGTCTCCT CAGCAAGCACAAAAGGTCCTTCAG TGTTCCCTCTGGCACCTTGCTCAC GCAGCACCTCTGAGAGTACAGCC GCCCTGGGCTGCCTGGTAAAGGA CTACTTTCCCGAACCAGTCACTGT GTCCTGGAATAGCGGGGCCTTGA CCTCTGGAGTGCACACATTTCCAG CTGTACTGCAGTCATCTGGACTCT ACAGCCTGTCCAGTGTGGTCACC GTACCTTCCTCCAACTTTGGCACT CAAACATATACATGTAACGTGGAT CATAAGCCCTCTAACACCAAAGTG GATAAAACTGTGGAGCGTAAGTGT TGTGTCGAGTGTCCTCCTTGTCCT GCTCCTCCTGTGGCAGGCCCATCT GTGTTTCTCTTTCCCCCAAAGCCA AAGGACACTTTGATGATATCCCGG ACCCCTGAGGTGACTTGCGTCGTC GTAGATGTTTCACACGAAGATCCA GAGGTGCAGTTCAACTGGTACGTG GATGGCGTGGAAGTGCATAATGC CAAGACAAAGCCCCGCGAAGAGC AGTTTAATTCCACCTTCCGCGTGG TGTCTGTGCTGACCGTGGTACATC AGGATTGGCTTAACGGTAAGGAGT ACAAGTGCAAGGTGAGTAACAAGG GGCTGCCCGCCCCTATCGAGAAG ACTATCAGTAAAACCAAGGGCCAG CCAAGGGAGCCACAGGTGTACAC ACTTCCACCATCTAGGGAGGAAAT GACAAAGAACCAGGTGAGTTTGAC CTGTCTCGTGAAAGGCTTTTATCC CAGTGATATAGCCGTGGAATGGGA AAGTAACGGGCAGCCCGAGAACA ACTATAAGACCACACCACCCATGC TGGACTCCGACGGTTCTTTCTTCC TTTATAGCAAGCTGACAGTGGATA AATCCAGGTGGCAGCAGGGTAAC GTATTCAGTTGCAGTGTCATGCAC GAGGCACTCCACAACCACTATACT

			CAGAAAAGTCTTTCCCTGAGTCCA GGCAAG

SEQ ID 2397	QVQLQESGPGLVKPSE TLSLTCTVSGGSISSYY WSWIRQPPGKGLEWIG YIYYTGSTNYNPSLKSR VTISVDTSKNQFSLKLSS VTTADTAVYYCARGGR GDGAAFDIWGQGTMVT VSSASTKGPSVFPLAPC SRSTSESTAALGCLVKD YFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSL SSVVTVPSSNFGTQTYT CNVDHKPSNTKVDKTV ERKCCVECPPCPAPPV AGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHE DPEVQFNWYVDGVEVH NAKTKPREEQFNSTFRV VSVLTVVHQDWLNGKE YKCKVSNKGLPAPIEKTI SKTKGQPREPQVYTLPP SREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQ PENNYKTTPPMLDSDG SFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHN HYTQKSLSLSPGK	SEQ ID 2505	CAGGTGCAGCTGCAGGAGTCCGG CCCAGGACTGGTGAAGCCTTCGG AGACCCTGTCCCTCACCTGCACTG TCTCTGGTGGCTCCATCAGTAGTT ACTACTGGAGCTGGATCCGGCAG CCCCCAGGGAAGGGACTGGAGTG GATTGGCTATATCTATTACACTGG GAGCACCAACTACAACCCCTCCCT CAAGAGCCGAGTCACCATATCAGT AGACACGTCCAAGAACCAGTTCTC CCTGAAGCTGAGCTCTGTGACCAC TGCGGACACGGCCGTGTATTACTG TGCGAGAGGTGGGAGGGGGGATG GGGCCGCTTTTGACATCTGGGGC CAAGGGACAATGGTCACCGTCTCT TCAGCAAGCACAAAAGGTCCTTCA GTGTTCCCTCTGGCACCTTGCTCA CGCAGCACCTCTGAGAGTACAGC CGCCCTGGGCTGCCTGGTAAAGG ACTACTTTCCCGAACCAGTCACTG TGTCCTGGAATAGCGGGGCCTTG ACCTCTGGAGTGCACACATTTCCA GCTGTACTGCAGTCATCTGGACTC TACAGCCTGTCCAGTGTGGTCACC GTACCTTCCTCCAACTTTGGCACT CAAACATATACATGTAACGTGGAT CATAAGCCCTCTAACACCAAAGTG GATAAAACTGTGGAGCGTAAGTGT TGTGTCGAGTGTCCTCCTTGTCCT GCTCCTCCTGTGGCAGGCCCATCT GTGTTTCTCTTTCCCCCAAAGCCA AAGGACACTTTGATGATATCCCGG ACCCCTGAGGTGACTTGCGTCGTC GTAGATGTTTCACACGAAGATCCA GAGGTGCAGTTCAACTGGTACGTG GATGGCGTGGAAGTGCATAATGC CAAGACAAAGCCCCGCGAAGAGC AGTTTAATTCCACCTTCCGCGTGG TGTCTGTGCTGACCGTGGTACATC AGGATTGGCTTAACGGTAAGGAGT ACAAGTGCAAGGTGAGTAACAAGG GGCTGCCCGCCCCTATCGAGAAG ACTATCAGTAAAACCAAGGGCCAG CCAAGGGAGCCACAGGTGTACAC ACTTCCACCATCTAGGGAGGAAAT GACAAAGAACCAGGTGAGTTTGAC CTGTCTCGTGAAAGGCTTTTATCC CAGTGATATAGCCGTGGAATGGGA AAGTAACGGGCAGCCCGAGAACA ACTATAAGACCACACCACCCATGC TGGACTCCGACGGTTCTTTCTTCC TTTATAGCAAGCTGACAGTGGATA AATCCAGGTGGCAGCAGGGTAAC GTATTCAGTTGCAGTGTCATGCAC GAGGCACTCCACAACCACTATACT

			CAGAAAAGTCTTTCCCTGAGTCCA GGCAAG

SEQ ID 2398	QVQLVQSGGGVVQPGR SLRLSCAASGFTFSSSA MHWVRQAPGKGLEWV AMIWHDESKKYYADSV KGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCA RPPDGGNSGRWYFDL WGRGTLVTVSSASTKG PSVFPLAPCSRSTSEST AALGCLVKDYFPEPVTV SWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVP SSNFGTQTYTCNVDHK PSNTKVDKTVERKCCVE CPPCPAPPVAGPSVFLF PPKPKDTLMISRTPEVT CVVVDVSHEDPEVQFN WYVDGVEVHNAKTKPR EEQFNSTFRVVSVLTVV HQDWLNGKEYKCKVSN KGLPAPIEKTISKTKGQP REPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDI AVEWESNGQPENNYKT TPPMLDSDGSFFLYSKL TVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSL SPGK	SEQ ID 2506	CAGGTGCAGCTGGTGCAATCTGG GGGAGGCGTGGTCCAGCCTGGGA GGTCCCTGAGACTCTCCTGTGCAG CGTCTGGATTCACCTTCAGCAGCT CTGCCATGCACTGGGTCCGCCAG GCTCCAGGCAAGGGACTGGAGTG GGTGGCAATGATTTGGCATGATGA GAGTAAGAAATACTATGCAGACTC CGTGAAGGGCCGATTCACTATCTC CAGAGACAATTCCAAGAACACGCT GTATCTGCAAATGAACAGCCTGAG AGCTGAGGACACGGCTGTGTATTA CTGTGCGAGACCCCCCGACGGTG GTAACTCCGGTCGCTGGTACTTCG ATCTCTGGGGCCGTGGCACCCTG GTCACCGTCTCCTCAGCAAGCACA AAAGGTCCTTCAGTGTTCCCTCTG GCACCTTGCTCACGCAGCACCTCT GAGAGTACAGCCGCCCTGGGCTG CCTGGTAAAGGACTACTTTCCCGA ACCAGTCACTGTGTCCTGGAATAG CGGGGCCTTGACCTCTGGAGTGC ACACATTTCCAGCTGTACTGCAGT CATCTGGACTCTACAGCCTGTCCA GTGTGGTCACCGTACCTTCCTCCA ACTTTGGCACTCAAACATATACAT GTAACGTGGATCATAAGCCCTCTA ACACCAAAGTGGATAAAACTGTGG AGCGTAAGTGTTGTGTCGAGTGTC CTCCTTGTCCTGCTCCTCCTGTGG CAGGCCCATCTGTGTTTCTCTTTC CCCCAAAGCCAAAGGACACTTTGA TGATATCCCGGACCCCTGAGGTGA CTTGCGTCGTCGTAGATGTTTCAC ACGAAGATCCAGAGGTGCAGTTCA ACTGGTACGTGGATGGCGTGGAA GTGCATAATGCCAAGACAAAGCCC CGCGAAGAGCAGTTTAATTCCACC TTCCGCGTGGTGTCTGTGCTGACC GTGGTACATCAGGATTGGCTTAAC GGTAAGGAGTACAAGTGCAAGGT GAGTAACAAGGGGCTGCCCGCCC CTATCGAGAAGACTATCAGTAAAA CCAAGGGCCAGCCAAGGGAGCCA CAGGTGTACACACTTCCACCATCT AGGGAGGAAATGACAAAGAACCA GGTGAGTTTGACCTGTCTCGTGAA AGGCTTTTATCCCAGTGATATAGC CGTGGAATGGGAAAGTAACGGGC AGCCCGAGAACAACTATAAGACCA CACCACCCATGCTGGACTCCGAC GGTTCTTTCTTCCTTTATAGCAAGC TGACAGTGGATAAATCCAGGTGGC AGCAGGGTAACGTATTCAGTTGCA GTGTCATGCACGAGGCACTCCACA

			ACCACTATACTCAGAAAAGTCTTTC CCTGAGTCCAGGCAAG

SEQ ID 2399	QMQLVQSGGGLVQPG GSLRLSCAASGFTFSSY AMSWVRQAPGKGLEW VSAISGSGGSTYYADSV KGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCA KDKNVRKHDYGDHPYG GYFDYWGQGTLVTVSS ASTKGPSVFPLAPCSRS TSESTAALGCLVKDYFP EPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSS VVTVPSSNFGTQTYTCN VDHKPSNTKVDKTVERK CCVECPPCPAPPVAGP SVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEV QFNWYVDGVEVHNAKT KPREEQFNSTFRVVSVL TVVHQDWLNGKEYKCK VSNKGLPAPIEKTISKTK GQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFY PSDIAVEWESNGQPEN NYKTTPPMLDSDGSFFL YSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQ KSLSLSPGK	SEQ ID 2507	CAGATGCAGCTGGTGCAATCTGG GGGAGGCTTGGTACAGCCTGGGG GGTCCCTGAGACTCTCCTGTGCAG CCTCTGGATTCACCTTTAGCAGCT ATGCCATGAGCTGGGTCCGCCAG GCTCCAGGGAAGGGGCTGGAGTG GGTCTCAGCTATTAGTGGTAGTGG TGGTAGCACATACTACGCAGACTC CGTGAAGGGCCGGTTCACCATCT CCAGAGACAATTCCAAGAACACGC TGTATCTGCAAATGAACAGCCTGA GAGCCGAGGACACGGCCGTATAT TACTGTGCGAAAGACAAGAACGTC CGAAAACATGACTACGGTGACCAC CCCTACGGGGGGTACTTTGACTAC TGGGGCCAGGGCACCCTGGTGAC CGTCTCCTCAGCAAGCACAAAAGG TCCTTCAGTGTTCCCTCTGGCACC TTGCTCACGCAGCACCTCTGAGAG TACAGCCGCCCTGGGCTGCCTGG TAAAGGACTACTTTCCCGAACCAG TCACTGTGTCCTGGAATAGCGGG GCCTTGACCTCTGGAGTGCACACA TTTCCAGCTGTACTGCAGTCATCT GGACTCTACAGCCTGTCCAGTGTG GTCACCGTACCTTCCTCCAACTTT GGCACTCAAACATATACATGTAAC GTGGATCATAAGCCCTCTAACACC AAAGTGGATAAAACTGTGGAGCGT AAGTGTTGTGTCGAGTGTCCTCCT TGTCCTGCTCCTCCTGTGGCAGGC CCATCTGTGTTTCTCTTTCCCCCAA AGCCAAAGGACACTTTGATGATAT CCCGGACCCCTGAGGTGACTTGC GTCGTCGTAGATGTTTCACACGAA GATCCAGAGGTGCAGTTCAACTGG TACGTGGATGGCGTGGAAGTGCA TAATGCCAAGACAAAGCCCCGCGA AGAGCAGTTTAATTCCACCTTCCG CGTGGTGTCTGTGCTGACCGTGG TACATCAGGATTGGCTTAACGGTA AGGAGTACAAGTGCAAGGTGAGTA ACAAGGGGCTGCCCGCCCCTATC GAGAAGACTATCAGTAAAACCAAG GGCCAGCCAAGGGAGCCACAGGT GTACACACTTCCACCATCTAGGGA GGAAATGACAAAGAACCAGGTGA GTTTGACCTGTCTCGTGAAAGGCT TTTATCCCAGTGATATAGCCGTGG AATGGGAAAGTAACGGGCAGCCC GAGAACAACTATAAGACCACACCA CCCATGCTGGACTCCGACGGTTCT TTCTTCCTTTATAGCAAGCTGACA GTGGATAAATCCAGGTGGCAGCA GGGTAACGTATTCAGTTGCAGTGT CATGCACGAGGCACTCCACAACCA

			CTATACTCAGAAAAGTCTTTCCCT GAGTCCAGGCAAG

SEQ ID 2400	EVQLVQSGAEVKKPGA SVKVSCKASGYTFTSYA MHWVRQAPGQRLEWM GWINAGNGNTKYSQKF QGRVTITRDTSASTAYM ELSSLRSEDTAVYYCAR VAGATSLWYWGQGTLV TVSSASTKGPSVFPLAP CSRSTSESTAALGCLVK DYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLY SLSSVVTVPSSNFGTQT YTCNVDHKPSNTKVDKT VERKCCVECPPCPAPP VAGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSH EDPEVQFNWYVDGVEV HNAKTKPREEQFNSTFR VVSVLTVVHQDWLNGK EYKCKVSNKGLPAPIEK TISKTKGQPREPQVYTL PPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNG QPENNYKTTPPMLDSD GSFFLYSKLTVDKSRW QQGNVFSCSVMHEALH NHYTQKSLSLSPGK	SEQ ID 2508	GAGGTCCAGCTGGTACAGTCTGG GGCTGAGGTGAAGAAGCCTGGGG CCTCAGTGAAGGTTTCCTGCAAGG CTTCTGGATACACCTTCACTAGCT ATGCTATGCATTGGGTGCGCCAG GCCCCCGGACAAAGGCTTGAGTG GATGGGATGGATCAACGCTGGCA ATGGTAACACAAAATATTCACAGA AGTTCCAGGGCAGAGTCACCATTA CCAGGGACACATCCGCGAGCACA GCCTACATGGAGCTGAGCAGCCT GAGATCTGAAGACACGGCTGTGTA TTACTGTGCGAGAGTGGCGGGAG CTACTTCCCTATGGTACTGGGGCC AGGGCACCCTGGTCACCGTCTCC TCAGCAAGCACAAAAGGTCCTTCA GTGTTCCCTCTGGCACCTTGCTCA CGCAGCACCTCTGAGAGTACAGC CGCCCTGGGCTGCCTGGTAAAGG ACTACTTTCCCGAACCAGTCACTG TGTCCTGGAATAGCGGGGCCTTG ACCTCTGGAGTGCACACATTTCCA GCTGTACTGCAGTCATCTGGACTC TACAGCCTGTCCAGTGTGGTCACC GTACCTTCCTCCAACTTTGGCACT CAAACATATACATGTAACGTGGAT CATAAGCCCTCTAACACCAAAGTG GATAAAACTGTGGAGCGTAAGTGT TGTGTCGAGTGTCCTCCTTGTCCT GCTCCTCCTGTGGCAGGCCCATCT GTGTTTCTCTTTCCCCCAAAGCCA AAGGACACTTTGATGATATCCCGG ACCCCTGAGGTGACTTGCGTCGTC GTAGATGTTTCACACGAAGATCCA GAGGTGCAGTTCAACTGGTACGTG GATGGCGTGGAAGTGCATAATGC CAAGACAAAGCCCCGCGAAGAGC AGTTTAATTCCACCTTCCGCGTGG TGTCTGTGCTGACCGTGGTACATC AGGATTGGCTTAACGGTAAGGAGT ACAAGTGCAAGGTGAGTAACAAGG GGCTGCCCGCCCCTATCGAGAAG ACTATCAGTAAAACCAAGGGCCAG CCAAGGGAGCCACAGGTGTACAC ACTTCCACCATCTAGGGAGGAAAT GACAAAGAACCAGGTGAGTTTGAC CTGTCTCGTGAAAGGCTTTTATCC CAGTGATATAGCCGTGGAATGGGA AAGTAACGGGCAGCCCGAGAACA ACTATAAGACCACACCACCCATGC TGGACTCCGACGGTTCTTTCTTCC TTTATAGCAAGCTGACAGTGGATA AATCCAGGTGGCAGCAGGGTAAC GTATTCAGTTGCAGTGTCATGCAC GAGGCACTCCACAACCACTATACT

			CAGAAAAGTCTTTCCCTGAGTCCA GGCAAG

SEQ ID 2401	QVQLQQSGPGLVKPSQ SLSLTCAISGDSVSSNS AAWNWIRQSPSRGLEW LGRTYYRSKWYNDYAV SVKSRITIKPDTSKNQFS LQLNSVTPEDTAVYYCT RLANSDGVDVWGQGT MVTVSSASTKGPSVFPL APCSRSTSESTAALGCL VKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSG LYSLSSVVTVPSSNFGT QTYTCNVDHKPSNTKV DKTVERKCCVECPPCP APPVAGPSVFLFPPKPK DTLMISRTPEVTCVVVD VSHEDPEVQFNWYVDG VEVHNAKTKPREEQFN STFRVVSVLTVVHQDWL NGKEYKCKVSNKGLPA PIEKTISKTKGQPREPQV YTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWE SNGQPENNYKTTPPML DSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK	SEQ ID 2509	CAGGTACAGCTGCAGCAGTCAGG TCCAGGACTGGTGAAGCCCTCGC AGAGCCTCTCACTCACCTGTGCCA TCTCCGGGGACAGTGTCTCTAGCA ACAGTGCTGCTTGGAACTGGATCA GGCAGTCCCCATCGAGAGGCCTT GAGTGGCTGGGAAGGACATACTA CAGGTCCAAGTGGTATAATGATTA TGCAGTATCTGTGAAGAGTCGAAT AACCATCAAACCAGACACATCCAA GAACCAGTTCTCCCTGCAGCTGAA CTCTGTGACTCCCGAGGACACGG CTGTGTATTACTGTACAAGGCTAG CTAATTCCGACGGTGTGGACGTCT GGGGCCAAGGGACAATGGTCACC GTCTCCTCAGCAAGCACAAAAGGT CCTTCAGTGTTCCCTCTGGCACCT TGCTCACGCAGCACCTCTGAGAGT ACAGCCGCCCTGGGCTGCCTGGT AAAGGACTACTTTCCCGAACCAGT CACTGTGTCCTGGAATAGCGGGG CCTTGACCTCTGGAGTGCACACAT TTCCAGCTGTACTGCAGTCATCTG GACTCTACAGCCTGTCCAGTGTGG TCACCGTACCTTCCTCCAACTTTG GCACTCAAACATATACATGTAACG TGGATCATAAGCCCTCTAACACCA AAGTGGATAAAACTGTGGAGCGTA AGTGTTGTGTCGAGTGTCCTCCTT GTCCTGCTCCTCCTGTGGCAGGC CCATCTGTGTTTCTCTTTCCCCCAA AGCCAAAGGACACTTTGATGATAT CCCGGACCCCTGAGGTGACTTGC GTCGTCGTAGATGTTTCACACGAA GATCCAGAGGTGCAGTTCAACTGG TACGTGGATGGCGTGGAAGTGCA TAATGCCAAGACAAAGCCCCGCGA AGAGCAGTTTAATTCCACCTTCCG CGTGGTGTCTGTGCTGACCGTGG TACATCAGGATTGGCTTAACGGTA AGGAGTACAAGTGCAAGGTGAGTA ACAAGGGGCTGCCCGCCCCTATC GAGAAGACTATCAGTAAAACCAAG GGCCAGCCAAGGGAGCCACAGGT GTACACACTTCCACCATCTAGGGA GGAAATGACAAAGAACCAGGTGA GTTTGACCTGTCTCGTGAAAGGCT TTTATCCCAGTGATATAGCCGTGG AATGGGAAAGTAACGGGCAGCCC GAGAACAACTATAAGACCACACCA CCCATGCTGGACTCCGACGGTTCT TTCTTCCTTTATAGCAAGCTGACA GTGGATAAATCCAGGTGGCAGCA GGGTAACGTATTCAGTTGCAGTGT CATGCACGAGGCACTCCACAACCA

			CTATACTCAGAAAAGTCTTTCCCT GAGTCCAGGCAAG

SEQ ID 2402	QVQLQQSGPGLVKPSQ TLSLTCAISGDSVSSDS AVWTWIRQSPSRGLEW LGRTYYKSKWYNDYAA SVKSRITINPDTSKNQFS LHLNSVTPEDTAVYYCA RGVTRTFDYWGQGTTV TVSSASTKGPSVFPLAP CSRSTSESTAALGCLVK DYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLY SLSSVVTVPSSNFGTQT YTCNVDHKPSNTKVDKT VERKCCVECPPCPAPP VAGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSH EDPEVQFNWYVDGVEV HNAKTKPREEQFNSTFR VVSVLTVVHQDWLNGK EYKCKVSNKGLPAPIEK TISKTKGQPREPQVYTL PPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNG QPENNYKTTPPMLDSD GSFFLYSKLTVDKSRW QQGNVFSCSVMHEALH NHYTQKSLSLSPGK	SEQ ID 2510	CAGGTACAGCTGCAGCAGTCAGG TCCAGGACTGGTGAAGCCCTCGC AGACCCTCTCACTCACCTGTGCCA TCTCCGGGGACAGTGTCTCTAGC GACAGTGCTGTTTGGACCTGGATC AGGCAGTCCCCATCGAGAGGCCT TGAGTGGCTGGGAAGGACATACTA CAAGTCGAAGTGGTATAATGATTA TGCAGCATCTGTGAAAAGTCGAAT AACCATCAACCCAGACACATCCAA GAACCAGTTCTCCCTGCACCTGAA CTCTGTGACTCCCGAGGACACGG CTGTGTATTACTGTGCAAGAGGTG TAACCCGGACCTTTGACTACTGGG GCCAGGGGACCACGGTCACCGTC TCCTCAGCAAGCACAAAAGGTCCT TCAGTGTTCCCTCTGGCACCTTGC TCACGCAGCACCTCTGAGAGTACA GCCGCCCTGGGCTGCCTGGTAAA GGACTACTTTCCCGAACCAGTCAC TGTGTCCTGGAATAGCGGGGCCTT GACCTCTGGAGTGCACACATTTCC AGCTGTACTGCAGTCATCTGGACT CTACAGCCTGTCCAGTGTGGTCAC CGTACCTTCCTCCAACTTTGGCAC TCAAACATATACATGTAACGTGGA TCATAAGCCCTCTAACACCAAAGT GGATAAAACTGTGGAGCGTAAGTG TTGTGTCGAGTGTCCTCCTTGTCC TGCTCCTCCTGTGGCAGGCCCATC TGTGTTTCTCTTTCCCCCAAAGCC AAAGGACACTTTGATGATATCCCG GACCCCTGAGGTGACTTGCGTCG TCGTAGATGTTTCACACGAAGATC CAGAGGTGCAGTTCAACTGGTACG TGGATGGCGTGGAAGTGCATAATG CCAAGACAAAGCCCCGCGAAGAG CAGTTTAATTCCACCTTCCGCGTG GTGTCTGTGCTGACCGTGGTACAT CAGGATTGGCTTAACGGTAAGGAG TACAAGTGCAAGGTGAGTAACAAG GGGCTGCCCGCCCCTATCGAGAA GACTATCAGTAAAACCAAGGGCCA GCCAAGGGAGCCACAGGTGTACA CACTTCCACCATCTAGGGAGGAAA TGACAAAGAACCAGGTGAGTTTGA CCTGTCTCGTGAAAGGCTTTTATC CCAGTGATATAGCCGTGGAATGG GAAAGTAACGGGCAGCCCGAGAA CAACTATAAGACCACACCACCCAT GCTGGACTCCGACGGTTCTTTCTT CCTTTATAGCAAGCTGACAGTGGA TAAATCCAGGTGGCAGCAGGGTAA CGTATTCAGTTGCAGTGTCATGCA CGAGGCACTCCACAACCACTATAC

			TCAGAAAAGTCTTTCCCTGAGTCC AGGCAAG

SEQ ID 2403	QLQLQESGPGLVKPSQ TLSLTCAISGDSVSSNS AAWNWIRQSPSRGLEW LGRTYYRSKWYNDYAV SVKSRITINPDTSKNQFS LQLNSVTPEDTAVYYCA EGNGPFDPWGQGTLVT VSSASTKGPSVFPLAPC SRSTSESTAALGCLVKD YFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSL SSVVTVPSSNFGTQTYT CNVDHKPSNTKVDKTV ERKCCVECPPCPAPPV AGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHE DPEVQFNWYVDGVEVH NAKTKPREEQFNSTFRV VSVLTVVHQDWLNGKE YKCKVSNKGLPAPIEKTI SKTKGQPREPQVYTLPP SREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQ PENNYKTTPPMLDSDG SFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHN HYTQKSLSLSPGK	SEQ ID 2511	CAGCTGCAGCTGCAGGAGTCGGG TCCAGGACTGGTGAAGCCCTCGC AGACCCTCTCACTCACCTGTGCCA TCTCCGGGGACAGTGTCTCTAGCA ACAGTGCTGCTTGGAACTGGATCA GGCAGTCCCCATCGAGAGGCCTT GAGTGGCTGGGAAGGACATACTA CAGGTCCAAGTGGTATAATGATTA TGCAGTATCTGTGAAAAGTCGAAT AACCATCAACCCAGACACATCCAA GAACCAGTTCTCCCTGCAGCTGAA CTCTGTGACTCCCGAGGACACGG CTGTGTATTACTGTGCAGAAGGCA ATGGGCCGTTCGACCCCTGGGGC CAGGGAACCCTGGTGACCGTCTC CTCAGCAAGCACAAAAGGTCCTTC AGTGTTCCCTCTGGCACCTTGCTC ACGCAGCACCTCTGAGAGTACAG CCGCCCTGGGCTGCCTGGTAAAG GACTACTTTCCCGAACCAGTCACT GTGTCCTGGAATAGCGGGGCCTT GACCTCTGGAGTGCACACATTTCC AGCTGTACTGCAGTCATCTGGACT CTACAGCCTGTCCAGTGTGGTCAC CGTACCTTCCTCCAACTTTGGCAC TCAAACATATACATGTAACGTGGA TCATAAGCCCTCTAACACCAAAGT GGATAAAACTGTGGAGCGTAAGTG TTGTGTCGAGTGTCCTCCTTGTCC TGCTCCTCCTGTGGCAGGCCCATC TGTGTTTCTCTTTCCCCCAAAGCC AAAGGACACTTTGATGATATCCCG GACCCCTGAGGTGACTTGCGTCG TCGTAGATGTTTCACACGAAGATC CAGAGGTGCAGTTCAACTGGTACG TGGATGGCGTGGAAGTGCATAATG CCAAGACAAAGCCCCGCGAAGAG CAGTTTAATTCCACCTTCCGCGTG GTGTCTGTGCTGACCGTGGTACAT CAGGATTGGCTTAACGGTAAGGAG TACAAGTGCAAGGTGAGTAACAAG GGGCTGCCCGCCCCTATCGAGAA GACTATCAGTAAAACCAAGGGCCA GCCAAGGGAGCCACAGGTGTACA CACTTCCACCATCTAGGGAGGAAA TGACAAAGAACCAGGTGAGTTTGA CCTGTCTCGTGAAAGGCTTTTATC CCAGTGATATAGCCGTGGAATGG GAAAGTAACGGGCAGCCCGAGAA CAACTATAAGACCACACCACCCAT GCTGGACTCCGACGGTTCTTTCTT CCTTTATAGCAAGCTGACAGTGGA TAAATCCAGGTGGCAGCAGGGTAA CGTATTCAGTTGCAGTGTCATGCA CGAGGCACTCCACAACCACTATAC

			TCAGAAAAGTCTTTCCCTGAGTCC AGGCAAG

SEQ ID 2404	QITLKESGGGVVQPGRS LRLSCVASGFTFSTYPM HWVRQAPGKGLEWVA VISYDGRNEYYADSVKG RFTISRDNSKNTLYLQM NSLRAEDTAVYYCATRD TPLVGVSIYWGQGTLVT VSSASTKGPSVFPLAPC SRSTSESTAALGCLVKD YFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSL SSVVTVPSSNFGTQTYT CNVDHKPSNTKVDKTV ERKCCVECPPCPAPPV AGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHE DPEVQFNWYVDGVEVH NAKTKPREEQFNSTFRV VSVLTVVHQDWLNGKE YKCKVSNKGLPAPIEKTI SKTKGQPREPQVYTLPP SREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQ PENNYKTTPPMLDSDG SFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHN HYTQKSLSLSPGK	SEQ ID 2512	CAGATCACCTTGAAGGAGTCTGGG GGAGGCGTGGTCCAGCCTGGGAG GTCCCTGAGACTCTCCTGTGTAGC CTCTGGATTCACCTTCAGTACCTA TCCCATGCACTGGGTCCGCCAGG CTCCAGGCAAGGGGCTGGAGTGG GTGGCAGTTATATCATATGATGGA CGTAATGAATACTACGCAGACTCC GTGAAGGGCCGATTCACCATCTCC AGAGACAATTCCAAAAACACGCTG TATCTGCAAATGAACAGTCTGCGA GCTGAAGACACGGCTGTCTATTAT TGTGCGACTCGGGATACACCTTTG GTTGGGGTTTCGATATACTGGGGC CAGGGCACCCTGGTCACCGTCTC CTCAGCAAGCACAAAAGGTCCTTC AGTGTTCCCTCTGGCACCTTGCTC ACGCAGCACCTCTGAGAGTACAG CCGCCCTGGGCTGCCTGGTAAAG GACTACTTTCCCGAACCAGTCACT GTGTCCTGGAATAGCGGGGCCTT GACCTCTGGAGTGCACACATTTCC AGCTGTACTGCAGTCATCTGGACT CTACAGCCTGTCCAGTGTGGTCAC CGTACCTTCCTCCAACTTTGGCAC TCAAACATATACATGTAACGTGGA TCATAAGCCCTCTAACACCAAAGT GGATAAAACTGTGGAGCGTAAGTG TTGTGTCGAGTGTCCTCCTTGTCC TGCTCCTCCTGTGGCAGGCCCATC TGTGTTTCTCTTTCCCCCAAAGCC AAAGGACACTTTGATGATATCCCG GACCCCTGAGGTGACTTGCGTCG TCGTAGATGTTTCACACGAAGATC CAGAGGTGCAGTTCAACTGGTACG TGGATGGCGTGGAAGTGCATAATG CCAAGACAAAGCCCCGCGAAGAG CAGTTTAATTCCACCTTCCGCGTG GTGTCTGTGCTGACCGTGGTACAT CAGGATTGGCTTAACGGTAAGGAG TACAAGTGCAAGGTGAGTAACAAG GGGCTGCCCGCCCCTATCGAGAA GACTATCAGTAAAACCAAGGGCCA GCCAAGGGAGCCACAGGTGTACA CACTTCCACCATCTAGGGAGGAAA TGACAAAGAACCAGGTGAGTTTGA CCTGTCTCGTGAAAGGCTTTTATC CCAGTGATATAGCCGTGGAATGG GAAAGTAACGGGCAGCCCGAGAA CAACTATAAGACCACACCACCCAT GCTGGACTCCGACGGTTCTTTCTT CCTTTATAGCAAGCTGACAGTGGA TAAATCCAGGTGGCAGCAGGGTAA CGTATTCAGTTGCAGTGTCATGCA CGAGGCACTCCACAACCACTATAC

			TCAGAAAAGTCTTTCCCTGAGTCC AGGCAAG

SEQ ID 2405	QMQLVQSGGGLVKAGG SLRLSCSASGFTFSSYA MHWVRQAPGKGLEYVS AISSNGGSTYYADSVKG RFTISRDNSKNTLYLQM SSLRAEDTAVYYCVNRA GYGDYRHFQHWGQGT LVTVSSASTKGPSVFPL APCSRSTSESTAALGCL VKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSG LYSLSSVVTVPSSNFGT QTYTCNVDHKPSNTKV DKTVERKCCVECPPCP APPVAGPSVFLFPPKPK DTLMISRTPEVTCVVVD VSHEDPEVQFNWYVDG VEVHNAKTKPREEQFN STFRVVSVLTVVHQDWL NGKEYKCKVSNKGLPA PIEKTISKTKGQPREPQV YTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWE SNGQPENNYKTTPPML DSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK	SEQ ID 2513	CAGATGCAGCTGGTGCAATCTGG GGGAGGCCTGGTCAAGGCTGGGG GGTCCCTGAGACTCTCCTGTTCAG CCTCTGGATTCACCTTCAGTAGCT ATGCTATGCACTGGGTCCGCCAG GCTCCAGGGAAGGGACTGGAATA TGTTTCAGCTATTAGTAGTAATGG GGGTAGCACATACTACGCAGACTC AGTGAAGGGCAGATTCACCATCTC CAGAGACAATTCCAAGAACACGCT GTATCTTCAAATGAGCAGTCTGAG AGCTGAGGACACGGCTGTGTATTA CTGTGTGAATCGGGCGGGTTACG GTGACTACAGACACTTCCAGCACT GGGGCCAGGGCACCCTGGTCACC GTCTCCTCAGCAAGCACAAAAGGT CCTTCAGTGTTCCCTCTGGCACCT TGCTCACGCAGCACCTCTGAGAGT ACAGCCGCCCTGGGCTGCCTGGT AAAGGACTACTTTCCCGAACCAGT CACTGTGTCCTGGAATAGCGGGG CCTTGACCTCTGGAGTGCACACAT TTCCAGCTGTACTGCAGTCATCTG GACTCTACAGCCTGTCCAGTGTGG TCACCGTACCTTCCTCCAACTTTG GCACTCAAACATATACATGTAACG TGGATCATAAGCCCTCTAACACCA AAGTGGATAAAACTGTGGAGCGTA AGTGTTGTGTCGAGTGTCCTCCTT GTCCTGCTCCTCCTGTGGCAGGC CCATCTGTGTTTCTCTTTCCCCCAA AGCCAAAGGACACTTTGATGATAT CCCGGACCCCTGAGGTGACTTGC GTCGTCGTAGATGTTTCACACGAA GATCCAGAGGTGCAGTTCAACTGG TACGTGGATGGCGTGGAAGTGCA TAATGCCAAGACAAAGCCCCGCGA AGAGCAGTTTAATTCCACCTTCCG CGTGGTGTCTGTGCTGACCGTGG TACATCAGGATTGGCTTAACGGTA AGGAGTACAAGTGCAAGGTGAGTA ACAAGGGGCTGCCCGCCCCTATC GAGAAGACTATCAGTAAAACCAAG GGCCAGCCAAGGGAGCCACAGGT GTACACACTTCCACCATCTAGGGA GGAAATGACAAAGAACCAGGTGA GTTTGACCTGTCTCGTGAAAGGCT TTTATCCCAGTGATATAGCCGTGG AATGGGAAAGTAACGGGCAGCCC GAGAACAACTATAAGACCACACCA CCCATGCTGGACTCCGACGGTTCT TTCTTCCTTTATAGCAAGCTGACA GTGGATAAATCCAGGTGGCAGCA GGGTAACGTATTCAGTTGCAGTGT CATGCACGAGGCACTCCACAACCA

			CTATACTCAGAAAAGTCTTTCCCT GAGTCCAGGCAAG

SEQ ID 2406	EVQLVQSGGGVVQPGG SLRLSCAASGFTFSSYG MHWVRQAPGKGLEWV AFISYDGSNKYYADSVK GRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCATT GDRFQEFDYWGQGTLV TVSSASTKGPSVFPLAP CSRSTSESTAALGCLVK DYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLY SLSSVVTVPSSNFGTQT YTCNVDHKPSNTKVDKT VERKCCVECPPCPAPP VAGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSH EDPEVQFNWYVDGVEV HNAKTKPREEQFNSTFR VVSVLTVVHQDWLNGK EYKCKVSNKGLPAPIEK TISKTKGQPREPQVYTL PPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNG QPENNYKTTPPMLDSD GSFFLYSKLTVDKSRW QQGNVFSCSVMHEALH NHYTQKSLSLSPGK	SEQ ID 2514	GAGGTGCAGCTGGTGCAGTCTGG GGGAGGCGTGGTCCAGCCTGGGG GGTCCCTGAGACTCTCCTGTGCAG CGTCTGGATTCACCTTCAGTAGCT ATGGCATGCACTGGGTCCGCCAG GCTCCAGGCAAGGGGCTGGAGTG GGTGGCATTTATATCATATGATGG AAGTAATAAATACTACGCAGACTC CGTGAAGGGCCGATTCACCATCTC CAGAGACAATTCCAAGAACACGCT GTATCTGCAAATGAACAGCCTGAG AGCCGAGGACACGGCCGTATATTA CTGTGCGACAACAGGGGACCGCT TCCAAGAGTTTGACTACTGGGGCC AGGGAACCCTGGTCACCGTCTCCT CAGCAAGCACAAAAGGTCCTTCAG TGTTCCCTCTGGCACCTTGCTCAC GCAGCACCTCTGAGAGTACAGCC GCCCTGGGCTGCCTGGTAAAGGA CTACTTTCCCGAACCAGTCACTGT GTCCTGGAATAGCGGGGCCTTGA CCTCTGGAGTGCACACATTTCCAG CTGTACTGCAGTCATCTGGACTCT ACAGCCTGTCCAGTGTGGTCACC GTACCTTCCTCCAACTTTGGCACT CAAACATATACATGTAACGTGGAT CATAAGCCCTCTAACACCAAAGTG GATAAAACTGTGGAGCGTAAGTGT TGTGTCGAGTGTCCTCCTTGTCCT GCTCCTCCTGTGGCAGGCCCATCT GTGTTTCTCTTTCCCCCAAAGCCA AAGGACACTTTGATGATATCCCGG ACCCCTGAGGTGACTTGCGTCGTC GTAGATGTTTCACACGAAGATCCA GAGGTGCAGTTCAACTGGTACGTG GATGGCGTGGAAGTGCATAATGC CAAGACAAAGCCCCGCGAAGAGC AGTTTAATTCCACCTTCCGCGTGG TGTCTGTGCTGACCGTGGTACATC AGGATTGGCTTAACGGTAAGGAGT ACAAGTGCAAGGTGAGTAACAAGG GGCTGCCCGCCCCTATCGAGAAG ACTATCAGTAAAACCAAGGGCCAG CCAAGGGAGCCACAGGTGTACAC ACTTCCACCATCTAGGGAGGAAAT GACAAAGAACCAGGTGAGTTTGAC CTGTCTCGTGAAAGGCTTTTATCC CAGTGATATAGCCGTGGAATGGGA AAGTAACGGGCAGCCCGAGAACA ACTATAAGACCACACCACCCATGC TGGACTCCGACGGTTCTTTCTTCC TTTATAGCAAGCTGACAGTGGATA AATCCAGGTGGCAGCAGGGTAAC GTATTCAGTTGCAGTGTCATGCAC GAGGCACTCCACAACCACTATACT

			CAGAAAAGTCTTTCCCTGAGTCCA GGCAAG

SEQ ID 2407	QMQLVQSGGVLLQPGR SLRLSCTASGFTFAAYNI NWFRQGPGGGLEWVG FIRANADSGTTEYAASV KGRFFISRDDSRSTAYL QMTSLKTEDTAVYYCAR DDRGRGDDFDYWGQG TLVTVSSASTKGPSVFP LAPCSRSTSESTAALGC LVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSS GLYSLSSVVTVPSSNFG TQTYTCNVDHKPSNTKV DKTVERKCCVECPPCP APPVAGPSVFLFPPKPK DTLMISRTPEVTCVVVD VSHEDPEVQFNWYVDG VEVHNAKTKPREEQFN STFRVVSVLTVVHQDWL NGKEYKCKVSNKGLPA PIEKTISKTKGQPREPQV YTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWE SNGQPENNYKTTPPML DSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK	SEQ ID 2515	CAGATGCAGCTGGTGCAGTCTGG GGGAGTCTTGCTTCAGCCAGGGC GGTCCCTGAGACTCTCCTGTACAG CTTCTGGATTCACCTTTGCTGCTTA TAATATCAACTGGTTCCGCCAGGG TCCTGGGGGGGGGCTGGAGTGG GTAGGTTTCATTAGAGCCAACGCT GATAGTGGGACAACAGAGTACGC CGCGTCTGTGAAAGGCAGATTCTT CATCTCAAGAGATGATTCCAGAAG CACCGCCTACCTGCAAATGACTAG CCTTAAAACCGAGGACACAGCCGT TTATTACTGTGCCAGAGATGATCG GGGTCGGGGAGATGACTTTGACT ACTGGGGCCAGGGCACCCTGGTC ACCGTCTCCTCAGCAAGCACAAAA GGTCCTTCAGTGTTCCCTCTGGCA CCTTGCTCACGCAGCACCTCTGAG AGTACAGCCGCCCTGGGCTGCCT GGTAAAGGACTACTTTCCCGAACC AGTCACTGTGTCCTGGAATAGCGG GGCCTTGACCTCTGGAGTGCACA CATTTCCAGCTGTACTGCAGTCAT CTGGACTCTACAGCCTGTCCAGTG TGGTCACCGTACCTTCCTCCAACT TTGGCACTCAAACATATACATGTAA CGTGGATCATAAGCCCTCTAACAC CAAAGTGGATAAAACTGTGGAGCG TAAGTGTTGTGTCGAGTGTCCTCC TTGTCCTGCTCCTCCTGTGGCAGG CCCATCTGTGTTTCTCTTTCCCCC AAAGCCAAAGGACACTTTGATGAT ATCCCGGACCCCTGAGGTGACTT GCGTCGTCGTAGATGTTTCACACG AAGATCCAGAGGTGCAGTTCAACT GGTACGTGGATGGCGTGGAAGTG CATAATGCCAAGACAAAGCCCCGC GAAGAGCAGTTTAATTCCACCTTC CGCGTGGTGTCTGTGCTGACCGT GGTACATCAGGATTGGCTTAACGG TAAGGAGTACAAGTGCAAGGTGAG TAACAAGGGGCTGCCCGCCCCTA TCGAGAAGACTATCAGTAAAACCA AGGGCCAGCCAAGGGAGCCACAG GTGTACACACTTCCACCATCTAGG GAGGAAATGACAAAGAACCAGGT GAGTTTGACCTGTCTCGTGAAAGG CTTTTATCCCAGTGATATAGCCGT GGAATGGGAAAGTAACGGGCAGC CCGAGAACAACTATAAGACCACAC CACCCATGCTGGACTCCGACGGTT CTTTCTTCCTTTATAGCAAGCTGAC AGTGGATAAATCCAGGTGGCAGCA GGGTAACGTATTCAGTTGCAGTGT CATGCACGAGGCACTCCACAACCA

			CTATACTCAGAAAAGTCTTTCCCT GAGTCCAGGCAAG

SEQ ID 2408	QVQLVQSGGGLVQPGG SLRLSCAASGFTFSSYG MTWVRQAPGKGLEWV STISGNGVGTYYPDSVK DRFTISRDSSKNTVYLQ MNSLRAEDTAVYYCVK HGRAGINWYFDLWGRG TLVTVSSASTKGPSVFP LAPCSRSTSESTAALGC LVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSS GLYSLSSVVTVPSSNFG TQTYTCNVDHKPSNTKV DKTVERKCCVECPPCP APPVAGPSVFLFPPKPK DTLMISRTPEVTCVVVD VSHEDPEVQFNWYVDG VEVHNAKTKPREEQFN STFRVVSVLTVVHQDWL NGKEYKCKVSNKGLPA PIEKTISKTKGQPREPQV YTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWE SNGQPENNYKTTPPML DSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK	SEQ ID 2516	CAGGTGCAGCTGGTGCAATCTGG GGGAGGCTTGGTACAGCCTGGGG GGTCCCTGAGACTCTCCTGTGCAG CCTCTGGATTCACCTTTAGCAGCT ATGGCATGACGTGGGTCCGCCAG GCTCCAGGGAAGGGGCTGGAGTG GGTCTCAACTATTAGTGGTAATGG TGTTGGCACATACTACCCAGACTC CGTGAAGGACCGGTTCACCATCTC CAGAGACAGTTCCAAGAACACGGT GTATCTGCAAATGAACAGCCTGAG AGCCGAGGACACGGCCGTATATTA CTGTGTGAAACATGGTAGGGCCG GAATAAACTGGTACTTCGATCTCT GGGGCCGTGGCACCCTGGTGACC GTCTCCTCAGCAAGCACAAAAGGT CCTTCAGTGTTCCCTCTGGCACCT TGCTCACGCAGCACCTCTGAGAGT ACAGCCGCCCTGGGCTGCCTGGT AAAGGACTACTTTCCCGAACCAGT CACTGTGTCCTGGAATAGCGGGG CCTTGACCTCTGGAGTGCACACAT TTCCAGCTGTACTGCAGTCATCTG GACTCTACAGCCTGTCCAGTGTGG TCACCGTACCTTCCTCCAACTTTG GCACTCAAACATATACATGTAACG TGGATCATAAGCCCTCTAACACCA AAGTGGATAAAACTGTGGAGCGTA AGTGTTGTGTCGAGTGTCCTCCTT GTCCTGCTCCTCCTGTGGCAGGC CCATCTGTGTTTCTCTTTCCCCCAA AGCCAAAGGACACTTTGATGATAT CCCGGACCCCTGAGGTGACTTGC GTCGTCGTAGATGTTTCACACGAA GATCCAGAGGTGCAGTTCAACTGG TACGTGGATGGCGTGGAAGTGCA TAATGCCAAGACAAAGCCCCGCGA AGAGCAGTTTAATTCCACCTTCCG CGTGGTGTCTGTGCTGACCGTGG TACATCAGGATTGGCTTAACGGTA AGGAGTACAAGTGCAAGGTGAGTA ACAAGGGGCTGCCCGCCCCTATC GAGAAGACTATCAGTAAAACCAAG GGCCAGCCAAGGGAGCCACAGGT GTACACACTTCCACCATCTAGGGA GGAAATGACAAAGAACCAGGTGA GTTTGACCTGTCTCGTGAAAGGCT TTTATCCCAGTGATATAGCCGTGG AATGGGAAAGTAACGGGCAGCCC GAGAACAACTATAAGACCACACCA CCCATGCTGGACTCCGACGGTTCT TTCTTCCTTTATAGCAAGCTGACA GTGGATAAATCCAGGTGGCAGCA GGGTAACGTATTCAGTTGCAGTGT CATGCACGAGGCACTCCACAACCA

			CTATACTCAGAAAAGTCTTTCCCT GAGTCCAGGCAAG

SEQ ID 2409	QVQLQQSGPGLVKPSQ TLSLTCAISGDSVSSNS AAWNWIRQSPSRGLEW LGRTYYRSKWYNDYAV SVKSRITINPDTSKNQFS LQLNSVTPEDTAVYYCA RGGGLWAFDIWGQGTT VTVSSASTKGPSVFPLA PCSRSTSESTAALGCLV KDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGL YSLSSVVTVPSSNFGTQ TYTCNVDHKPSNTKVDK TVERKCCVECPPCPAP PVAGPSVFLFPPKPKDT LMISRTPEVTCVVVDVS HEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTF RVVSVLTVVHQDWLNG KEYKCKVSNKGLPAPIE KTISKTKGQPREPQVYT LPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESN GQPENNYKTTPPMLDS DGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALH NHYTQKSLSLSPGK	SEQ ID 2517	CAGGTACAGCTGCAGCAGTCAGG TCCAGGACTGGTGAAGCCCTCGC AGACCCTCTCACTCACCTGTGCCA TCTCCGGGGACAGTGTCTCTAGCA ACAGTGCTGCTTGGAACTGGATCA GGCAGTCCCCATCGAGAGGCCTT GAGTGGCTGGGAAGGACATACTA CAGGTCCAAGTGGTATAATGATTA TGCAGTATCTGTGAAAAGTCGAAT AACCATCAACCCAGACACATCCAA GAACCAGTTCTCCCTGCAGCTGAA CTCTGTGACTCCCGAGGACACGG CTGTGTATTACTGTGCAAGAGGGG GAGGGCTTTGGGCTTTTGATATCT GGGGCCAAGGGACCACGGTCACC GTCTCCTCAGCAAGCACAAAAGGT CCTTCAGTGTTCCCTCTGGCACCT TGCTCACGCAGCACCTCTGAGAGT ACAGCCGCCCTGGGCTGCCTGGT AAAGGACTACTTTCCCGAACCAGT CACTGTGTCCTGGAATAGCGGGG CCTTGACCTCTGGAGTGCACACAT TTCCAGCTGTACTGCAGTCATCTG GACTCTACAGCCTGTCCAGTGTGG TCACCGTACCTTCCTCCAACTTTG GCACTCAAACATATACATGTAACG TGGATCATAAGCCCTCTAACACCA AAGTGGATAAAACTGTGGAGCGTA AGTGTTGTGTCGAGTGTCCTCCTT GTCCTGCTCCTCCTGTGGCAGGC CCATCTGTGTTTCTCTTTCCCCCAA AGCCAAAGGACACTTTGATGATAT CCCGGACCCCTGAGGTGACTTGC GTCGTCGTAGATGTTTCACACGAA GATCCAGAGGTGCAGTTCAACTGG TACGTGGATGGCGTGGAAGTGCA TAATGCCAAGACAAAGCCCCGCGA AGAGCAGTTTAATTCCACCTTCCG CGTGGTGTCTGTGCTGACCGTGG TACATCAGGATTGGCTTAACGGTA AGGAGTACAAGTGCAAGGTGAGTA ACAAGGGGCTGCCCGCCCCTATC GAGAAGACTATCAGTAAAACCAAG GGCCAGCCAAGGGAGCCACAGGT GTACACACTTCCACCATCTAGGGA GGAAATGACAAAGAACCAGGTGA GTTTGACCTGTCTCGTGAAAGGCT TTTATCCCAGTGATATAGCCGTGG AATGGGAAAGTAACGGGCAGCCC GAGAACAACTATAAGACCACACCA CCCATGCTGGACTCCGACGGTTCT TTCTTCCTTTATAGCAAGCTGACA GTGGATAAATCCAGGTGGCAGCA GGGTAACGTATTCAGTTGCAGTGT CATGCACGAGGCACTCCACAACCA

			CTATACTCAGAAAAGTCTTTCCCT GAGTCCAGGCAAG

SEQ ID 2410	EVQLVQSGAEVKKPGA SVKVSCKASGYTFTGYY MHWVRQAPGQGLEWM GWINPNSGGTNYAQKF QGRVTMTRDTSISTAYM ELSRLRSDDTAVYYCAR DKIGSCPYWGQGTLVT VSSASTKGPSVFPLAPC SRSTSESTAALGCLVKD YFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSL SSVVTVPSSNFGTQTYT CNVDHKPSNTKVDKTV ERKCCVECPPCPAPPV AGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHE DPEVQFNWYVDGVEVH NAKTKPREEQFNSTFRV VSVLTVVHQDWLNGKE YKCKVSNKGLPAPIEKTI SKTKGQPREPQVYTLPP SREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQ PENNYKTTPPMLDSDG SFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHN HYTQKSLSLSPGK	SEQ ID 2518	GAGGTCCAGCTGGTGCAGTCTGG GGCTGAGGTGAAGAAGCCTGGGG CCTCAGTGAAGGTCTCCTGCAAGG CTTCTGGATACACCTTCACCGGCT ACTATATGCACTGGGTGCGACAGG CCCCTGGACAAGGGCTTGAGTGG ATGGGATGGATCAACCCTAACAGT GGTGGCACAAACTATGCACAGAAG TTTCAGGGCAGGGTCACCATGACC AGGGACACGTCCATCAGCACAGC CTACATGGAGCTGAGCAGGCTGA GATCTGACGACACGGCCGTGTATT ACTGTGCGAGAGACAAGATCGGC AGCTGTCCTTACTGGGGCCAGGG AACCCTGGTCACCGTCTCCTCAGC AAGCACAAAAGGTCCTTCAGTGTT CCCTCTGGCACCTTGCTCACGCAG CACCTCTGAGAGTACAGCCGCCCT GGGCTGCCTGGTAAAGGACTACTT TCCCGAACCAGTCACTGTGTCCTG GAATAGCGGGGCCTTGACCTCTG GAGTGCACACATTTCCAGCTGTAC TGCAGTCATCTGGACTCTACAGCC TGTCCAGTGTGGTCACCGTACCTT CCTCCAACTTTGGCACTCAAACAT ATACATGTAACGTGGATCATAAGC CCTCTAACACCAAAGTGGATAAAA CTGTGGAGCGTAAGTGTTGTGTCG AGTGTCCTCCTTGTCCTGCTCCTC CTGTGGCAGGCCCATCTGTGTTTC TCTTTCCCCCAAAGCCAAAGGACA CTTTGATGATATCCCGGACCCCTG AGGTGACTTGCGTCGTCGTAGATG TTTCACACGAAGATCCAGAGGTGC AGTTCAACTGGTACGTGGATGGCG TGGAAGTGCATAATGCCAAGACAA AGCCCCGCGAAGAGCAGTTTAATT CCACCTTCCGCGTGGTGTCTGTGC TGACCGTGGTACATCAGGATTGGC TTAACGGTAAGGAGTACAAGTGCA AGGTGAGTAACAAGGGGCTGCCC GCCCCTATCGAGAAGACTATCAGT AAAACCAAGGGCCAGCCAAGGGA GCCACAGGTGTACACACTTCCACC ATCTAGGGAGGAAATGACAAAGAA CCAGGTGAGTTTGACCTGTCTCGT GAAAGGCTTTTATCCCAGTGATAT AGCCGTGGAATGGGAAAGTAACG GGCAGCCCGAGAACAACTATAAGA CCACACCACCCATGCTGGACTCC GACGGTTCTTTCTTCCTTTATAGCA AGCTGACAGTGGATAAATCCAGGT GGCAGCAGGGTAACGTATTCAGTT GCAGTGTCATGCACGAGGCACTC CACAACCACTATACTCAGAAAAGT CTTTCCCTGAGTCCAGGCAAG

SEQ ID 2411	QVTLKESGPTLVKPTQT LTLTCTFSGFSLSTSGV GVGWIRQPPGKALEWL ALIYWDDDKRYSPSLKS RLTITKDTSKNQVVLTM TNMDPVDTATYYCAHR PDSSSQCFDYWGQGTL VTVSSASTKGPSVFPLA PCSRSTSESTAALGCLV KDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGL YSLSSVVTVPSSNFGTQ TYTCNVDHKPSNTKVDK TVERKCCVECPPCPAP PVAGPSVFLFPPKPKDT LMISRTPEVTCVVVDVS HEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTF RVVSVLTVVHQDWLNG KEYKCKVSNKGLPAPIE KTISKTKGQPREPQVYT LPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESN GQPENNYKTTPPMLDS DGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALH NHYTQKSLSLSPGK	SEQ ID 2519	CAGGTCACCTTGAAGGAGTCTGGT CCTACGCTGGTGAAACCCACACAG ACCCTCACGCTGACCTGCACCTTC TCTGGGTTCTCACTCAGCACTAGT GGAGTGGGTGTGGGCTGGATCCG TCAGCCCCCAGGAAAGGCCCTGG AGTGGCTTGCACTCATTTATTGGG ATGATGATAAGCGCTACAGCCCAT CTCTGAAGAGCAGGCTCACCATCA CCAAGGACACCTCCAAAAACCAGG TGGTCCTTACAATGACCAACATGG ACCCTGTGGACACAGCCACATATT ACTGTGCACACAGACCGGATAGCA GCAGTCAATGTTTTGACTACTGGG GCCAGGGAACCCTGGTCACCGTC TCCTCAGCAAGCACAAAAGGTCCT TCAGTGTTCCCTCTGGCACCTTGC TCACGCAGCACCTCTGAGAGTACA GCCGCCCTGGGCTGCCTGGTAAA GGACTACTTTCCCGAACCAGTCAC TGTGTCCTGGAATAGCGGGGCCTT GACCTCTGGAGTGCACACATTTCC AGCTGTACTGCAGTCATCTGGACT CTACAGCCTGTCCAGTGTGGTCAC CGTACCTTCCTCCAACTTTGGCAC TCAAACATATACATGTAACGTGGA TCATAAGCCCTCTAACACCAAAGT GGATAAAACTGTGGAGCGTAAGTG TTGTGTCGAGTGTCCTCCTTGTCC TGCTCCTCCTGTGGCAGGCCCATC TGTGTTTCTCTTTCCCCCAAAGCC AAAGGACACTTTGATGATATCCCG GACCCCTGAGGTGACTTGCGTCG TCGTAGATGTTTCACACGAAGATC CAGAGGTGCAGTTCAACTGGTACG TGGATGGCGTGGAAGTGCATAATG CCAAGACAAAGCCCCGCGAAGAG CAGTTTAATTCCACCTTCCGCGTG GTGTCTGTGCTGACCGTGGTACAT CAGGATTGGCTTAACGGTAAGGAG TACAAGTGCAAGGTGAGTAACAAG GGGCTGCCCGCCCCTATCGAGAA GACTATCAGTAAAACCAAGGGCCA GCCAAGGGAGCCACAGGTGTACA CACTTCCACCATCTAGGGAGGAAA TGACAAAGAACCAGGTGAGTTTGA CCTGTCTCGTGAAAGGCTTTTATC CCAGTGATATAGCCGTGGAATGG GAAAGTAACGGGCAGCCCGAGAA CAACTATAAGACCACACCACCCAT GCTGGACTCCGACGGTTCTTTCTT CCTTTATAGCAAGCTGACAGTGGA TAAATCCAGGTGGCAGCAGGGTAA CGTATTCAGTTGCAGTGTCATGCA CGAGGCACTCCACAACCACTATAC

			TCAGAAAAGTCTTTCCCTGAGTCC AGGCAAG

SEQ ID 2412	QVTLKESGGGVVQPGR SLRLSCAASGFTFSSYA MHWVRQAPGKGLEWV AVISYDGSNKYYADSVK GRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCAR SSGWSLPEDYWGQGTL VTVSSASTKGPSVFPLA PCSRSTSESTAALGCLV KDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGL YSLSSVVTVPSSNFGTQ TYTCNVDHKPSNTKVDK TVERKCCVECPPCPAP PVAGPSVFLFPPKPKDT LMISRTPEVTCVVVDVS HEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTF RVVSVLTVVHQDWLNG KEYKCKVSNKGLPAPIE KTISKTKGQPREPQVYT LPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESN GQPENNYKTTPPMLDS DGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALH NHYTQKSLSLSPGK	SEQ ID 2520	CAGGTCACCTTGAAGGAGTCTGG GGGAGGCGTGGTCCAGCCTGGGA GGTCCCTGAGACTCTCCTGTGCAG CCTCTGGATTCACCTTCAGTAGCT ATGCTATGCACTGGGTCCGCCAG GCTCCAGGCAAGGGGCTGGAGTG GGTGGCAGTTATATCATATGATGG AAGTAATAAATACTACGCAGACTC CGTGAAGGGCCGATTCACCATCTC CAGAGACAATTCCAAGAACACGCT GTATCTGCAAATGAACAGCCTGAG AGCTGAGGACACGGCTGTGTATTA CTGTGCGAGAAGCAGTGGCTGGT CACTGCCTGAAGACTACTGGGGC CAGGGAACCCTGGTCACCGTCTC CTCAGCAAGCACAAAAGGTCCTTC AGTGTTCCCTCTGGCACCTTGCTC ACGCAGCACCTCTGAGAGTACAG CCGCCCTGGGCTGCCTGGTAAAG GACTACTTTCCCGAACCAGTCACT GTGTCCTGGAATAGCGGGGCCTT GACCTCTGGAGTGCACACATTTCC AGCTGTACTGCAGTCATCTGGACT CTACAGCCTGTCCAGTGTGGTCAC CGTACCTTCCTCCAACTTTGGCAC TCAAACATATACATGTAACGTGGA TCATAAGCCCTCTAACACCAAAGT GGATAAAACTGTGGAGCGTAAGTG TTGTGTCGAGTGTCCTCCTTGTCC TGCTCCTCCTGTGGCAGGCCCATC TGTGTTTCTCTTTCCCCCAAAGCC AAAGGACACTTTGATGATATCCCG GACCCCTGAGGTGACTTGCGTCG TCGTAGATGTTTCACACGAAGATC CAGAGGTGCAGTTCAACTGGTACG TGGATGGCGTGGAAGTGCATAATG CCAAGACAAAGCCCCGCGAAGAG CAGTTTAATTCCACCTTCCGCGTG GTGTCTGTGCTGACCGTGGTACAT CAGGATTGGCTTAACGGTAAGGAG TACAAGTGCAAGGTGAGTAACAAG GGGCTGCCCGCCCCTATCGAGAA GACTATCAGTAAAACCAAGGGCCA GCCAAGGGAGCCACAGGTGTACA CACTTCCACCATCTAGGGAGGAAA TGACAAAGAACCAGGTGAGTTTGA CCTGTCTCGTGAAAGGCTTTTATC CCAGTGATATAGCCGTGGAATGG GAAAGTAACGGGCAGCCCGAGAA CAACTATAAGACCACACCACCCAT GCTGGACTCCGACGGTTCTTTCTT CCTTTATAGCAAGCTGACAGTGGA TAAATCCAGGTGGCAGCAGGGTAA CGTATTCAGTTGCAGTGTCATGCA CGAGGCACTCCACAACCACTATAC

			TCAGAAAAGTCTTTCCCTGAGTCC AGGCAAG

SEQ ID 2413	QVQLVQSGAEVKKPGA SVKVSCKVSGYTLTELS MHWVRQAPGKGLEWM GGFDPEDGETIYAQKFQ GRVTMTEDTSTDTAYM ELSSLRSEDTAVYYCAT DVNPELLGAGFDYWGQ GTLVTVSSASTKGPSVF PLAPCSRSTSESTAALG CLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSNF GTQTYTCNVDHKPSNT KVDKTVERKCCVECPP CPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVV VDVSHEDPEVQFNWYV DGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQD WLNGKEYKCKVSNKGL PAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPP MLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVM HEALHNHYTQKSLSLSP GK	SEQ ID 2521	CAGGTCCAGCTGGTACAGTCTGG GGCTGAGGTGAAGAAGCCTGGGG CCTCAGTGAAGGTCTCCTGCAAGG TTTCCGGATACACCCTCACTGAAT TATCCATGCACTGGGTGCGACAG GCTCCTGGAAAAGGGCTTGAGTG GATGGGAGGTTTTGATCCTGAAGA TGGTGAAACAATCTACGCACAGAA GTTCCAGGGCAGAGTCACCATGA CCGAGGACACATCTACAGACACAG CCTACATGGAGCTGAGCAGCCTG AGATCTGAGGACACGGCCGTGTAT TACTGTGCAACGGATGTGAACCCG GAGCTACTGGGGGCGGGATTTGA CTACTGGGGCCAGGGCACCCTGG TCACCGTCTCCTCAGCAAGCACAA AAGGTCCTTCAGTGTTCCCTCTGG CACCTTGCTCACGCAGCACCTCTG AGAGTACAGCCGCCCTGGGCTGC CTGGTAAAGGACTACTTTCCCGAA CCAGTCACTGTGTCCTGGAATAGC GGGGCCTTGACCTCTGGAGTGCA CACATTTCCAGCTGTACTGCAGTC ATCTGGACTCTACAGCCTGTCCAG TGTGGTCACCGTACCTTCCTCCAA CTTTGGCACTCAAACATATACATGT AACGTGGATCATAAGCCCTCTAAC ACCAAAGTGGATAAAACTGTGGAG CGTAAGTGTTGTGTCGAGTGTCCT CCTTGTCCTGCTCCTCCTGTGGCA GGCCCATCTGTGTTTCTCTTTCCC CCAAAGCCAAAGGACACTTTGATG ATATCCCGGACCCCTGAGGTGACT TGCGTCGTCGTAGATGTTTCACAC GAAGATCCAGAGGTGCAGTTCAAC TGGTACGTGGATGGCGTGGAAGT GCATAATGCCAAGACAAAGCCCCG CGAAGAGCAGTTTAATTCCACCTT CCGCGTGGTGTCTGTGCTGACCG TGGTACATCAGGATTGGCTTAACG GTAAGGAGTACAAGTGCAAGGTGA GTAACAAGGGGCTGCCCGCCCCT ATCGAGAAGACTATCAGTAAAACC AAGGGCCAGCCAAGGGAGCCACA GGTGTACACACTTCCACCATCTAG GGAGGAAATGACAAAGAACCAGG TGAGTTTGACCTGTCTCGTGAAAG GCTTTTATCCCAGTGATATAGCCG TGGAATGGGAAAGTAACGGGCAG CCCGAGAACAACTATAAGACCACA CCACCCATGCTGGACTCCGACGG TTCTTTCTTCCTTTATAGCAAGCTG ACAGTGGATAAATCCAGGTGGCAG CAGGGTAACGTATTCAGTTGCAGT GTCATGCACGAGGCACTCCACAAC

			CACTATACTCAGAAAAGTCTTTCC CTGAGTCCAGGCAAG

SEQ ID 2414	QVTLKESGGGLVQPGG SLRLSCAASGFTFSDQY MDWVRQAPGKGLEWV GRVRNKANSYTTEYAA SVKGRFTISRDDSKNSL YLQMNSLNTEDTAMYF CASSLNSGGYRCFHHW GQGTLVTVSSASTKGPS VFPLAPCSRSTSESTAA LGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSN FGTQTYTCNVDHKPSN TKVDKTVERKCCVECPP CPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVV VDVSHEDPEVQFNWYV DGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQD WLNGKEYKCKVSNKGL PAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPP MLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVM HEALHNHYTQKSLSLSP GK	SEQ ID 2522	CAGGTCACCTTGAAGGAGTCTGG GGGAGGCTTGGTCCAGCCTGGAG GGTCCCTGAGACTCTCCTGTGCAG CCTCTGGATTCACCTTCAGTGACC AGTACATGGACTGGGTCCGCCAG GCTCCAGGGAAGGGGCTGGAGTG GGTTGGCCGTGTTAGAAACAAAGC TAACAGTTACACCACAGAATACGC CGCGTCTGTGAAAGGCAGATTCAC CATCTCAAGAGATGATTCAAAGAA CTCACTGTATCTGCAAATGAATAG TCTGAACACCGAGGACACGGCCA TGTATTTCTGTGCTAGTAGTCTCAA TAGTGGGGGCTACCGATGCTTCCA TCACTGGGGCCAGGGCACCCTGG TGACCGTCTCCTCAGCAAGCACAA AAGGTCCTTCAGTGTTCCCTCTGG CACCTTGCTCACGCAGCACCTCTG AGAGTACAGCCGCCCTGGGCTGC CTGGTAAAGGACTACTTTCCCGAA CCAGTCACTGTGTCCTGGAATAGC GGGGCCTTGACCTCTGGAGTGCA CACATTTCCAGCTGTACTGCAGTC ATCTGGACTCTACAGCCTGTCCAG TGTGGTCACCGTACCTTCCTCCAA CTTTGGCACTCAAACATATACATGT AACGTGGATCATAAGCCCTCTAAC ACCAAAGTGGATAAAACTGTGGAG CGTAAGTGTTGTGTCGAGTGTCCT CCTTGTCCTGCTCCTCCTGTGGCA GGCCCATCTGTGTTTCTCTTTCCC CCAAAGCCAAAGGACACTTTGATG ATATCCCGGACCCCTGAGGTGACT TGCGTCGTCGTAGATGTTTCACAC GAAGATCCAGAGGTGCAGTTCAAC TGGTACGTGGATGGCGTGGAAGT GCATAATGCCAAGACAAAGCCCCG CGAAGAGCAGTTTAATTCCACCTT CCGCGTGGTGTCTGTGCTGACCG TGGTACATCAGGATTGGCTTAACG GTAAGGAGTACAAGTGCAAGGTGA GTAACAAGGGGCTGCCCGCCCCT ATCGAGAAGACTATCAGTAAAACC AAGGGCCAGCCAAGGGAGCCACA GGTGTACACACTTCCACCATCTAG GGAGGAAATGACAAAGAACCAGG TGAGTTTGACCTGTCTCGTGAAAG GCTTTTATCCCAGTGATATAGCCG TGGAATGGGAAAGTAACGGGCAG CCCGAGAACAACTATAAGACCACA CCACCCATGCTGGACTCCGACGG TTCTTTCTTCCTTTATAGCAAGCTG ACAGTGGATAAATCCAGGTGGCAG CAGGGTAACGTATTCAGTTGCAGT GTCATGCACGAGGCACTCCACAAC

			CACTATACTCAGAAAAGTCTTTCC CTGAGTCCAGGCAAG

SEQ ID 2415	QVQLVQSGGGLVQPGG SLRLSCSASGFTFSSYA MHWVRQAPGKGLEYVS AISSNGGSTYYADSVKG RFTISRDNSKNTLYLQM SSLRAEDTAVYYCVKAP RGVVPAAMRGGYWGQ GTLVTVSSASTKGPSVF PLAPCSRSTSESTAALG CLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSNF GTQTYTCNVDHKPSNT KVDKTVERKCCVECPP CPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVV VDVSHEDPEVQFNWYV DGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQD WLNGKEYKCKVSNKGL PAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPP MLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVM HEALHNHYTQKSLSLSP GK	SEQ ID 2523	CAGGTCCAGCTGGTGCAGTCTGG GGGAGGCTTGGTCCAGCCTGGGG GGTCCCTGAGACTCTCCTGTTCAG CCTCTGGATTCACCTTCAGTAGCT ATGCTATGCACTGGGTCCGCCAG GCTCCAGGGAAGGGACTGGAATA TGTTTCAGCTATTAGTAGTAATGG GGGTAGCACATACTACGCAGACTC AGTGAAGGGCAGATTCACCATCTC CAGAGACAATTCCAAGAACACGCT GTATCTTCAAATGAGCAGTCTGAG AGCTGAGGACACGGCTGTGTATTA CTGTGTGAAAGCGCCGAGGGGTG TAGTACCAGCTGCTATGCGGGGG GGCTACTGGGGCCAGGGAACCCT GGTCACCGTCTCCTCAGCAAGCAC AAAAGGTCCTTCAGTGTTCCCTCT GGCACCTTGCTCACGCAGCACCT CTGAGAGTACAGCCGCCCTGGGC TGCCTGGTAAAGGACTACTTTCCC GAACCAGTCACTGTGTCCTGGAAT AGCGGGGCCTTGACCTCTGGAGT GCACACATTTCCAGCTGTACTGCA GTCATCTGGACTCTACAGCCTGTC CAGTGTGGTCACCGTACCTTCCTC CAACTTTGGCACTCAAACATATAC ATGTAACGTGGATCATAAGCCCTC TAACACCAAAGTGGATAAAACTGT GGAGCGTAAGTGTTGTGTCGAGT GTCCTCCTTGTCCTGCTCCTCCTG TGGCAGGCCCATCTGTGTTTCTCT TTCCCCCAAAGCCAAAGGACACTT TGATGATATCCCGGACCCCTGAGG TGACTTGCGTCGTCGTAGATGTTT CACACGAAGATCCAGAGGTGCAG TTCAACTGGTACGTGGATGGCGTG GAAGTGCATAATGCCAAGACAAAG CCCCGCGAAGAGCAGTTTAATTCC ACCTTCCGCGTGGTGTCTGTGCTG ACCGTGGTACATCAGGATTGGCTT AACGGTAAGGAGTACAAGTGCAAG GTGAGTAACAAGGGGCTGCCCGC CCCTATCGAGAAGACTATCAGTAA AACCAAGGGCCAGCCAAGGGAGC CACAGGTGTACACACTTCCACCAT CTAGGGAGGAAATGACAAAGAACC AGGTGAGTTTGACCTGTCTCGTGA AAGGCTTTTATCCCAGTGATATAG CCGTGGAATGGGAAAGTAACGGG CAGCCCGAGAACAACTATAAGACC ACACCACCCATGCTGGACTCCGAC GGTTCTTTCTTCCTTTATAGCAAGC TGACAGTGGATAAATCCAGGTGGC AGCAGGGTAACGTATTCAGTTGCA GTGTCATGCACGAGGCACTCCACA

			ACCACTATACTCAGAAAAGTCTTTC CCTGAGTCCAGGCAAG

SEQ ID 2416	QVQLQESGGGLVQPGR SLRLSCTASGFTFGDYA MSWFRQAPGKGLEWV GFIRSKAYGGTTEYAAS VKGRFTISRDDSKSIAYL QMNSLKTEDTAVYYCT RLVGNSGSYYPFGYWG QGTLVTVSSASTKGPSV FPLAPCSRSTSESTAAL GCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSN FGTQTYTCNVDHKPSN TKVDKTVERKCCVECPP CPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVV VDVSHEDPEVQFNWYV DGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQD WLNGKEYKCKVSNKGL PAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPP MLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVM HEALHNHYTQKSLSLSP GK	SEQ ID 2524	CAGGTGCAGCTGCAGGAGTCGGG GGGAGGCTTGGTACAGCCAGGGC GGTCCCTGAGACTCTCCTGTACAG CTTCTGGATTCACCTTTGGTGATTA TGCTATGAGCTGGTTCCGCCAGG CTCCAGGGAAGGGGCTGGAGTGG GTAGGTTTCATTAGAAGCAAAGCT TATGGTGGGACAACAGAATACGCC GCGTCTGTGAAAGGCAGATTCACC ATCTCAAGAGATGATTCCAAAAGC ATCGCCTATCTGCAAATGAACAGC CTGAAAACCGAGGACACAGCCGT GTATTACTGTACTAGATTGGTGGG CAATAGTGGGAGCTACTATCCGTT TGGGTACTGGGGCCAGGGAACCC TGGTGACCGTCTCCTCAGCAAGCA CAAAAGGTCCTTCAGTGTTCCCTC TGGCACCTTGCTCACGCAGCACCT CTGAGAGTACAGCCGCCCTGGGC TGCCTGGTAAAGGACTACTTTCCC GAACCAGTCACTGTGTCCTGGAAT AGCGGGGCCTTGACCTCTGGAGT GCACACATTTCCAGCTGTACTGCA GTCATCTGGACTCTACAGCCTGTC CAGTGTGGTCACCGTACCTTCCTC CAACTTTGGCACTCAAACATATAC ATGTAACGTGGATCATAAGCCCTC TAACACCAAAGTGGATAAAACTGT GGAGCGTAAGTGTTGTGTCGAGT GTCCTCCTTGTCCTGCTCCTCCTG TGGCAGGCCCATCTGTGTTTCTCT TTCCCCCAAAGCCAAAGGACACTT TGATGATATCCCGGACCCCTGAGG TGACTTGCGTCGTCGTAGATGTTT CACACGAAGATCCAGAGGTGCAG TTCAACTGGTACGTGGATGGCGTG GAAGTGCATAATGCCAAGACAAAG CCCCGCGAAGAGCAGTTTAATTCC ACCTTCCGCGTGGTGTCTGTGCTG ACCGTGGTACATCAGGATTGGCTT AACGGTAAGGAGTACAAGTGCAAG GTGAGTAACAAGGGGCTGCCCGC CCCTATCGAGAAGACTATCAGTAA AACCAAGGGCCAGCCAAGGGAGC CACAGGTGTACACACTTCCACCAT CTAGGGAGGAAATGACAAAGAACC AGGTGAGTTTGACCTGTCTCGTGA AAGGCTTTTATCCCAGTGATATAG CCGTGGAATGGGAAAGTAACGGG CAGCCCGAGAACAACTATAAGACC ACACCACCCATGCTGGACTCCGAC GGTTCTTTCTTCCTTTATAGCAAGC TGACAGTGGATAAATCCAGGTGGC AGCAGGGTAACGTATTCAGTTGCA GTGTCATGCACGAGGCACTCCACA

			ACCACTATACTCAGAAAAGTCTTTC CCTGAGTCCAGGCAAG

SEQ ID 2417	QVQLQQWGAGLLKPSE TLSLTCAVYGGSFSGYY WSWIRQPPGKGLEWIG EINHSGSTNYNPSLKSR VTISVDTSKNQFSLKLSS VTAADTAVYYCARGRSL PYRGLAPRSFGGYYFD YWGQGTLVTVSSASTK GPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVT VSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTV PSSNFGTQTYTCNVDH KPSNTKVDKTVERKCCV ECPPCPAPPVAGPSVFL FPPKPKDTLMISRTPEV TCVVVDVSHEDPEVQF NWYVDGVEVHNAKTKP REEQFNSTFRVVSVLTV VHQDWLNGKEYKCKVS NKGLPAPIEKTISKTKGQ PREPQVYTLPPSREEMT KNQVSLTCLVKGFYPSD IAVEWESNGQPENNYK TTPPMLDSDGSFFLYSK LTVDKSRWQQGNVFSC SVMHEALHNHYTQKSL SLSPGK	SEQ ID 2525	CAGGTGCAGCTACAGCAGTGGGG CGCAGGACTGTTGAAGCCTTCGG AGACCCTGTCCCTCACCTGCGCTG TCTATGGTGGGTCCTTCAGTGGTT ACTACTGGAGCTGGATCCGCCAG CCCCCAGGGAAGGGGCTGGAGTG GATTGGGGAAATCAATCATAGTGG AAGCACCAACTACAACCCGTCCCT CAAGAGTCGAGTCACCATATCAGT AGACACGTCCAAGAACCAGTTCTC CCTGAAGCTGAGCTCGGTGACCG CCGCGGACACGGCTGTGTATTACT GTGCGAGAGGCCGGTCCCTTCCC TACCGGGGGTTGGCTCCTAGATCT TTCGGAGGATACTACTTTGACTAC TGGGGCCAGGGAACCCTGGTCAC CGTCTCCTCAGCAAGCACAAAAGG TCCTTCAGTGTTCCCTCTGGCACC TTGCTCACGCAGCACCTCTGAGAG TACAGCCGCCCTGGGCTGCCTGG TAAAGGACTACTTTCCCGAACCAG TCACTGTGTCCTGGAATAGCGGG GCCTTGACCTCTGGAGTGCACACA TTTCCAGCTGTACTGCAGTCATCT GGACTCTACAGCCTGTCCAGTGTG GTCACCGTACCTTCCTCCAACTTT GGCACTCAAACATATACATGTAAC GTGGATCATAAGCCCTCTAACACC AAAGTGGATAAAACTGTGGAGCGT AAGTGTTGTGTCGAGTGTCCTCCT TGTCCTGCTCCTCCTGTGGCAGGC CCATCTGTGTTTCTCTTTCCCCCAA AGCCAAAGGACACTTTGATGATAT CCCGGACCCCTGAGGTGACTTGC GTCGTCGTAGATGTTTCACACGAA GATCCAGAGGTGCAGTTCAACTGG TACGTGGATGGCGTGGAAGTGCA TAATGCCAAGACAAAGCCCCGCGA AGAGCAGTTTAATTCCACCTTCCG CGTGGTGTCTGTGCTGACCGTGG TACATCAGGATTGGCTTAACGGTA AGGAGTACAAGTGCAAGGTGAGTA ACAAGGGGCTGCCCGCCCCTATC GAGAAGACTATCAGTAAAACCAAG GGCCAGCCAAGGGAGCCACAGGT GTACACACTTCCACCATCTAGGGA GGAAATGACAAAGAACCAGGTGA GTTTGACCTGTCTCGTGAAAGGCT TTTATCCCAGTGATATAGCCGTGG AATGGGAAAGTAACGGGCAGCCC GAGAACAACTATAAGACCACACCA CCCATGCTGGACTCCGACGGTTCT TTCTTCCTTTATAGCAAGCTGACA GTGGATAAATCCAGGTGGCAGCA GGGTAACGTATTCAGTTGCAGTGT CATGCACGAGGCACTCCACAACCA

			CTATACTCAGAAAAGTCTTTCCCT GAGTCCAGGCAAG

SEQ ID 2418	QVQLQESGGGLVRPGG SLRLSCGDSGFNFSGY EMNWVRQAPGKGLEW VSYVSTSGSTRYYADSV KGRFTISRDNAKNTLYL QMNSLRVEDTAVYYCA RGRTHWGPQDFDYWG QGTLVTVSSASTKGPSV FPLAPCSRSTSESTAAL GCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSN FGTQTYTCNVDHKPSN TKVDKTVERKCCVECPP CPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVV VDVSHEDPEVQFNWYV DGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQD WLNGKEYKCKVSNKGL PAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPP MLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVM HEALHNHYTQKSLSLSP GK	SEQ ID 2526	CAGGTGCAGCTGCAGGAGTCGGG GGGAGGCTTGGTACGGCCTGGAG GGTCCCTGAGACTCTCCTGTGGA GACTCTGGATTCAACTTCAGTGGA TATGAAATGAACTGGGTCCGCCAG GCTCCAGGGAAGGGGCTGGAGTG GGTTTCATACGTCAGTACTAGTGG TAGTACCAGATACTACGCAGACTC TGTGAAGGGCCGATTTACCATCTC CAGAGACAACGCCAAGAACACCCT GTATTTGCAAATGAACAGTCTGAG AGTCGAGGACACGGCTGTGTATTA CTGTGCAAGAGGACGGACTCACT GGGGCCCCCAGGACTTTGACTAC TGGGGCCAGGGAACCCTGGTCAC CGTCTCCTCAGCAAGCACAAAAGG TCCTTCAGTGTTCCCTCTGGCACC TTGCTCACGCAGCACCTCTGAGAG TACAGCCGCCCTGGGCTGCCTGG TAAAGGACTACTTTCCCGAACCAG TCACTGTGTCCTGGAATAGCGGG GCCTTGACCTCTGGAGTGCACACA TTTCCAGCTGTACTGCAGTCATCT GGACTCTACAGCCTGTCCAGTGTG GTCACCGTACCTTCCTCCAACTTT GGCACTCAAACATATACATGTAAC GTGGATCATAAGCCCTCTAACACC AAAGTGGATAAAACTGTGGAGCGT AAGTGTTGTGTCGAGTGTCCTCCT TGTCCTGCTCCTCCTGTGGCAGGC CCATCTGTGTTTCTCTTTCCCCCAA AGCCAAAGGACACTTTGATGATAT CCCGGACCCCTGAGGTGACTTGC GTCGTCGTAGATGTTTCACACGAA GATCCAGAGGTGCAGTTCAACTGG TACGTGGATGGCGTGGAAGTGCA TAATGCCAAGACAAAGCCCCGCGA AGAGCAGTTTAATTCCACCTTCCG CGTGGTGTCTGTGCTGACCGTGG TACATCAGGATTGGCTTAACGGTA AGGAGTACAAGTGCAAGGTGAGTA ACAAGGGGCTGCCCGCCCCTATC GAGAAGACTATCAGTAAAACCAAG GGCCAGCCAAGGGAGCCACAGGT GTACACACTTCCACCATCTAGGGA GGAAATGACAAAGAACCAGGTGA GTTTGACCTGTCTCGTGAAAGGCT TTTATCCCAGTGATATAGCCGTGG AATGGGAAAGTAACGGGCAGCCC GAGAACAACTATAAGACCACACCA CCCATGCTGGACTCCGACGGTTCT TTCTTCCTTTATAGCAAGCTGACA GTGGATAAATCCAGGTGGCAGCA GGGTAACGTATTCAGTTGCAGTGT CATGCACGAGGCACTCCACAACCA

			CTATACTCAGAAAAGTCTTTCCCT GAGTCCAGGCAAG

SEQ ID 2419	QVQLQESGGGLVQPGG SLRLSCAASGFTFSSYA MSWVRQAPGKGLEWV SAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCAK GGMYYYGSGSSYFDY WGQGTLVTVSSASTKG PSVFPLAPCSRSTSEST AALGCLVKDYFPEPVTV SWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVP SSNFGTQTYTCNVDHK PSNTKVDKTVERKCCVE CPPCPAPPVAGPSVFLF PPKPKDTLMISRTPEVT CVVVDVSHEDPEVQFN WYVDGVEVHNAKTKPR EEQFNSTFRVVSVLTVV HQDWLNGKEYKCKVSN KGLPAPIEKTISKTKGQP REPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDI AVEWESNGQPENNYKT TPPMLDSDGSFFLYSKL TVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSL SPGK	SEQ ID 2527	CAGGTGCAGCTGCAGGAGTCGGG GGGAGGCTTGGTACAGCCTGGGG GGTCCCTGAGACTCTCCTGTGCAG CCTCTGGATTCACCTTTAGCAGCT ATGCCATGAGCTGGGTCCGCCAG GCTCCAGGGAAGGGGCTGGAGTG GGTCTCAGCTATTAGTGGTAGTGG TGGTAGCACATACTACGCAGACTC CGTGAAGGGCCGGTTCACCATCT CCAGAGACAATTCCAAGAACACGC TGTATCTGCAAATGAACAGCCTGA GAGCCGAGGACACGGCCGTATAT TACTGTGCGAAAGGAGGAATGTAT TACTATGGTTCGGGGAGCTCGTAC TTTGACTACTGGGGCCAGGGAAC CCTGGTGACCGTCTCCTCAGCAAG CACAAAAGGTCCTTCAGTGTTCCC TCTGGCACCTTGCTCACGCAGCAC CTCTGAGAGTACAGCCGCCCTGG GCTGCCTGGTAAAGGACTACTTTC CCGAACCAGTCACTGTGTCCTGGA ATAGCGGGGCCTTGACCTCTGGA GTGCACACATTTCCAGCTGTACTG CAGTCATCTGGACTCTACAGCCTG TCCAGTGTGGTCACCGTACCTTCC TCCAACTTTGGCACTCAAACATATA CATGTAACGTGGATCATAAGCCCT CTAACACCAAAGTGGATAAAACTG TGGAGCGTAAGTGTTGTGTCGAGT GTCCTCCTTGTCCTGCTCCTCCTG TGGCAGGCCCATCTGTGTTTCTCT TTCCCCCAAAGCCAAAGGACACTT TGATGATATCCCGGACCCCTGAGG TGACTTGCGTCGTCGTAGATGTTT CACACGAAGATCCAGAGGTGCAG TTCAACTGGTACGTGGATGGCGTG GAAGTGCATAATGCCAAGACAAAG CCCCGCGAAGAGCAGTTTAATTCC ACCTTCCGCGTGGTGTCTGTGCTG ACCGTGGTACATCAGGATTGGCTT AACGGTAAGGAGTACAAGTGCAAG GTGAGTAACAAGGGGCTGCCCGC CCCTATCGAGAAGACTATCAGTAA AACCAAGGGCCAGCCAAGGGAGC CACAGGTGTACACACTTCCACCAT CTAGGGAGGAAATGACAAAGAACC AGGTGAGTTTGACCTGTCTCGTGA AAGGCTTTTATCCCAGTGATATAG CCGTGGAATGGGAAAGTAACGGG CAGCCCGAGAACAACTATAAGACC ACACCACCCATGCTGGACTCCGAC GGTTCTTTCTTCCTTTATAGCAAGC TGACAGTGGATAAATCCAGGTGGC AGCAGGGTAACGTATTCAGTTGCA GTGTCATGCACGAGGCACTCCACA

			ACCACTATACTCAGAAAAGTCTTTC CCTGAGTCCAGGCAAG

SEQ ID 2420	QVQLVQSGGGLVQPGG SLRLSCAASGFTFSSYA MSWVRQAPGKGLEWV SGISGSGGSTYYADSVK GRFTISRDNSKNMLFLQ MNSPRAEDTAVYYCAK KIAAAGKQPVDYWGQG TLVTVSSASTKGPSVFP LAPCSRSTSESTAALGC LVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSS GLYSLSSVVTVPSSNFG TQTYTCNVDHKPSNTKV DKTVERKCCVECPPCP APPVAGPSVFLFPPKPK DTLMISRTPEVTCVVVD VSHEDPEVQFNWYVDG VEVHNAKTKPREEQFN STFRVVSVLTVVHQDWL NGKEYKCKVSNKGLPA PIEKTISKTKGQPREPQV YTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWE SNGQPENNYKTTPPML DSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK	SEQ ID 2528	CAGGTGCAGCTGGTGCAATCTGG GGGAGGCTTGGTACAGCCTGGGG GGTCCCTGAGACTCTCCTGTGCAG CCTCTGGATTCACCTTTAGCAGCT ATGCCATGAGCTGGGTCCGCCAG GCTCCAGGGAAGGGGCTGGAATG GGTCTCAGGTATTAGTGGTAGTGG TGGTAGCACATACTACGCAGACTC CGTGAAGGGCCGGTTCACCATCT CCAGAGACAATTCCAAGAACATGC TGTTTCTGCAAATGAACAGCCCGA GAGCCGAGGACACGGCCGTATAT TACTGTGCGAAGAAAATAGCAGCA GCTGGTAAGCAACCTGTTGACTAC TGGGGCCAGGGAACCCTGGTCAC CGTCTCCTCAGCAAGCACAAAAGG TCCTTCAGTGTTCCCTCTGGCACC TTGCTCACGCAGCACCTCTGAGAG TACAGCCGCCCTGGGCTGCCTGG TAAAGGACTACTTTCCCGAACCAG TCACTGTGTCCTGGAATAGCGGG GCCTTGACCTCTGGAGTGCACACA TTTCCAGCTGTACTGCAGTCATCT GGACTCTACAGCCTGTCCAGTGTG GTCACCGTACCTTCCTCCAACTTT GGCACTCAAACATATACATGTAAC GTGGATCATAAGCCCTCTAACACC AAAGTGGATAAAACTGTGGAGCGT AAGTGTTGTGTCGAGTGTCCTCCT TGTCCTGCTCCTCCTGTGGCAGGC CCATCTGTGTTTCTCTTTCCCCCAA AGCCAAAGGACACTTTGATGATAT CCCGGACCCCTGAGGTGACTTGC GTCGTCGTAGATGTTTCACACGAA GATCCAGAGGTGCAGTTCAACTGG TACGTGGATGGCGTGGAAGTGCA TAATGCCAAGACAAAGCCCCGCGA AGAGCAGTTTAATTCCACCTTCCG CGTGGTGTCTGTGCTGACCGTGG TACATCAGGATTGGCTTAACGGTA AGGAGTACAAGTGCAAGGTGAGTA ACAAGGGGCTGCCCGCCCCTATC GAGAAGACTATCAGTAAAACCAAG GGCCAGCCAAGGGAGCCACAGGT GTACACACTTCCACCATCTAGGGA GGAAATGACAAAGAACCAGGTGA GTTTGACCTGTCTCGTGAAAGGCT TTTATCCCAGTGATATAGCCGTGG AATGGGAAAGTAACGGGCAGCCC GAGAACAACTATAAGACCACACCA CCCATGCTGGACTCCGACGGTTCT TTCTTCCTTTATAGCAAGCTGACA GTGGATAAATCCAGGTGGCAGCA GGGTAACGTATTCAGTTGCAGTGT CATGCACGAGGCACTCCACAACCA

			CTATACTCAGAAAAGTCTTTCCCT GAGTCCAGGCAAG

SEQ ID 2421	QVQLQQWGAGLLKPSE TLSLTCAVYGGSFSGYY WSWIRQPPGKGLEWIG EINHSGSTNYNPSLKSR VTISVDTSKNQFSLKLSS VTAADTAVYYCARRKVY DYVWGSYRLPGSVSYY FDYWGQGTLVTVSSAS TKGPSVFPLAPCSRSTS ESTAALGCLVKDYFPEP VTVSWNSGALTSGVHT FPAVLQSSGLYSLSSVV TVPSSNFGTQTYTCNVD HKPSNTKVDKTVERKC CVECPPCPAPPVAGPS VFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEV QFNWYVDGVEVHNAKT KPREEQFNSTFRVVSVL TVVHQDWLNGKEYKCK VSNKGLPAPIEKTISKTK GQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFY PSDIAVEWESNGQPEN NYKTTPPMLDSDGSFFL YSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQ KSLSLSPGK	SEQ ID 2529	CAGGTGCAGCTACAGCAGTGGGG CGCAGGACTGTTGAAGCCTTCGG AGACCCTGTCCCTCACCTGCGCTG TCTATGGTGGGTCCTTCAGTGGTT ACTACTGGAGCTGGATCCGCCAG CCCCCAGGGAAGGGGCTGGAGTG GATTGGGGAAATCAATCATAGTGG AAGCACCAACTACAACCCGTCCCT CAAGAGTCGAGTCACCATATCAGT AGACACGTCCAAGAACCAGTTCTC CCTGAAGCTGAGCTCTGTGACCG CCGCGGACACGGCTGTGTATTACT GTGCGAGAAGGAAGGTGTATGATT ACGTTTGGGGGAGTTATCGCCTCC CCGGGTCGGTATCGTACTACTTTG ACTACTGGGGCCAGGGAACCCTG GTCACCGTCTCCTCAGCAAGCACA AAAGGTCCTTCAGTGTTCCCTCTG GCACCTTGCTCACGCAGCACCTCT GAGAGTACAGCCGCCCTGGGCTG CCTGGTAAAGGACTACTTTCCCGA ACCAGTCACTGTGTCCTGGAATAG CGGGGCCTTGACCTCTGGAGTGC ACACATTTCCAGCTGTACTGCAGT CATCTGGACTCTACAGCCTGTCCA GTGTGGTCACCGTACCTTCCTCCA ACTTTGGCACTCAAACATATACAT GTAACGTGGATCATAAGCCCTCTA ACACCAAAGTGGATAAAACTGTGG AGCGTAAGTGTTGTGTCGAGTGTC CTCCTTGTCCTGCTCCTCCTGTGG CAGGCCCATCTGTGTTTCTCTTTC CCCCAAAGCCAAAGGACACTTTGA TGATATCCCGGACCCCTGAGGTGA CTTGCGTCGTCGTAGATGTTTCAC ACGAAGATCCAGAGGTGCAGTTCA ACTGGTACGTGGATGGCGTGGAA GTGCATAATGCCAAGACAAAGCCC CGCGAAGAGCAGTTTAATTCCACC TTCCGCGTGGTGTCTGTGCTGACC GTGGTACATCAGGATTGGCTTAAC GGTAAGGAGTACAAGTGCAAGGT GAGTAACAAGGGGCTGCCCGCCC CTATCGAGAAGACTATCAGTAAAA CCAAGGGCCAGCCAAGGGAGCCA CAGGTGTACACACTTCCACCATCT AGGGAGGAAATGACAAAGAACCA GGTGAGTTTGACCTGTCTCGTGAA AGGCTTTTATCCCAGTGATATAGC CGTGGAATGGGAAAGTAACGGGC AGCCCGAGAACAACTATAAGACCA CACCACCCATGCTGGACTCCGAC GGTTCTTTCTTCCTTTATAGCAAGC TGACAGTGGATAAATCCAGGTGGC AGCAGGGTAACGTATTCAGTTGCA GTGTCATGCACGAGGCACTCCACA

			ACCACTATACTCAGAAAAGTCTTTC CCTGAGTCCAGGCAAG

SEQ ID 2422	QVQLVQSGAEVKKPGE SLKISCKGSGYSFTSYW IGWVRQMPGKGLEWM GIIYPGDSDTRYSPSFQ GQVTISADKSISTAYLQ WSSLKASDTAMYYCAR LPGRAARPDYWGQGTL VTVSSASTKGPSVFPLA PCSRSTSESTAALGCLV KDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGL YSLSSVVTVPSSNFGTQ TYTCNVDHKPSNTKVDK TVERKCCVECPPCPAP PVAGPSVFLFPPKPKDT LMISRTPEVTCVVVDVS HEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTF RVVSVLTVVHQDWLNG KEYKCKVSNKGLPAPIE KTISKTKGQPREPQVYT LPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESN GQPENNYKTTPPMLDS DGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALH NHYTQKSLSLSPGK	SEQ ID 2530	CAGGTCCAGCTGGTACAGTCTGG AGCAGAGGTGAAAAAGCCCGGGG AGTCTCTGAAGATCTCCTGTAAGG GTTCTGGATACAGCTTTACCAGCT ACTGGATCGGCTGGGTGCGCCAG ATGCCCGGGAAAGGCCTGGAGTG GATGGGGATCATCTATCCTGGTGA CTCTGATACCAGATACAGCCCGTC CTTCCAAGGCCAGGTCACCATCTC AGCCGACAAGTCCATCAGCACCG CCTACCTGCAGTGGAGCAGCCTG AAGGCCTCGGACACCGCCATGTAT TACTGTGCGAGACTCCCGGGGAG AGCAGCTCGTCCAGACTACTGGG GCCAGGGCACCCTGGTCACCGTC TCCTCAGCAAGCACAAAAGGTCCT TCAGTGTTCCCTCTGGCACCTTGC TCACGCAGCACCTCTGAGAGTACA GCCGCCCTGGGCTGCCTGGTAAA GGACTACTTTCCCGAACCAGTCAC TGTGTCCTGGAATAGCGGGGCCTT GACCTCTGGAGTGCACACATTTCC AGCTGTACTGCAGTCATCTGGACT CTACAGCCTGTCCAGTGTGGTCAC CGTACCTTCCTCCAACTTTGGCAC TCAAACATATACATGTAACGTGGA TCATAAGCCCTCTAACACCAAAGT GGATAAAACTGTGGAGCGTAAGTG TTGTGTCGAGTGTCCTCCTTGTCC TGCTCCTCCTGTGGCAGGCCCATC TGTGTTTCTCTTTCCCCCAAAGCC AAAGGACACTTTGATGATATCCCG GACCCCTGAGGTGACTTGCGTCG TCGTAGATGTTTCACACGAAGATC CAGAGGTGCAGTTCAACTGGTACG TGGATGGCGTGGAAGTGCATAATG CCAAGACAAAGCCCCGCGAAGAG CAGTTTAATTCCACCTTCCGCGTG GTGTCTGTGCTGACCGTGGTACAT CAGGATTGGCTTAACGGTAAGGAG TACAAGTGCAAGGTGAGTAACAAG GGGCTGCCCGCCCCTATCGAGAA GACTATCAGTAAAACCAAGGGCCA GCCAAGGGAGCCACAGGTGTACA CACTTCCACCATCTAGGGAGGAAA TGACAAAGAACCAGGTGAGTTTGA CCTGTCTCGTGAAAGGCTTTTATC CCAGTGATATAGCCGTGGAATGG GAAAGTAACGGGCAGCCCGAGAA CAACTATAAGACCACACCACCCAT GCTGGACTCCGACGGTTCTTTCTT CCTTTATAGCAAGCTGACAGTGGA TAAATCCAGGTGGCAGCAGGGTAA CGTATTCAGTTGCAGTGTCATGCA CGAGGCACTCCACAACCACTATAC

			TCAGAAAAGTCTTTCCCTGAGTCC AGGCAAG

SEQ ID 2423	QVTLKESGGGVVQPGR SLRLSCAASGFTFSSYA MHWVRQAPGKGLEWV AVISYDGSNKYYADSVK GRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCAR GPGAVAGTKPKYYFDY WGQGTLVTVSSASTKG PSVFPLAPCSRSTSEST AALGCLVKDYFPEPVTV SWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVP SSNFGTQTYTCNVDHK PSNTKVDKTVERKCCVE CPPCPAPPVAGPSVFLF PPKPKDTLMISRTPEVT CVVVDVSHEDPEVQFN WYVDGVEVHNAKTKPR EEQFNSTFRVVSVLTVV HQDWLNGKEYKCKVSN KGLPAPIEKTISKTKGQP REPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDI AVEWESNGQPENNYKT TPPMLDSDGSFFLYSKL TVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSL SPGK	SEQ ID 2531	CAGGTCACCTTGAAGGAGTCTGG GGGAGGCGTGGTCCAGCCTGGGA GGTCCCTGAGACTCTCCTGTGCAG CCTCTGGATTCACCTTCAGTAGCT ATGCTATGCACTGGGTCCGCCAG GCTCCAGGCAAGGGGCTGGAGTG GGTGGCAGTTATATCATATGATGG AAGTAATAAATACTACGCAGACTC CGTGAAGGGCCGATTCACCATCTC CAGAGACAATTCCAAGAACACGCT GTATCTGCAAATGAACAGCCTGAG AGCTGAGGACACGGCTGTGTATTA CTGTGCGAGAGGCCCCGGGGCAG TGGCTGGTACTAAGCCAAAGTACT ACTTTGACTACTGGGGCCAGGGAA CCCTGGTCACCGTCTCCTCAGCAA GCACAAAAGGTCCTTCAGTGTTCC CTCTGGCACCTTGCTCACGCAGCA CCTCTGAGAGTACAGCCGCCCTG GGCTGCCTGGTAAAGGACTACTTT CCCGAACCAGTCACTGTGTCCTGG AATAGCGGGGCCTTGACCTCTGG AGTGCACACATTTCCAGCTGTACT GCAGTCATCTGGACTCTACAGCCT GTCCAGTGTGGTCACCGTACCTTC CTCCAACTTTGGCACTCAAACATA TACATGTAACGTGGATCATAAGCC CTCTAACACCAAAGTGGATAAAAC TGTGGAGCGTAAGTGTTGTGTCGA GTGTCCTCCTTGTCCTGCTCCTCC TGTGGCAGGCCCATCTGTGTTTCT CTTTCCCCCAAAGCCAAAGGACAC TTTGATGATATCCCGGACCCCTGA GGTGACTTGCGTCGTCGTAGATGT TTCACACGAAGATCCAGAGGTGCA GTTCAACTGGTACGTGGATGGCGT GGAAGTGCATAATGCCAAGACAAA GCCCCGCGAAGAGCAGTTTAATTC CACCTTCCGCGTGGTGTCTGTGCT GACCGTGGTACATCAGGATTGGCT TAACGGTAAGGAGTACAAGTGCAA GGTGAGTAACAAGGGGCTGCCCG CCCCTATCGAGAAGACTATCAGTA AAACCAAGGGCCAGCCAAGGGAG CCACAGGTGTACACACTTCCACCA TCTAGGGAGGAAATGACAAAGAAC CAGGTGAGTTTGACCTGTCTCGTG AAAGGCTTTTATCCCAGTGATATA GCCGTGGAATGGGAAAGTAACGG GCAGCCCGAGAACAACTATAAGAC CACACCACCCATGCTGGACTCCGA CGGTTCTTTCTTCCTTTATAGCAAG CTGACAGTGGATAAATCCAGGTGG CAGCAGGGTAACGTATTCAGTTGC AGTGTCATGCACGAGGCACTCCAC

			AACCACTATACTCAGAAAAGTCTTT CCCTGAGTCCAGGCAAG

SEQ ID 2424	EVQLVQSGGGVVQPGR SLRLSCAASGFTFSSYA MHWVRQAPGKGLEWV AVISYDGSNKYYADSVK GRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCAR ATYYYDSSGYRFDYWG QGTLVTVSSASTKGPSV FPLAPCSRSTSESTAAL GCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSN FGTQTYTCNVDHKPSN TKVDKTVERKCCVECPP CPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVV VDVSHEDPEVQFNWYV DGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQD WLNGKEYKCKVSNKGL PAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPP MLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVM HEALHNHYTQKSLSLSP GK	SEQ ID 2532	GAGGTCCAGCTGGTGCAGTCTGG GGGAGGCGTGGTCCAGCCTGGGA GGTCCCTGAGACTCTCCTGTGCAG CCTCTGGATTCACCTTCAGTAGCT ATGCTATGCACTGGGTCCGCCAG GCTCCAGGCAAGGGGCTGGAGTG GGTGGCAGTTATATCATATGATGG AAGTAATAAATACTACGCAGACTC CGTGAAGGGCCGATTCACCATCTC CAGAGACAATTCCAAGAACACGCT GTATCTGCAAATGAACAGCCTGAG AGCTGAGGACACGGCTGTGTATTA CTGTGCGAGGGCCACGTATTACTA TGATAGTAGTGGTTATAGGTTTGA CTACTGGGGCCAGGGAACCCTGG TCACCGTCTCCTCAGCAAGCACAA AAGGTCCTTCAGTGTTCCCTCTGG CACCTTGCTCACGCAGCACCTCTG AGAGTACAGCCGCCCTGGGCTGC CTGGTAAAGGACTACTTTCCCGAA CCAGTCACTGTGTCCTGGAATAGC GGGGCCTTGACCTCTGGAGTGCA CACATTTCCAGCTGTACTGCAGTC ATCTGGACTCTACAGCCTGTCCAG TGTGGTCACCGTACCTTCCTCCAA CTTTGGCACTCAAACATATACATGT AACGTGGATCATAAGCCCTCTAAC ACCAAAGTGGATAAAACTGTGGAG CGTAAGTGTTGTGTCGAGTGTCCT CCTTGTCCTGCTCCTCCTGTGGCA GGCCCATCTGTGTTTCTCTTTCCC CCAAAGCCAAAGGACACTTTGATG ATATCCCGGACCCCTGAGGTGACT TGCGTCGTCGTAGATGTTTCACAC GAAGATCCAGAGGTGCAGTTCAAC TGGTACGTGGATGGCGTGGAAGT GCATAATGCCAAGACAAAGCCCCG CGAAGAGCAGTTTAATTCCACCTT CCGCGTGGTGTCTGTGCTGACCG TGGTACATCAGGATTGGCTTAACG GTAAGGAGTACAAGTGCAAGGTGA GTAACAAGGGGCTGCCCGCCCCT ATCGAGAAGACTATCAGTAAAACC AAGGGCCAGCCAAGGGAGCCACA GGTGTACACACTTCCACCATCTAG GGAGGAAATGACAAAGAACCAGG TGAGTTTGACCTGTCTCGTGAAAG GCTTTTATCCCAGTGATATAGCCG TGGAATGGGAAAGTAACGGGCAG CCCGAGAACAACTATAAGACCACA CCACCCATGCTGGACTCCGACGG TTCTTTCTTCCTTTATAGCAAGCTG ACAGTGGATAAATCCAGGTGGCAG CAGGGTAACGTATTCAGTTGCAGT GTCATGCACGAGGCACTCCACAAC

			CACTATACTCAGAAAAGTCTTTCC CTGAGTCCAGGCAAG

SEQ ID 2425	EVQLVQSGGGLVEPGG SLRLSCAASRFTFSDAW MSWVRQAPGKGLEWV GRIKSKISGGTTDYAAP VQGRFTISRDDSKNTLY LQMDSLKTEDTAVYYCA NRNLGYWGQGTLVTVS SASTKGPSVFPLAPCSR STSESTAALGCLVKDYF PEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLS SVVTVPSSNFGTQTYTC NVDHKPSNTKVDKTVE RKCCVECPPCPAPPVA GPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHED PEVQFNWYVDGVEVHN AKTKPREEQFNSTFRVV SVLTVVHQDWLNGKEY KCKVSNKGLPAPIEKTIS KTKGQPREPQVYTLPPS REEMTKNQVSLTCLVK GFYPSDIAVEWESNGQ PENNYKTTPPMLDSDG SFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHN HYTQKSLSLSPGK	SEQ ID 2533	GAGGTCCAGCTGGTACAGTCTGG GGGAGGCTTGGTAGAACCGGGGG GGTCCCTTAGACTCTCCTGTGCAG CCTCTCGATTCACTTTCAGTGACG CCTGGATGAGCTGGGTCCGCCAG GCTCCAGGTAAGGGGCTGGAGTG GGTTGGCCGTATTAAAAGCAAAAT AAGTGGTGGGACAACAGACTACG CTGCACCCGTGCAAGGCAGATTCA CCATCTCAAGAGATGATTCAAAAA ACACGCTGTATCTGCAAATGGACA GCCTGAAAACCGAGGACACAGCC GTGTATTACTGTGCGAACCGAAAC TTAGGCTACTGGGGCCAGGGCAC CCTGGTGACCGTCTCCTCAGCAAG CACAAAAGGTCCTTCAGTGTTCCC TCTGGCACCTTGCTCACGCAGCAC CTCTGAGAGTACAGCCGCCCTGG GCTGCCTGGTAAAGGACTACTTTC CCGAACCAGTCACTGTGTCCTGGA ATAGCGGGGCCTTGACCTCTGGA GTGCACACATTTCCAGCTGTACTG CAGTCATCTGGACTCTACAGCCTG TCCAGTGTGGTCACCGTACCTTCC TCCAACTTTGGCACTCAAACATATA CATGTAACGTGGATCATAAGCCCT CTAACACCAAAGTGGATAAAACTG TGGAGCGTAAGTGTTGTGTCGAGT GTCCTCCTTGTCCTGCTCCTCCTG TGGCAGGCCCATCTGTGTTTCTCT TTCCCCCAAAGCCAAAGGACACTT TGATGATATCCCGGACCCCTGAGG TGACTTGCGTCGTCGTAGATGTTT CACACGAAGATCCAGAGGTGCAG TTCAACTGGTACGTGGATGGCGTG GAAGTGCATAATGCCAAGACAAAG CCCCGCGAAGAGCAGTTTAATTCC ACCTTCCGCGTGGTGTCTGTGCTG ACCGTGGTACATCAGGATTGGCTT AACGGTAAGGAGTACAAGTGCAAG GTGAGTAACAAGGGGCTGCCCGC CCCTATCGAGAAGACTATCAGTAA AACCAAGGGCCAGCCAAGGGAGC CACAGGTGTACACACTTCCACCAT CTAGGGAGGAAATGACAAAGAACC AGGTGAGTTTGACCTGTCTCGTGA AAGGCTTTTATCCCAGTGATATAG CCGTGGAATGGGAAAGTAACGGG CAGCCCGAGAACAACTATAAGACC ACACCACCCATGCTGGACTCCGAC GGTTCTTTCTTCCTTTATAGCAAGC TGACAGTGGATAAATCCAGGTGGC AGCAGGGTAACGTATTCAGTTGCA GTGTCATGCACGAGGCACTCCACA ACCACTATACTCAGAAAAGTCTTTC CCTGAGTCCAGGCAAG

SEQ ID 2426	EVQLVQSGAEVKKPGA SVKVSCKASGYTFTSYA MHWVRQAPGQRLEWM GWINAGNGNTKYSQKF QGRVTMTTDTSTSTAY MELRSLRSDDTAVYYCA RARYYDSSGYIAPSGYF DYWGQGTLVTVSSAST KGPSVFPLAPCSRSTSE STAALGCLVKDYFPEPV TVSWNSGALTSGVHTF PAVLQSSGLYSLSSVVT VPSSNFGTQTYTCNVD HKPSNTKVDKTVERKC CVECPPCPAPPVAGPS VFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEV QFNWYVDGVEVHNAKT KPREEQFNSTFRVVSVL TVVHQDWLNGKEYKCK VSNKGLPAPIEKTISKTK GQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFY PSDIAVEWESNGQPEN NYKTTPPMLDSDGSFFL YSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQ KSLSLSPGK	SEQ ID 2534	GAGGTCCAGCTGGTGCAGTCTGG GGCTGAGGTGAAGAAGCCTGGGG CCTCAGTGAAGGTTTCCTGCAAGG CTTCTGGATACACCTTCACTAGCT ATGCTATGCATTGGGTGCGCCAG GCCCCCGGACAAAGGCTTGAGTG GATGGGATGGATCAACGCTGGCA ATGGTAACACAAAATATTCACAGA AGTTCCAGGGCAGAGTCACCATGA CCACAGACACATCCACGAGCACA GCCTACATGGAGCTGAGGAGCCT GAGATCTGACGACACGGCCGTGT ATTACTGTGCGAGAGCTCGTTACT ATGATAGTAGTGGTTATATTGCCC CATCGGGTTACTTTGACTACTGGG GCCAGGGAACCCTGGTCACCGTC TCCTCAGCAAGCACAAAAGGTCCT TCAGTGTTCCCTCTGGCACCTTGC TCACGCAGCACCTCTGAGAGTACA GCCGCCCTGGGCTGCCTGGTAAA GGACTACTTTCCCGAACCAGTCAC TGTGTCCTGGAATAGCGGGGCCTT GACCTCTGGAGTGCACACATTTCC AGCTGTACTGCAGTCATCTGGACT CTACAGCCTGTCCAGTGTGGTCAC CGTACCTTCCTCCAACTTTGGCAC TCAAACATATACATGTAACGTGGA TCATAAGCCCTCTAACACCAAAGT GGATAAAACTGTGGAGCGTAAGTG TTGTGTCGAGTGTCCTCCTTGTCC TGCTCCTCCTGTGGCAGGCCCATC TGTGTTTCTCTTTCCCCCAAAGCC AAAGGACACTTTGATGATATCCCG GACCCCTGAGGTGACTTGCGTCG TCGTAGATGTTTCACACGAAGATC CAGAGGTGCAGTTCAACTGGTACG TGGATGGCGTGGAAGTGCATAATG CCAAGACAAAGCCCCGCGAAGAG CAGTTTAATTCCACCTTCCGCGTG GTGTCTGTGCTGACCGTGGTACAT CAGGATTGGCTTAACGGTAAGGAG TACAAGTGCAAGGTGAGTAACAAG GGGCTGCCCGCCCCTATCGAGAA GACTATCAGTAAAACCAAGGGCCA GCCAAGGGAGCCACAGGTGTACA CACTTCCACCATCTAGGGAGGAAA TGACAAAGAACCAGGTGAGTTTGA CCTGTCTCGTGAAAGGCTTTTATC CCAGTGATATAGCCGTGGAATGG GAAAGTAACGGGCAGCCCGAGAA CAACTATAAGACCACACCACCCAT GCTGGACTCCGACGGTTCTTTCTT CCTTTATAGCAAGCTGACAGTGGA TAAATCCAGGTGGCAGCAGGGTAA CGTATTCAGTTGCAGTGTCATGCA CGAGGCACTCCACAACCACTATAC

			TCAGAAAAGTCTTTCCCTGAGTCC AGGCAAG

SEQ ID 2427	QVQLVQSGAEVKKPGA SVKVSCKASGYTFTSYA MHWVRQAPGQRLEWM GWINAGNGNTKYSQKF QGRVTITRDTSASTAYM ELSSLRSEDTAVYYCAR DGPAVDGAEYFQHWG QGTLVTVSSASTKGPSV FPLAPCSRSTSESTAAL GCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSN FGTQTYTCNVDHKPSN TKVDKTVERKCCVECPP CPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVV VDVSHEDPEVQFNWYV DGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQD WLNGKEYKCKVSNKGL PAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPP MLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVM HEALHNHYTQKSLSLSP GK	SEQ ID 2535	CAGGTGCAGCTGGTGCAGTCTGG GGCTGAGGTGAAGAAGCCTGGGG CCTCAGTGAAGGTTTCCTGCAAGG CTTCTGGATACACCTTCACTAGCT ATGCTATGCATTGGGTGCGCCAG GCCCCCGGACAAAGGCTTGAGTG GATGGGATGGATCAACGCTGGCA ATGGTAACACAAAATATTCACAGA AGTTCCAGGGCAGAGTCACCATTA CCAGGGACACATCCGCGAGCACA GCCTACATGGAGCTGAGCAGCCT GAGATCTGAAGACACGGCTGTGTA TTACTGTGCGAGAGATGGCCCCG CCGTTGATGGTGCTGAATACTTCC AGCACTGGGGCCAGGGCACCCTG GTCACCGTCTCCTCAGCAAGCACA AAAGGTCCTTCAGTGTTCCCTCTG GCACCTTGCTCACGCAGCACCTCT GAGAGTACAGCCGCCCTGGGCTG CCTGGTAAAGGACTACTTTCCCGA ACCAGTCACTGTGTCCTGGAATAG CGGGGCCTTGACCTCTGGAGTGC ACACATTTCCAGCTGTACTGCAGT CATCTGGACTCTACAGCCTGTCCA GTGTGGTCACCGTACCTTCCTCCA ACTTTGGCACTCAAACATATACAT GTAACGTGGATCATAAGCCCTCTA ACACCAAAGTGGATAAAACTGTGG AGCGTAAGTGTTGTGTCGAGTGTC CTCCTTGTCCTGCTCCTCCTGTGG CAGGCCCATCTGTGTTTCTCTTTC CCCCAAAGCCAAAGGACACTTTGA TGATATCCCGGACCCCTGAGGTGA CTTGCGTCGTCGTAGATGTTTCAC ACGAAGATCCAGAGGTGCAGTTCA ACTGGTACGTGGATGGCGTGGAA GTGCATAATGCCAAGACAAAGCCC CGCGAAGAGCAGTTTAATTCCACC TTCCGCGTGGTGTCTGTGCTGACC GTGGTACATCAGGATTGGCTTAAC GGTAAGGAGTACAAGTGCAAGGT GAGTAACAAGGGGCTGCCCGCCC CTATCGAGAAGACTATCAGTAAAA CCAAGGGCCAGCCAAGGGAGCCA CAGGTGTACACACTTCCACCATCT AGGGAGGAAATGACAAAGAACCA GGTGAGTTTGACCTGTCTCGTGAA AGGCTTTTATCCCAGTGATATAGC CGTGGAATGGGAAAGTAACGGGC AGCCCGAGAACAACTATAAGACCA CACCACCCATGCTGGACTCCGAC GGTTCTTTCTTCCTTTATAGCAAGC TGACAGTGGATAAATCCAGGTGGC AGCAGGGTAACGTATTCAGTTGCA GTGTCATGCACGAGGCACTCCACA

			ACCACTATACTCAGAAAAGTCTTTC CCTGAGTCCAGGCAAG

SEQ ID 2428	QLQLQESGPGLVKPSQ TLSLTCAISGDSVSSNS AAWNWIRQSPSRGLEW LGRTYYRSKWYNDYAV SLKSRITINPDTSKNQFS LQLNSVTPEDTAVYYCA SLASGSPPPGDYWGQG TLVTVSSASTKGPSVFP LAPCSRSTSESTAALGC LVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSS GLYSLSSVVTVPSSNFG TQTYTCNVDHKPSNTKV DKTVERKCCVECPPCP APPVAGPSVFLFPPKPK DTLMISRTPEVTCVVVD VSHEDPEVQFNWYVDG VEVHNAKTKPREEQFN STFRVVSVLTVVHQDWL NGKEYKCKVSNKGLPA PIEKTISKTKGQPREPQV YTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWE SNGQPENNYKTTPPML DSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK	SEQ ID 2536	CAGCTGCAGCTGCAGGAGTCGGG TCCAGGACTGGTGAAGCCCTCGC AGACCCTCTCACTCACCTGTGCCA TCTCCGGGGACAGTGTCTCTAGCA ACAGTGCTGCTTGGAACTGGATCA GGCAGTCCCCATCGCGAGGCCTT GAGTGGCTGGGAAGGACTTACTA CAGGTCCAAGTGGTATAATGATTA TGCAGTATCTCTGAAAAGTCGAAT AACCATCAACCCGGACACATCCAA GAACCAGTTCTCCCTGCAGCTGAA CTCTGTGACTCCCGAGGACACGG CTGTATATTACTGTGCAAGTTTGG CGAGTGGTTCCCCCCCTCCGGGG GACTACTGGGGCCAGGGAACCCT GGTGACCGTCTCCTCAGCAAGCA CAAAAGGTCCTTCAGTGTTCCCTC TGGCACCTTGCTCACGCAGCACCT CTGAGAGTACAGCCGCCCTGGGC TGCCTGGTAAAGGACTACTTTCCC GAACCAGTCACTGTGTCCTGGAAT AGCGGGGCCTTGACCTCTGGAGT GCACACATTTCCAGCTGTACTGCA GTCATCTGGACTCTACAGCCTGTC CAGTGTGGTCACCGTACCTTCCTC CAACTTTGGCACTCAAACATATAC ATGTAACGTGGATCATAAGCCCTC TAACACCAAAGTGGATAAAACTGT GGAGCGTAAGTGTTGTGTCGAGT GTCCTCCTTGTCCTGCTCCTCCTG TGGCAGGCCCATCTGTGTTTCTCT TTCCCCCAAAGCCAAAGGACACTT TGATGATATCCCGGACCCCTGAGG TGACTTGCGTCGTCGTAGATGTTT CACACGAAGATCCAGAGGTGCAG TTCAACTGGTACGTGGATGGCGTG GAAGTGCATAATGCCAAGACAAAG CCCCGCGAAGAGCAGTTTAATTCC ACCTTCCGCGTGGTGTCTGTGCTG ACCGTGGTACATCAGGATTGGCTT AACGGTAAGGAGTACAAGTGCAAG GTGAGTAACAAGGGGCTGCCCGC CCCTATCGAGAAGACTATCAGTAA AACCAAGGGCCAGCCAAGGGAGC CACAGGTGTACACACTTCCACCAT CTAGGGAGGAAATGACAAAGAACC AGGTGAGTTTGACCTGTCTCGTGA AAGGCTTTTATCCCAGTGATATAG CCGTGGAATGGGAAAGTAACGGG CAGCCCGAGAACAACTATAAGACC ACACCACCCATGCTGGACTCCGAC GGTTCTTTCTTCCTTTATAGCAAGC TGACAGTGGATAAATCCAGGTGGC AGCAGGGTAACGTATTCAGTTGCA GTGTCATGCACGAGGCACTCCACA

			ACCACTATACTCAGAAAAGTCTTTC CCTGAGTCCAGGCAAG

SEQ ID 2429	QVTLKESGGGVVQPGR SLRLSCAASGFTFSTYG MHWVRQAPGKGLEWV ALISYDGSKKYYANSVK GRFTISRDNSKNTLYLQ MKSLRAEDTAMYYCAK GPIVGATMDYWGQGAL VTVSSASTKGPSVFPLA PCSRSTSESTAALGCLV KDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGL YSLSSVVTVPSSNFGTQ TYTCNVDHKPSNTKVDK TVERKCCVECPPCPAP PVAGPSVFLFPPKPKDT LMISRTPEVTCVVVDVS HEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTF RVVSVLTVVHQDWLNG KEYKCKVSNKGLPAPIE KTISKTKGQPREPQVYT LPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESN GQPENNYKTTPPMLDS DGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALH NHYTQKSLSLSPGK	SEQ ID 2537	CAGGTCACCTTGAAGGAGTCTGG GGGAGGCGTGGTCCAGCCTGGGA GGTCCCTGAGACTCTCCTGTGCAG CCTCTGGATTCACCTTCAGTACCT ATGGCATGCACTGGGTCCGCCAG GCTCCAGGCAAGGGGCTGGAGTG GGTGGCACTTATATCATATGATGG AAGTAAAAAATACTATGCAAACTCC GTGAAGGGCCGATTCACCATCTCC AGAGACAATTCCAAGAACACGTTG TATCTGCAAATGAAAAGTCTGAGA GCTGAGGACACGGCTATGTATTAC TGTGCGAAAGGCCCTATAGTGGG AGCGACTATGGACTACTGGGGCC AGGGAGCCCTGGTCACCGTCTCC TCAGCAAGCACAAAAGGTCCTTCA GTGTTCCCTCTGGCACCTTGCTCA CGCAGCACCTCTGAGAGTACAGC CGCCCTGGGCTGCCTGGTAAAGG ACTACTTTCCCGAACCAGTCACTG TGTCCTGGAATAGCGGGGCCTTG ACCTCTGGAGTGCACACATTTCCA GCTGTACTGCAGTCATCTGGACTC TACAGCCTGTCCAGTGTGGTCACC GTACCTTCCTCCAACTTTGGCACT CAAACATATACATGTAACGTGGAT CATAAGCCCTCTAACACCAAAGTG GATAAAACTGTGGAGCGTAAGTGT TGTGTCGAGTGTCCTCCTTGTCCT GCTCCTCCTGTGGCAGGCCCATCT GTGTTTCTCTTTCCCCCAAAGCCA AAGGACACTTTGATGATATCCCGG ACCCCTGAGGTGACTTGCGTCGTC GTAGATGTTTCACACGAAGATCCA GAGGTGCAGTTCAACTGGTACGTG GATGGCGTGGAAGTGCATAATGC CAAGACAAAGCCCCGCGAAGAGC AGTTTAATTCCACCTTCCGCGTGG TGTCTGTGCTGACCGTGGTACATC AGGATTGGCTTAACGGTAAGGAGT ACAAGTGCAAGGTGAGTAACAAGG GGCTGCCCGCCCCTATCGAGAAG ACTATCAGTAAAACCAAGGGCCAG CCAAGGGAGCCACAGGTGTACAC ACTTCCACCATCTAGGGAGGAAAT GACAAAGAACCAGGTGAGTTTGAC CTGTCTCGTGAAAGGCTTTTATCC CAGTGATATAGCCGTGGAATGGGA AAGTAACGGGCAGCCCGAGAACA ACTATAAGACCACACCACCCATGC TGGACTCCGACGGTTCTTTCTTCC TTTATAGCAAGCTGACAGTGGATA AATCCAGGTGGCAGCAGGGTAAC GTATTCAGTTGCAGTGTCATGCAC GAGGCACTCCACAACCACTATACT

			CAGAAAAGTCTTTCCCTGAGTCCA GGCAAG

SEQ ID 2430	EVQLVQSGAEVKKPGS SVKVSCKASGGTFSSYA ISWVRQAPGQGLEWMG WISAYNGNTNYAQKLQ GRVTMTTDTSTSTAYM ELRSLRSDDTAVYYCAR WYGDYGLDYWGQGTL VTVSSASTKGPSVFPLA PCSRSTSESTAALGCLV KDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGL YSLSSVVTVPSSNFGTQ TYTCNVDHKPSNTKVDK TVERKCCVECPPCPAP PVAGPSVFLFPPKPKDT LMISRTPEVTCVVVDVS HEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTF RVVSVLTVVHQDWLNG KEYKCKVSNKGLPAPIE KTISKTKGQPREPQVYT LPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESN GQPENNYKTTPPMLDS DGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALH NHYTQKSLSLSPGK	SEQ ID 2538	GAGGTGCAGCTGGTGCAGTCTGG GGCTGAGGTGAAGAAGCCTGGGT CCTCGGTGAAGGTCTCCTGCAAG GCTTCTGGAGGCACCTTCAGCAG CTATGCTATCAGCTGGGTGCGACA GGCCCCTGGACAAGGGCTTGAGT GGATGGGATGGATCAGCGCTTAC AATGGTAACACAAACTATGCACAG AAGCTCCAGGGCAGAGTCACCAT GACCACAGACACATCCACGAGCA CAGCCTACATGGAGCTGAGGAGC CTGAGATCTGACGACACGGCCGT GTATTACTGTGCGAGATGGTACGG TGACTACGGCCTTGACTACTGGGG CCAGGGAACCCTGGTCACCGTCT CCTCAGCAAGCACAAAAGGTCCTT CAGTGTTCCCTCTGGCACCTTGCT CACGCAGCACCTCTGAGAGTACA GCCGCCCTGGGCTGCCTGGTAAA GGACTACTTTCCCGAACCAGTCAC TGTGTCCTGGAATAGCGGGGCCTT GACCTCTGGAGTGCACACATTTCC AGCTGTACTGCAGTCATCTGGACT CTACAGCCTGTCCAGTGTGGTCAC CGTACCTTCCTCCAACTTTGGCAC TCAAACATATACATGTAACGTGGA TCATAAGCCCTCTAACACCAAAGT GGATAAAACTGTGGAGCGTAAGTG TTGTGTCGAGTGTCCTCCTTGTCC TGCTCCTCCTGTGGCAGGCCCATC TGTGTTTCTCTTTCCCCCAAAGCC AAAGGACACTTTGATGATATCCCG GACCCCTGAGGTGACTTGCGTCG TCGTAGATGTTTCACACGAAGATC CAGAGGTGCAGTTCAACTGGTACG TGGATGGCGTGGAAGTGCATAATG CCAAGACAAAGCCCCGCGAAGAG CAGTTTAATTCCACCTTCCGCGTG GTGTCTGTGCTGACCGTGGTACAT CAGGATTGGCTTAACGGTAAGGAG TACAAGTGCAAGGTGAGTAACAAG GGGCTGCCCGCCCCTATCGAGAA GACTATCAGTAAAACCAAGGGCCA GCCAAGGGAGCCACAGGTGTACA CACTTCCACCATCTAGGGAGGAAA TGACAAAGAACCAGGTGAGTTTGA CCTGTCTCGTGAAAGGCTTTTATC CCAGTGATATAGCCGTGGAATGG GAAAGTAACGGGCAGCCCGAGAA CAACTATAAGACCACACCACCCAT GCTGGACTCCGACGGTTCTTTCTT CCTTTATAGCAAGCTGACAGTGGA TAAATCCAGGTGGCAGCAGGGTAA CGTATTCAGTTGCAGTGTCATGCA CGAGGCACTCCACAACCACTATAC

			TCAGAAAAGTCTTTCCCTGAGTCC AGGCAAG

SEQ ID 2431	EVQLVQSGAEVKKPGA SVKVSCKASGYTFTSYA MHWVRQAPGQRLAWM GWINAGNGNTKYSEKF EGRVTITRDTSASTAYM ELSSLRSEDTAVYYCAR VAKYYYESGGYRASNW FDPWGQGTLVTVSSAS TKGPSVFPLAPCSRSTS ESTAALGCLVKDYFPEP VTVSWNSGALTSGVHT FPAVLQSSGLYSLSSVV TVPSSNFGTQTYTCNVD HKPSNTKVDKTVERKC CVECPPCPAPPVAGPS VFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEV QFNWYVDGVEVHNAKT KPREEQFNSTFRVVSVL TVVHQDWLNGKEYKCK VSNKGLPAPIEKTISKTK GQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFY PSDIAVEWESNGQPEN NYKTTPPMLDSDGSFFL YSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQ KSLSLSPGK	SEQ ID 2539	GAGGTCCAGCTGGTGCAGTCTGG GGCTGAGGTGAAGAAGCCTGGGG CCTCAGTGAAGGTTTCCTGCAAGG CTTCTGGATACACCTTCACTAGCT ATGCTATGCATTGGGTGCGCCAG GCCCCCGGACAAAGGCTTGCGTG GATGGGATGGATCAACGCTGGCA ATGGTAACACAAAATATTCAGAGA AGTTCGAAGGCAGAGTCACCATCA CCAGGGACACATCCGCGAGCACA GCCTACATGGAGCTGAGCAGCCT GAGATCTGAAGACACGGCTGTGTA TTACTGTGCGAGGGTCGCCAAATA TTATTACGAGAGTGGTGGTTATCG GGCCTCCAACTGGTTCGACCCCT GGGGCCAGGGCACCCTGGTCACC GTCTCCTCAGCAAGCACAAAAGGT CCTTCAGTGTTCCCTCTGGCACCT TGCTCACGCAGCACCTCTGAGAGT ACAGCCGCCCTGGGCTGCCTGGT AAAGGACTACTTTCCCGAACCAGT CACTGTGTCCTGGAATAGCGGGG CCTTGACCTCTGGAGTGCACACAT TTCCAGCTGTACTGCAGTCATCTG GACTCTACAGCCTGTCCAGTGTGG TCACCGTACCTTCCTCCAACTTTG GCACTCAAACATATACATGTAACG TGGATCATAAGCCCTCTAACACCA AAGTGGATAAAACTGTGGAGCGTA AGTGTTGTGTCGAGTGTCCTCCTT GTCCTGCTCCTCCTGTGGCAGGC CCATCTGTGTTTCTCTTTCCCCCAA AGCCAAAGGACACTTTGATGATAT CCCGGACCCCTGAGGTGACTTGC GTCGTCGTAGATGTTTCACACGAA GATCCAGAGGTGCAGTTCAACTGG TACGTGGATGGCGTGGAAGTGCA TAATGCCAAGACAAAGCCCCGCGA AGAGCAGTTTAATTCCACCTTCCG CGTGGTGTCTGTGCTGACCGTGG TACATCAGGATTGGCTTAACGGTA AGGAGTACAAGTGCAAGGTGAGTA ACAAGGGGCTGCCCGCCCCTATC GAGAAGACTATCAGTAAAACCAAG GGCCAGCCAAGGGAGCCACAGGT GTACACACTTCCACCATCTAGGGA GGAAATGACAAAGAACCAGGTGA GTTTGACCTGTCTCGTGAAAGGCT TTTATCCCAGTGATATAGCCGTGG AATGGGAAAGTAACGGGCAGCCC GAGAACAACTATAAGACCACACCA CCCATGCTGGACTCCGACGGTTCT TTCTTCCTTTATAGCAAGCTGACA GTGGATAAATCCAGGTGGCAGCA GGGTAACGTATTCAGTTGCAGTGT CATGCACGAGGCACTCCACAACCA

			CTATACTCAGAAAAGTCTTTCCCT GAGTCCAGGCAAG

SEQ ID 2432	QVQLQESGPGLVKPSQ TLSLTCAISGDSVSSNS AAWNWIRQSPSRGLEW LGRTYYRSKWYNDYAV SVKSRITINPDTSKNQFS LQLNSVTPEDTAVYYCA RAPPPTVGWYAPVFDY WGQGTLVTVSSASTKG PSVFPLAPCSRSTSEST AALGCLVKDYFPEPVTV SWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVP SSNFGTQTYTCNVDHK PSNTKVDKTVERKCCVE CPPCPAPPVAGPSVFLF PPKPKDTLMISRTPEVT CVVVDVSHEDPEVQFN WYVDGVEVHNAKTKPR EEQFNSTFRVVSVLTVV HQDWLNGKEYKCKVSN KGLPAPIEKTISKTKGQP REPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDI AVEWESNGQPENNYKT TPPMLDSDGSFFLYSKL TVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSL SPGK	SEQ ID 2540	CAGGTGCAGCTGCAGGAGTCAGG TCCAGGACTGGTGAAGCCCTCGC AGACCCTCTCACTCACCTGTGCCA TCTCCGGGGACAGTGTCTCTAGCA ACAGTGCTGCTTGGAACTGGATCA GGCAGTCCCCATCGAGAGGCCTT GAGTGGCTGGGAAGGACATACTA CAGGTCCAAGTGGTATAATGATTA TGCAGTATCTGTGAAAAGTCGAAT AACCATCAACCCAGACACATCCAA GAACCAGTTCTCCCTGCAGCTGAA CTCTGTGACTCCCGAGGACACGG CTGTGTATTACTGTGCAAGAGCGC CCCCTCCGACTGTTGGCTGGTAC GCCCCCGTCTTTGACTACTGGGG CCAGGGAACCCTGGTCACCGTCT CCTCAGCAAGCACAAAAGGTCCTT CAGTGTTCCCTCTGGCACCTTGCT CACGCAGCACCTCTGAGAGTACA GCCGCCCTGGGCTGCCTGGTAAA GGACTACTTTCCCGAACCAGTCAC TGTGTCCTGGAATAGCGGGGCCTT GACCTCTGGAGTGCACACATTTCC AGCTGTACTGCAGTCATCTGGACT CTACAGCCTGTCCAGTGTGGTCAC CGTACCTTCCTCCAACTTTGGCAC TCAAACATATACATGTAACGTGGA TCATAAGCCCTCTAACACCAAAGT GGATAAAACTGTGGAGCGTAAGTG TTGTGTCGAGTGTCCTCCTTGTCC TGCTCCTCCTGTGGCAGGCCCATC TGTGTTTCTCTTTCCCCCAAAGCC AAAGGACACTTTGATGATATCCCG GACCCCTGAGGTGACTTGCGTCG TCGTAGATGTTTCACACGAAGATC CAGAGGTGCAGTTCAACTGGTACG TGGATGGCGTGGAAGTGCATAATG CCAAGACAAAGCCCCGCGAAGAG CAGTTTAATTCCACCTTCCGCGTG GTGTCTGTGCTGACCGTGGTACAT CAGGATTGGCTTAACGGTAAGGAG TACAAGTGCAAGGTGAGTAACAAG GGGCTGCCCGCCCCTATCGAGAA GACTATCAGTAAAACCAAGGGCCA GCCAAGGGAGCCACAGGTGTACA CACTTCCACCATCTAGGGAGGAAA TGACAAAGAACCAGGTGAGTTTGA CCTGTCTCGTGAAAGGCTTTTATC CCAGTGATATAGCCGTGGAATGG GAAAGTAACGGGCAGCCCGAGAA CAACTATAAGACCACACCACCCAT GCTGGACTCCGACGGTTCTTTCTT CCTTTATAGCAAGCTGACAGTGGA TAAATCCAGGTGGCAGCAGGGTAA CGTATTCAGTTGCAGTGTCATGCA CGAGGCACTCCACAACCACTATAC

			TCAGAAAAGTCTTTCCCTGAGTCC AGGCAAG

SEQ ID 2433	QLQLQESGGGLVQPGG SLRLSCSASGISFRDYW MHWIRQTPGKGLVWVS RINPDGSSTSYADSVKG RFTISRDNSKNTLYLQM NSLRAEDTAVYYCAKVT GRRVGAHDYWGQGTL VTVSSASTKGPSVFPLA PCSRSTSESTAALGCLV KDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGL YSLSSVVTVPSSNFGTQ TYTCNVDHKPSNTKVDK TVERKCCVECPPCPAP PVAGPSVFLFPPKPKDT LMISRTPEVTCVVVDVS HEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTF RVVSVLTVVHQDWLNG KEYKCKVSNKGLPAPIE KTISKTKGQPREPQVYT LPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESN GQPENNYKTTPPMLDS DGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALH NHYTQKSLSLSPGK	SEQ ID 2541	CAGCTGCAGCTGCAGGAGTCCGG GGGAGGCTTAGTTCAGCCGGGGG GGTCCCTGAGACTCTCCTGCTCAG CCTCTGGAATCAGCTTCAGAGATT ACTGGATGCACTGGATCCGCCAAA CTCCAGGGAAGGGGCTGGTGTGG GTCTCACGTATTAATCCTGATGGG AGTAGCACAAGCTACGCGGACTC CGTGAAGGGCCGATTCACCATCTC CAGAGACAATTCCAAGAACACGCT GTATCTGCAAATGAACAGCCTGAG AGCTGAGGACACGGCTGTGTATTA CTGTGCGAAAGTTACGGGACGGA GAGTGGGAGCCCATGACTACTGG GGCCAGGGAACCCTGGTCACCGT CTCCTCAGCAAGCACAAAAGGTCC TTCAGTGTTCCCTCTGGCACCTTG CTCACGCAGCACCTCTGAGAGTAC AGCCGCCCTGGGCTGCCTGGTAA AGGACTACTTTCCCGAACCAGTCA CTGTGTCCTGGAATAGCGGGGCC TTGACCTCTGGAGTGCACACATTT CCAGCTGTACTGCAGTCATCTGGA CTCTACAGCCTGTCCAGTGTGGTC ACCGTACCTTCCTCCAACTTTGGC ACTCAAACATATACATGTAACGTG GATCATAAGCCCTCTAACACCAAA GTGGATAAAACTGTGGAGCGTAAG TGTTGTGTCGAGTGTCCTCCTTGT CCTGCTCCTCCTGTGGCAGGCCC ATCTGTGTTTCTCTTTCCCCCAAAG CCAAAGGACACTTTGATGATATCC CGGACCCCTGAGGTGACTTGCGT CGTCGTAGATGTTTCACACGAAGA TCCAGAGGTGCAGTTCAACTGGTA CGTGGATGGCGTGGAAGTGCATA ATGCCAAGACAAAGCCCCGCGAA GAGCAGTTTAATTCCACCTTCCGC GTGGTGTCTGTGCTGACCGTGGTA CATCAGGATTGGCTTAACGGTAAG GAGTACAAGTGCAAGGTGAGTAAC AAGGGGCTGCCCGCCCCTATCGA GAAGACTATCAGTAAAACCAAGGG CCAGCCAAGGGAGCCACAGGTGT ACACACTTCCACCATCTAGGGAGG AAATGACAAAGAACCAGGTGAGTT TGACCTGTCTCGTGAAAGGCTTTT ATCCCAGTGATATAGCCGTGGAAT GGGAAAGTAACGGGCAGCCCGAG AACAACTATAAGACCACACCACCC ATGCTGGACTCCGACGGTTCTTTC TTCCTTTATAGCAAGCTGACAGTG GATAAATCCAGGTGGCAGCAGGG TAACGTATTCAGTTGCAGTGTCAT GCACGAGGCACTCCACAACCACTA

			TACTCAGAAAAGTCTTTCCCTGAG TCCAGGCAAG

SEQ ID 2434	QVQLVQSGAEVKKPGA SVKVSCKASGYTFTGYY MHWVRQAPGQGLEWM GWINPNSGGTNYAQKF QGRVTMTRDTSISTAYM ELSRLRSDDTAVYYCAF AQPGAETLNFDLWGRG TLVTVSSASTKGPSVFP LAPCSRSTSESTAALGC LVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSS GLYSLSSVVTVPSSNFG TQTYTCNVDHKPSNTKV DKTVERKCCVECPPCP APPVAGPSVFLFPPKPK DTLMISRTPEVTCVVVD VSHEDPEVQFNWYVDG VEVHNAKTKPREEQFN STFRVVSVLTVVHQDWL NGKEYKCKVSNKGLPA PIEKTISKTKGQPREPQV YTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWE SNGQPENNYKTTPPML DSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK	SEQ ID 2542	CAGGTGCAGCTGGTGCAGTCTGG GGCTGAGGTGAAGAAGCCTGGGG CCTCAGTGAAGGTCTCCTGCAAGG CTTCTGGATACACCTTCACCGGCT ACTATATGCACTGGGTGCGACAGG CCCCTGGACAAGGGCTTGAGTGG ATGGGATGGATCAACCCTAACAGT GGTGGCACAAACTATGCACAGAAG TTTCAGGGCAGGGTCACCATGACC AGGGACACGTCCATCAGCACAGC CTACATGGAGCTGAGCAGGCTGA GATCTGACGACACGGCCGTGTATT ACTGTGCCTTTGCCCAGCCGGGC GCTGAGACGTTGAACTTCGATCTC TGGGGCCGTGGCACCCTGGTCAC CGTCTCCTCAGCAAGCACAAAAGG TCCTTCAGTGTTCCCTCTGGCACC TTGCTCACGCAGCACCTCTGAGAG TACAGCCGCCCTGGGCTGCCTGG TAAAGGACTACTTTCCCGAACCAG TCACTGTGTCCTGGAATAGCGGG GCCTTGACCTCTGGAGTGCACACA TTTCCAGCTGTACTGCAGTCATCT GGACTCTACAGCCTGTCCAGTGTG GTCACCGTACCTTCCTCCAACTTT GGCACTCAAACATATACATGTAAC GTGGATCATAAGCCCTCTAACACC AAAGTGGATAAAACTGTGGAGCGT AAGTGTTGTGTCGAGTGTCCTCCT TGTCCTGCTCCTCCTGTGGCAGGC CCATCTGTGTTTCTCTTTCCCCCAA AGCCAAAGGACACTTTGATGATAT CCCGGACCCCTGAGGTGACTTGC GTCGTCGTAGATGTTTCACACGAA GATCCAGAGGTGCAGTTCAACTGG TACGTGGATGGCGTGGAAGTGCA TAATGCCAAGACAAAGCCCCGCGA AGAGCAGTTTAATTCCACCTTCCG CGTGGTGTCTGTGCTGACCGTGG TACATCAGGATTGGCTTAACGGTA AGGAGTACAAGTGCAAGGTGAGTA ACAAGGGGCTGCCCGCCCCTATC GAGAAGACTATCAGTAAAACCAAG GGCCAGCCAAGGGAGCCACAGGT GTACACACTTCCACCATCTAGGGA GGAAATGACAAAGAACCAGGTGA GTTTGACCTGTCTCGTGAAAGGCT TTTATCCCAGTGATATAGCCGTGG AATGGGAAAGTAACGGGCAGCCC GAGAACAACTATAAGACCACACCA CCCATGCTGGACTCCGACGGTTCT TTCTTCCTTTATAGCAAGCTGACA GTGGATAAATCCAGGTGGCAGCA GGGTAACGTATTCAGTTGCAGTGT CATGCACGAGGCACTCCACAACCA

			CTATACTCAGAAAAGTCTTTCCCT GAGTCCAGGCAAG

SEQ ID 2435	QVQLQQSGPGLVKPSQ TLSLTCAISGDSVSSKSA AWNWIRQSPSRGLEWL GRTYYRSKWNNDYALS VKSRITINPDTSKNQFSL QLKSVTPEDTALYYCVR QVAGGMDVWGQGTTV TVSSASTKGPSVFPLAP CSRSTSESTAALGCLVK DYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLY SLSSVVTVPSSNFGTQT YTCNVDHKPSNTKVDKT VERKCCVECPPCPAPP VAGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSH EDPEVQFNWYVDGVEV HNAKTKPREEQFNSTFR VVSVLTVVHQDWLNGK EYKCKVSNKGLPAPIEK TISKTKGQPREPQVYTL PPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNG QPENNYKTTPPMLDSD GSFFLYSKLTVDKSRW QQGNVFSCSVMHEALH NHYTQKSLSLSPGK	SEQ ID 2543	CAGGTACAGCTGCAGCAGTCAGG TCCAGGACTGGTGAAGCCCTCGC AGACCCTCTCACTCACCTGTGCCA TCTCCGGGGACAGTGTCTCTAGCA AAAGTGCTGCTTGGAACTGGATCA GGCAGTCCCCATCGAGAGGCCTT GAGTGGCTGGGAAGGACATACTA CAGGTCCAAATGGAATAATGATTA TGCATTATCTGTGAAAAGTCGAAT AACCATCAACCCAGACACATCCAA GAACCAGTTCTCCCTGCAGCTGAA GTCTGTGACTCCCGAGGACACGG CTCTGTATTACTGTGTAAGACAAG TCGCGGGCGGTATGGACGTCTGG GGCCAAGGGACCACGGTCACCGT CTCCTCAGCAAGCACAAAAGGTCC TTCAGTGTTCCCTCTGGCACCTTG CTCACGCAGCACCTCTGAGAGTAC AGCCGCCCTGGGCTGCCTGGTAA AGGACTACTTTCCCGAACCAGTCA CTGTGTCCTGGAATAGCGGGGCC TTGACCTCTGGAGTGCACACATTT CCAGCTGTACTGCAGTCATCTGGA CTCTACAGCCTGTCCAGTGTGGTC ACCGTACCTTCCTCCAACTTTGGC ACTCAAACATATACATGTAACGTG GATCATAAGCCCTCTAACACCAAA GTGGATAAAACTGTGGAGCGTAAG TGTTGTGTCGAGTGTCCTCCTTGT CCTGCTCCTCCTGTGGCAGGCCC ATCTGTGTTTCTCTTTCCCCCAAAG CCAAAGGACACTTTGATGATATCC CGGACCCCTGAGGTGACTTGCGT CGTCGTAGATGTTTCACACGAAGA TCCAGAGGTGCAGTTCAACTGGTA CGTGGATGGCGTGGAAGTGCATA ATGCCAAGACAAAGCCCCGCGAA GAGCAGTTTAATTCCACCTTCCGC GTGGTGTCTGTGCTGACCGTGGTA CATCAGGATTGGCTTAACGGTAAG GAGTACAAGTGCAAGGTGAGTAAC AAGGGGCTGCCCGCCCCTATCGA GAAGACTATCAGTAAAACCAAGGG CCAGCCAAGGGAGCCACAGGTGT ACACACTTCCACCATCTAGGGAGG AAATGACAAAGAACCAGGTGAGTT TGACCTGTCTCGTGAAAGGCTTTT ATCCCAGTGATATAGCCGTGGAAT GGGAAAGTAACGGGCAGCCCGAG AACAACTATAAGACCACACCACCC ATGCTGGACTCCGACGGTTCTTTC TTCCTTTATAGCAAGCTGACAGTG GATAAATCCAGGTGGCAGCAGGG TAACGTATTCAGTTGCAGTGTCAT GCACGAGGCACTCCACAACCACTA

			TACTCAGAAAAGTCTTTCCCTGAG TCCAGGCAAG

SEQ ID 2436	QVQLVQSGGGLVQPGR SLRLSCTASGFTFGDYA MSWFRQAPGKGLEWV SAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCAK GSVYSGSYYMLIDYWG QGTLVTVSSASTKGPSV FPLAPCSRSTSESTAAL GCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSN FGTQTYTCNVDHKPSN TKVDKTVERKCCVECPP CPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVV VDVSHEDPEVQFNWYV DGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQD WLNGKEYKCKVSNKGL PAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPP MLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVM HEALHNHYTQKSLSLSP GK	SEQ ID 2544	CAGGTGCAGCTGGTGCAATCTGG GGGAGGCTTGGTACAGCCAGGGC GGTCCCTGAGACTCTCCTGTACAG CTTCTGGATTCACCTTTGGTGATTA TGCTATGAGCTGGTTCCGCCAGG CTCCAGGGAAGGGGCTGGAGTGG GTCTCAGCTATTAGTGGTAGTGGT GGTAGCACATACTATGCAGACTCC GTGAAGGGCCGATTCACCATCTCC AGAGACAATTCCAAGAACACGCTG TATCTGCAAATGAACAGCCTGAGA GCTGAGGACACGGCTGTGTATTAC TGTGCGAAAGGATCGGTATATAGT GGGAGCTACTATATGCTCATTGAC TACTGGGGCCAGGGCACCCTGGT CACCGTCTCCTCAGCAAGCACAAA AGGTCCTTCAGTGTTCCCTCTGGC ACCTTGCTCACGCAGCACCTCTGA GAGTACAGCCGCCCTGGGCTGCC TGGTAAAGGACTACTTTCCCGAAC CAGTCACTGTGTCCTGGAATAGCG GGGCCTTGACCTCTGGAGTGCAC ACATTTCCAGCTGTACTGCAGTCA TCTGGACTCTACAGCCTGTCCAGT GTGGTCACCGTACCTTCCTCCAAC TTTGGCACTCAAACATATACATGTA ACGTGGATCATAAGCCCTCTAACA CCAAAGTGGATAAAACTGTGGAGC GTAAGTGTTGTGTCGAGTGTCCTC CTTGTCCTGCTCCTCCTGTGGCAG GCCCATCTGTGTTTCTCTTTCCCC CAAAGCCAAAGGACACTTTGATGA TATCCCGGACCCCTGAGGTGACTT GCGTCGTCGTAGATGTTTCACACG AAGATCCAGAGGTGCAGTTCAACT GGTACGTGGATGGCGTGGAAGTG CATAATGCCAAGACAAAGCCCCGC GAAGAGCAGTTTAATTCCACCTTC CGCGTGGTGTCTGTGCTGACCGT GGTACATCAGGATTGGCTTAACGG TAAGGAGTACAAGTGCAAGGTGAG TAACAAGGGGCTGCCCGCCCCTA TCGAGAAGACTATCAGTAAAACCA AGGGCCAGCCAAGGGAGCCACAG GTGTACACACTTCCACCATCTAGG GAGGAAATGACAAAGAACCAGGT GAGTTTGACCTGTCTCGTGAAAGG CTTTTATCCCAGTGATATAGCCGT GGAATGGGAAAGTAACGGGCAGC CCGAGAACAACTATAAGACCACAC CACCCATGCTGGACTCCGACGGTT CTTTCTTCCTTTATAGCAAGCTGAC AGTGGATAAATCCAGGTGGCAGCA GGGTAACGTATTCAGTTGCAGTGT CATGCACGAGGCACTCCACAACCA

			CTATACTCAGAAAAGTCTTTCCCT GAGTCCAGGCAAG

SEQ ID 2437	QVQLQQSGPGLVRPSQ TLSLTCVISGDSVSSGS AAWNWIRQSPSRGLEW LGRTYYRAKWYNEYAG SVKSRITISPDTSKNQFS LQLNSVTPEDTAVYFCT RQDKDNTRYSGLGVWG QGTTVTVSSASTKGPSV FPLAPCSRSTSESTAAL GCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSN FGTQTYTCNVDHKPSN TKVDKTVERKCCVECPP CPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVV VDVSHEDPEVQFNWYV DGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQD WLNGKEYKCKVSNKGL PAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPP MLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVM HEALHNHYTQKSLSLSP GK	SEQ ID 2545	CAGGTACAGCTGCAGCAGTCAGG TCCAGGACTGGTGAGGCCCTCGC AGACCCTCTCACTCACCTGTGTCA TCTCCGGGGACAGTGTCTCTAGC GGCAGTGCTGCTTGGAACTGGAT CAGGCAGTCCCCATCGAGAGGCC TTGAGTGGCTGGGAAGGACATATT ATAGGGCCAAGTGGTATAATGAAT ATGCAGGGTCTGTGAAAAGCCGAA TAACCATCAGTCCGGACACATCCA AGAACCAGTTCTCCCTGCAACTGA ACTCTGTGACTCCCGAGGACACG GCTGTGTATTTCTGTACAAGACAA GACAAAGACAACACGAGATATTCC GGTTTGGGCGTCTGGGGCCAAGG GACCACGGTGACCGTCTCCTCAG CAAGCACAAAAGGTCCTTCAGTGT TCCCTCTGGCACCTTGCTCACGCA GCACCTCTGAGAGTACAGCCGCC CTGGGCTGCCTGGTAAAGGACTA CTTTCCCGAACCAGTCACTGTGTC CTGGAATAGCGGGGCCTTGACCT CTGGAGTGCACACATTTCCAGCTG TACTGCAGTCATCTGGACTCTACA GCCTGTCCAGTGTGGTCACCGTAC CTTCCTCCAACTTTGGCACTCAAA CATATACATGTAACGTGGATCATA AGCCCTCTAACACCAAAGTGGATA AAACTGTGGAGCGTAAGTGTTGTG TCGAGTGTCCTCCTTGTCCTGCTC CTCCTGTGGCAGGCCCATCTGTGT TTCTCTTTCCCCCAAAGCCAAAGG ACACTTTGATGATATCCCGGACCC CTGAGGTGACTTGCGTCGTCGTAG ATGTTTCACACGAAGATCCAGAGG TGCAGTTCAACTGGTACGTGGATG GCGTGGAAGTGCATAATGCCAAGA CAAAGCCCCGCGAAGAGCAGTTTA ATTCCACCTTCCGCGTGGTGTCTG TGCTGACCGTGGTACATCAGGATT GGCTTAACGGTAAGGAGTACAAGT GCAAGGTGAGTAACAAGGGGCTG CCCGCCCCTATCGAGAAGACTATC AGTAAAACCAAGGGCCAGCCAAG GGAGCCACAGGTGTACACACTTCC ACCATCTAGGGAGGAAATGACAAA GAACCAGGTGAGTTTGACCTGTCT CGTGAAAGGCTTTTATCCCAGTGA TATAGCCGTGGAATGGGAAAGTAA CGGGCAGCCCGAGAACAACTATA AGACCACACCACCCATGCTGGACT CCGACGGTTCTTTCTTCCTTTATAG CAAGCTGACAGTGGATAAATCCAG GTGGCAGCAGGGTAACGTATTCA GTTGCAGTGTCATGCACGAGGCA

			CTCCACAACCACTATACTCAGAAA AGTCTTTCCCTGAGTCCAGGCAAG

SEQ ID 2438	EVQLVETGGGLVQPGG SLRLSCAASEFTLRNYG VSWVRQAPGKGLEWVS GMSGSGYSTYYADSVK GRFTISRDSSKNTLFLQ MDSLRAEDTAIYYCARG PRMWSSGIDAFDIWGH GTMVTVSSASTKGPSVF PLAPCSRSTSESTAALG CLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSNF GTQTYTCNVDHKPSNT KVDKTVERKCCVECPP CPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVV VDVSHEDPEVQFNWYV DGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQD WLNGKEYKCKVSNKGL PAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPP MLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVM HEALHNHYTQKSLSLSP GK	SEQ ID 2546	GAGGTGCAGCTGGTGGAGACCGG GGGAGGCTTAGTTCAGCCTGGGG GGTCCCTGAGACTCTCCTGTGCAG CCTCTGAATTCACCCTTAGGAACT ATGGCGTGAGCTGGGTCCGCCAG GCTCCAGGGAAGGGGCTGGAGTG GGTCTCAGGTATGAGTGGTAGTG GTTATAGTACATACTACGCAGACT CCGTGAAGGGCCGGTTCACCATC TCCAGAGACAGTTCCAAGAACACG CTGTTTCTGCAAATGGACAGCCTG AGAGCCGAGGACACGGCCATATA TTACTGTGCGAGAGGGCCCCGAA TGTGGAGCAGTGGCATTGATGCTT TTGATATCTGGGGCCACGGGACAA TGGTGACCGTCTCTTCAGCAAGCA CAAAAGGTCCTTCAGTGTTCCCTC TGGCACCTTGCTCACGCAGCACCT CTGAGAGTACAGCCGCCCTGGGC TGCCTGGTAAAGGACTACTTTCCC GAACCAGTCACTGTGTCCTGGAAT AGCGGGGCCTTGACCTCTGGAGT GCACACATTTCCAGCTGTACTGCA GTCATCTGGACTCTACAGCCTGTC CAGTGTGGTCACCGTACCTTCCTC CAACTTTGGCACTCAAACATATAC ATGTAACGTGGATCATAAGCCCTC TAACACCAAAGTGGATAAAACTGT GGAGCGTAAGTGTTGTGTCGAGT GTCCTCCTTGTCCTGCTCCTCCTG TGGCAGGCCCATCTGTGTTTCTCT TTCCCCCAAAGCCAAAGGACACTT TGATGATATCCCGGACCCCTGAGG TGACTTGCGTCGTCGTAGATGTTT CACACGAAGATCCAGAGGTGCAG TTCAACTGGTACGTGGATGGCGTG GAAGTGCATAATGCCAAGACAAAG CCCCGCGAAGAGCAGTTTAATTCC ACCTTCCGCGTGGTGTCTGTGCTG ACCGTGGTACATCAGGATTGGCTT AACGGTAAGGAGTACAAGTGCAAG GTGAGTAACAAGGGGCTGCCCGC CCCTATCGAGAAGACTATCAGTAA AACCAAGGGCCAGCCAAGGGAGC CACAGGTGTACACACTTCCACCAT CTAGGGAGGAAATGACAAAGAACC AGGTGAGTTTGACCTGTCTCGTGA AAGGCTTTTATCCCAGTGATATAG CCGTGGAATGGGAAAGTAACGGG CAGCCCGAGAACAACTATAAGACC ACACCACCCATGCTGGACTCCGAC GGTTCTTTCTTCCTTTATAGCAAGC TGACAGTGGATAAATCCAGGTGGC AGCAGGGTAACGTATTCAGTTGCA GTGTCATGCACGAGGCACTCCACA

			ACCACTATACTCAGAAAAGTCTTTC CCTGAGTCCAGGCAAG

SEQ ID 2439	QVQLQQWGAGLLKPSE TLSLTCAVYGGSVSGYY WSWIRQPPGKGLEWM GEIHHSGSTNYNPSLKS RVTISLDTPKNQFSLKLS SVTAADTAVYYCARRD WAGKRVWGQGTLVTVS SASTKGPSVFPLAPCSR STSESTAALGCLVKDYF PEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLS SVVTVPSSNFGTQTYTC NVDHKPSNTKVDKTVE RKCCVECPPCPAPPVA GPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHED PEVQFNWYVDGVEVHN AKTKPREEQFNSTFRVV SVLTVVHQDWLNGKEY KCKVSNKGLPAPIEKTIS KTKGQPREPQVYTLPPS REEMTKNQVSLTCLVK GFYPSDIAVEWESNGQ PENNYKTTPPMLDSDG SFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHN HYTQKSLSLSPGK	SEQ ID 2547	CAGGTGCAGCTACAGCAGTGGGG CGCAGGACTGTTGAAGCCTTCGG AGACCCTGTCCCTCACCTGCGCTG TCTATGGTGGGTCCGTCAGTGGTT ACTACTGGAGCTGGATCCGCCAG CCCCCAGGGAAGGGGCTGGAGTG GATGGGGGAAATCCATCATAGTGG AAGCACCAACTACAACCCGTCCCT CAAGAGTCGAGTCACCATATCACT AGACACGCCCAAGAACCAGTTCTC CCTGAAGCTAAGCTCTGTGACCGC CGCGGACACGGCTGTATATTACTG TGCGAGACGGGATTGGGCAGGAA AAAGGGTCTGGGGCCAGGGAACC CTGGTCACCGTCTCCTCAGCAAGC ACAAAAGGTCCTTCAGTGTTCCCT CTGGCACCTTGCTCACGCAGCAC CTCTGAGAGTACAGCCGCCCTGG GCTGCCTGGTAAAGGACTACTTTC CCGAACCAGTCACTGTGTCCTGGA ATAGCGGGGCCTTGACCTCTGGA GTGCACACATTTCCAGCTGTACTG CAGTCATCTGGACTCTACAGCCTG TCCAGTGTGGTCACCGTACCTTCC TCCAACTTTGGCACTCAAACATATA CATGTAACGTGGATCATAAGCCCT CTAACACCAAAGTGGATAAAACTG TGGAGCGTAAGTGTTGTGTCGAGT GTCCTCCTTGTCCTGCTCCTCCTG TGGCAGGCCCATCTGTGTTTCTCT TTCCCCCAAAGCCAAAGGACACTT TGATGATATCCCGGACCCCTGAGG TGACTTGCGTCGTCGTAGATGTTT CACACGAAGATCCAGAGGTGCAG TTCAACTGGTACGTGGATGGCGTG GAAGTGCATAATGCCAAGACAAAG CCCCGCGAAGAGCAGTTTAATTCC ACCTTCCGCGTGGTGTCTGTGCTG ACCGTGGTACATCAGGATTGGCTT AACGGTAAGGAGTACAAGTGCAAG GTGAGTAACAAGGGGCTGCCCGC CCCTATCGAGAAGACTATCAGTAA AACCAAGGGCCAGCCAAGGGAGC CACAGGTGTACACACTTCCACCAT CTAGGGAGGAAATGACAAAGAACC AGGTGAGTTTGACCTGTCTCGTGA AAGGCTTTTATCCCAGTGATATAG CCGTGGAATGGGAAAGTAACGGG CAGCCCGAGAACAACTATAAGACC ACACCACCCATGCTGGACTCCGAC GGTTCTTTCTTCCTTTATAGCAAGC TGACAGTGGATAAATCCAGGTGGC AGCAGGGTAACGTATTCAGTTGCA GTGTCATGCACGAGGCACTCCACA ACCACTATACTCAGAAAAGTCTTTC CCTGAGTCCAGGCAAG

SEQ ID 2440	QVQLQQSGPGLLKPSQ TLSLTCAISGDSVSSNTA TWNWIRQSPSRGLEWL GRTYYRSKWYKDNALS VKSRITINPDTSKNQFSL QLNSVTPEDTAVYYCAG GRAGIAAFDIWGQGTTV TVSSASTKGPSVFPLAP CSRSTSESTAALGCLVK DYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLY SLSSVVTVPSSNFGTQT YTCNVDHKPSNTKVDKT VERKCCVECPPCPAPP VAGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSH EDPEVQFNWYVDGVEV HNAKTKPREEQFNSTFR VVSVLTVVHQDWLNGK EYKCKVSNKGLPAPIEK TISKTKGQPREPQVYTL PPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNG QPENNYKTTPPMLDSD GSFFLYSKLTVDKSRW QQGNVFSCSVMHEALH NHYTQKSLSLSPGK	SEQ ID 2548	CAGGTACAGCTGCAGCAGTCAGG TCCAGGACTATTAAAGCCCTCGCA GACCCTCTCACTCACCTGTGCCAT CTCCGGGGACAGTGTCTCTAGCAA CACTGCTACTTGGAACTGGATCAG GCAGTCCCCATCGAGAGGCCTTG AGTGGCTGGGAAGGACATACTACA GGTCCAAGTGGTATAAGGATAATG CACTGTCTGTGAAAAGTCGAATAA CCATCAACCCAGACACATCCAAGA ACCAGTTCTCCCTGCAGCTGAACT CTGTGACTCCCGAGGACACGGCT GTGTATTACTGTGCAGGAGGTCGG GCTGGTATTGCCGCTTTTGATATC TGGGGCCAAGGGACCACGGTCAC CGTCTCCTCAGCAAGCACAAAAGG TCCTTCAGTGTTCCCTCTGGCACC TTGCTCACGCAGCACCTCTGAGAG TACAGCCGCCCTGGGCTGCCTGG TAAAGGACTACTTTCCCGAACCAG TCACTGTGTCCTGGAATAGCGGG GCCTTGACCTCTGGAGTGCACACA TTTCCAGCTGTACTGCAGTCATCT GGACTCTACAGCCTGTCCAGTGTG GTCACCGTACCTTCCTCCAACTTT GGCACTCAAACATATACATGTAAC GTGGATCATAAGCCCTCTAACACC AAAGTGGATAAAACTGTGGAGCGT AAGTGTTGTGTCGAGTGTCCTCCT TGTCCTGCTCCTCCTGTGGCAGGC CCATCTGTGTTTCTCTTTCCCCCAA AGCCAAAGGACACTTTGATGATAT CCCGGACCCCTGAGGTGACTTGC GTCGTCGTAGATGTTTCACACGAA GATCCAGAGGTGCAGTTCAACTGG TACGTGGATGGCGTGGAAGTGCA TAATGCCAAGACAAAGCCCCGCGA AGAGCAGTTTAATTCCACCTTCCG CGTGGTGTCTGTGCTGACCGTGG TACATCAGGATTGGCTTAACGGTA AGGAGTACAAGTGCAAGGTGAGTA ACAAGGGGCTGCCCGCCCCTATC GAGAAGACTATCAGTAAAACCAAG GGCCAGCCAAGGGAGCCACAGGT GTACACACTTCCACCATCTAGGGA GGAAATGACAAAGAACCAGGTGA GTTTGACCTGTCTCGTGAAAGGCT TTTATCCCAGTGATATAGCCGTGG AATGGGAAAGTAACGGGCAGCCC GAGAACAACTATAAGACCACACCA CCCATGCTGGACTCCGACGGTTCT TTCTTCCTTTATAGCAAGCTGACA GTGGATAAATCCAGGTGGCAGCA GGGTAACGTATTCAGTTGCAGTGT CATGCACGAGGCACTCCACAACCA

			CTATACTCAGAAAAGTCTTTCCCT GAGTCCAGGCAAG

SEQ ID 2441	QVQLVQSGGGLIQPGG SLRLSCAASGFTVSSNY MSWVRQAPGKGLEWV SLIYSDGRTNYADSVKG RFTISRDNSKNTLYLQM NSLRAEDTAVYYCAKGA LQGEWRRFDYWGQGT LVTVSSASTKGPSVFPL APCSRSTSESTAALGCL VKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSG LYSLSSVVTVPSSNFGT QTYTCNVDHKPSNTKV DKTVERKCCVECPPCP APPVAGPSVFLFPPKPK DTLMISRTPEVTCVVVD VSHEDPEVQFNWYVDG VEVHNAKTKPREEQFN STFRVVSVLTVVHQDWL NGKEYKCKVSNKGLPA PIEKTISKTKGQPREPQV YTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWE SNGQPENNYKTTPPML DSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK	SEQ ID 2549	CAGGTGCAGCTGGTGCAATCTGG AGGAGGCTTGATCCAGCCTGGGG GGTCCCTGAGACTCTCCTGTGCAG CCTCTGGGTTCACCGTCAGTAGCA ACTACATGAGCTGGGTCCGCCAG GCTCCAGGGAAGGGGCTGGAATG GGTCTCACTTATTTATAGTGATGGT CGCACAAACTATGCAGACTCCGTG AAGGGCCGATTCACCATCTCCAGA GACAATTCCAAGAACACGCTGTAT CTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCCGTATATTACTGT GCGAAGGGGGCCCTACAGGGCGA ATGGCGGAGATTTGACTACTGGG GCCAGGGCACCCTGGTCACCGTC TCCTCAGCAAGCACAAAAGGTCCT TCAGTGTTCCCTCTGGCACCTTGC TCACGCAGCACCTCTGAGAGTACA GCCGCCCTGGGCTGCCTGGTAAA GGACTACTTTCCCGAACCAGTCAC TGTGTCCTGGAATAGCGGGGCCTT GACCTCTGGAGTGCACACATTTCC AGCTGTACTGCAGTCATCTGGACT CTACAGCCTGTCCAGTGTGGTCAC CGTACCTTCCTCCAACTTTGGCAC TCAAACATATACATGTAACGTGGA TCATAAGCCCTCTAACACCAAAGT GGATAAAACTGTGGAGCGTAAGTG TTGTGTCGAGTGTCCTCCTTGTCC TGCTCCTCCTGTGGCAGGCCCATC TGTGTTTCTCTTTCCCCCAAAGCC AAAGGACACTTTGATGATATCCCG GACCCCTGAGGTGACTTGCGTCG TCGTAGATGTTTCACACGAAGATC CAGAGGTGCAGTTCAACTGGTACG TGGATGGCGTGGAAGTGCATAATG CCAAGACAAAGCCCCGCGAAGAG CAGTTTAATTCCACCTTCCGCGTG GTGTCTGTGCTGACCGTGGTACAT CAGGATTGGCTTAACGGTAAGGAG TACAAGTGCAAGGTGAGTAACAAG GGGCTGCCCGCCCCTATCGAGAA GACTATCAGTAAAACCAAGGGCCA GCCAAGGGAGCCACAGGTGTACA CACTTCCACCATCTAGGGAGGAAA TGACAAAGAACCAGGTGAGTTTGA CCTGTCTCGTGAAAGGCTTTTATC CCAGTGATATAGCCGTGGAATGG GAAAGTAACGGGCAGCCCGAGAA CAACTATAAGACCACACCACCCAT GCTGGACTCCGACGGTTCTTTCTT CCTTTATAGCAAGCTGACAGTGGA TAAATCCAGGTGGCAGCAGGGTAA CGTATTCAGTTGCAGTGTCATGCA CGAGGCACTCCACAACCACTATAC

			TCAGAAAAGTCTTTCCCTGAGTCC AGGCAAG

SEQ ID 2442	QVQLQQSGPGLVKPSQ TLSLTCAISGDSVSSNS AAWNWIRQSPSRGLEW LGRTYYRSKWYNDYAV SVKSRITINPDTSKNQFS LQLNSVTPEDTAVYYCT RTNQGYGGNSGVFDY WGQGTLVTVSSASTKG PSVFPLAPCSRSTSEST AALGCLVKDYFPEPVTV SWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVP SSNFGTQTYTCNVDHK PSNTKVDKTVERKCCVE CPPCPAPPVAGPSVFLF PPKPKDTLMISRTPEVT CVVVDVSHEDPEVQFN WYVDGVEVHNAKTKPR EEQFNSTFRVVSVLTVV HQDWLNGKEYKCKVSN KGLPAPIEKTISKTKGQP REPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDI AVEWESNGQPENNYKT TPPMLDSDGSFFLYSKL TVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSL SPGK	SEQ ID 2550	CAGGTGCAGCTACAGCAGTCAGG TCCAGGACTGGTGAAGCCCTCGC AGACCCTCTCACTCACCTGTGCCA TCTCCGGGGACAGTGTCTCTAGCA ACAGTGCTGCTTGGAACTGGATCA GGCAGTCCCCATCGAGAGGCCTT GAGTGGCTGGGAAGGACATATTAC AGGTCCAAGTGGTATAATGATTAT GCAGTATCTGTGAAAAGTCGAATA ACCATCAACCCAGACACATCCAAG AACCAGTTCTCCCTGCAGCTGAAC TCTGTGACTCCCGAGGACACGGC TGTGTATTACTGTACAAGAACCAA CCAGGGATACGGTGGTAACTCCG GGGTATTTGACTACTGGGGCCAG GGAACCCTGGTCACCGTCTCCTCA GCAAGCACAAAAGGTCCTTCAGTG TTCCCTCTGGCACCTTGCTCACGC AGCACCTCTGAGAGTACAGCCGC CCTGGGCTGCCTGGTAAAGGACT ACTTTCCCGAACCAGTCACTGTGT CCTGGAATAGCGGGGCCTTGACC TCTGGAGTGCACACATTTCCAGCT GTACTGCAGTCATCTGGACTCTAC AGCCTGTCCAGTGTGGTCACCGTA CCTTCCTCCAACTTTGGCACTCAA ACATATACATGTAACGTGGATCAT AAGCCCTCTAACACCAAAGTGGAT AAAACTGTGGAGCGTAAGTGTTGT GTCGAGTGTCCTCCTTGTCCTGCT CCTCCTGTGGCAGGCCCATCTGT GTTTCTCTTTCCCCCAAAGCCAAA GGACACTTTGATGATATCCCGGAC CCCTGAGGTGACTTGCGTCGTCGT AGATGTTTCACACGAAGATCCAGA GGTGCAGTTCAACTGGTACGTGGA TGGCGTGGAAGTGCATAATGCCAA GACAAAGCCCCGCGAAGAGCAGT TTAATTCCACCTTCCGCGTGGTGT CTGTGCTGACCGTGGTACATCAGG ATTGGCTTAACGGTAAGGAGTACA AGTGCAAGGTGAGTAACAAGGGG CTGCCCGCCCCTATCGAGAAGACT ATCAGTAAAACCAAGGGCCAGCCA AGGGAGCCACAGGTGTACACACTT CCACCATCTAGGGAGGAAATGACA AAGAACCAGGTGAGTTTGACCTGT CTCGTGAAAGGCTTTTATCCCAGT GATATAGCCGTGGAATGGGAAAGT AACGGGCAGCCCGAGAACAACTA TAAGACCACACCACCCATGCTGGA CTCCGACGGTTCTTTCTTCCTTTAT AGCAAGCTGACAGTGGATAAATCC AGGTGGCAGCAGGGTAACGTATT CAGTTGCAGTGTCATGCACGAGG CACTCCACAACCACTATACTCAGA

			AAAGTCTTTCCCTGAGTCCAGGCAAG

SEQ ID 2443	QVQLQQSGPGLVKPSQ TLSLTCAISGDSVSGNS AAWNWIRQSPSRGLEW LGRTYYRSKWYNDYAV SVKSRITINPDTSKNQFS LQLNSVTPEDTAVYYCA RIVGGAVDCWGQGTLV TVSSASTKGPSVFPLAP CSRSTSESTAALGCLVK DYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLY SLSSVVTVPSSNFGTQT YTCNVDHKPSNTKVDKT VERKCCVECPPCPAPP VAGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSH EDPEVQFNWYVDGVEV HNAKTKPREEQFNSTFR VVSVLTVVHQDWLNGK EYKCKVSNKGLPAPIEK TISKTKGQPREPQVYTL PPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNG QPENNYKTTPPMLDSD GSFFLYSKLTVDKSRW QQGNVFSCSVMHEALH NHYTQKSLSLSPGK	SEQ ID 2551	CAGGTGCAGCTACAGCAGTCAGG TCCAGGACTGGTGAAGCCCTCGC AGACCCTCTCACTCACCTGTGCCA TCTCCGGGGACAGTGTCTCTGGC AACAGTGCTGCTTGGAACTGGATC AGGCAGTCCCCATCGAGAGGCCT TGAGTGGCTGGGAAGGACATACTA CAGGTCCAAGTGGTATAATGATTA TGCAGTATCTGTGAAAAGTCGAAT AACCATCAACCCAGACACATCCAA GAACCAGTTCTCCCTGCAGTTGAA TTCTGTGACTCCCGAGGACACGG CTGTGTATTACTGTGCGAGGATAG TGGGAGGTGCCGTTGACTGCTGG GGCCAGGGAACCCTGGTGACCGT CTCCTCAGCAAGCACAAAAGGTCC TTCAGTGTTCCCTCTGGCACCTTG CTCACGCAGCACCTCTGAGAGTAC AGCCGCCCTGGGCTGCCTGGTAA AGGACTACTTTCCCGAACCAGTCA CTGTGTCCTGGAATAGCGGGGCC TTGACCTCTGGAGTGCACACATTT CCAGCTGTACTGCAGTCATCTGGA CTCTACAGCCTGTCCAGTGTGGTC ACCGTACCTTCCTCCAACTTTGGC ACTCAAACATATACATGTAACGTG GATCATAAGCCCTCTAACACCAAA GTGGATAAAACTGTGGAGCGTAAG TGTTGTGTCGAGTGTCCTCCTTGT CCTGCTCCTCCTGTGGCAGGCCC ATCTGTGTTTCTCTTTCCCCCAAAG CCAAAGGACACTTTGATGATATCC CGGACCCCTGAGGTGACTTGCGT CGTCGTAGATGTTTCACACGAAGA TCCAGAGGTGCAGTTCAACTGGTA CGTGGATGGCGTGGAAGTGCATA ATGCCAAGACAAAGCCCCGCGAA GAGCAGTTTAATTCCACCTTCCGC GTGGTGTCTGTGCTGACCGTGGTA CATCAGGATTGGCTTAACGGTAAG GAGTACAAGTGCAAGGTGAGTAAC AAGGGGCTGCCCGCCCCTATCGA GAAGACTATCAGTAAAACCAAGGG CCAGCCAAGGGAGCCACAGGTGT ACACACTTCCACCATCTAGGGAGG AAATGACAAAGAACCAGGTGAGTT TGACCTGTCTCGTGAAAGGCTTTT ATCCCAGTGATATAGCCGTGGAAT GGGAAAGTAACGGGCAGCCCGAG AACAACTATAAGACCACACCACCC ATGCTGGACTCCGACGGTTCTTTC TTCCTTTATAGCAAGCTGACAGTG GATAAATCCAGGTGGCAGCAGGG TAACGTATTCAGTTGCAGTGTCAT GCACGAGGCACTCCACAACCACTA

			TACTCAGAAAAGTCTTTCCCTGAG TCCAGGCAAG

SEQ ID 2444	EVQLVQSGAEVKKPGA SVKVSCKASGYTFTSYA MHWVRQAPGQRLEWM GWINAGNGNTKYSQKF QGRVTITRDTSASTAYM ELSSLRSEDTAVYYCAR VRVGATTVYDSWFDPW GQGTLVTVSSASTKGPS VFPLAPCSRSTSESTAA LGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSN FGTQTYTCNVDHKPSN TKVDKTVERKCCVECPP CPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVV VDVSHEDPEVQFNWYV DGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQD WLNGKEYKCKVSNKGL PAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPP MLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVM HEALHNHYTQKSLSLSP GK	SEQ ID 2552	GAGGTGCAGCTGGTGCAGTCTGG GGCTGAGGTGAAGAAGCCTGGGG CCTCAGTGAAGGTTTCCTGCAAGG CTTCTGGATACACCTTCACTAGCT ATGCTATGCATTGGGTGCGCCAG GCCCCCGGACAAAGGCTTGAGTG GATGGGATGGATCAACGCTGGCA ATGGTAACACAAAATATTCACAGA AGTTCCAGGGCAGAGTCACCATTA CCAGGGACACATCCGCGAGCACA GCCTACATGGAGCTGAGCAGCCT GAGATCTGAAGACACGGCTGTGTA TTACTGTGCGAGAGTTAGAGTGGG AGCTACTACTGTTTACGACAGCTG GTTCGACCCCTGGGGCCAGGGAA CCCTGGTGACCGTCTCCTCAGCAA GCACAAAAGGTCCTTCAGTGTTCC CTCTGGCACCTTGCTCACGCAGCA CCTCTGAGAGTACAGCCGCCCTG GGCTGCCTGGTAAAGGACTACTTT CCCGAACCAGTCACTGTGTCCTGG AATAGCGGGGCCTTGACCTCTGG AGTGCACACATTTCCAGCTGTACT GCAGTCATCTGGACTCTACAGCCT GTCCAGTGTGGTCACCGTACCTTC CTCCAACTTTGGCACTCAAACATA TACATGTAACGTGGATCATAAGCC CTCTAACACCAAAGTGGATAAAAC TGTGGAGCGTAAGTGTTGTGTCGA GTGTCCTCCTTGTCCTGCTCCTCC TGTGGCAGGCCCATCTGTGTTTCT CTTTCCCCCAAAGCCAAAGGACAC TTTGATGATATCCCGGACCCCTGA GGTGACTTGCGTCGTCGTAGATGT TTCACACGAAGATCCAGAGGTGCA GTTCAACTGGTACGTGGATGGCGT GGAAGTGCATAATGCCAAGACAAA GCCCCGCGAAGAGCAGTTTAATTC CACCTTCCGCGTGGTGTCTGTGCT GACCGTGGTACATCAGGATTGGCT TAACGGTAAGGAGTACAAGTGCAA GGTGAGTAACAAGGGGCTGCCCG CCCCTATCGAGAAGACTATCAGTA AAACCAAGGGCCAGCCAAGGGAG CCACAGGTGTACACACTTCCACCA TCTAGGGAGGAAATGACAAAGAAC CAGGTGAGTTTGACCTGTCTCGTG AAAGGCTTTTATCCCAGTGATATA GCCGTGGAATGGGAAAGTAACGG GCAGCCCGAGAACAACTATAAGAC CACACCACCCATGCTGGACTCCGA CGGTTCTTTCTTCCTTTATAGCAAG CTGACAGTGGATAAATCCAGGTGG CAGCAGGGTAACGTATTCAGTTGC AGTGTCATGCACGAGGCACTCCAC

			AACCACTATACTCAGAAAAGTCTTT CCCTGAGTCCAGGCAAG

SEQ ID 2445	QVQLVQSGGGLVQPGG SLRLSCAASGFTFSSYA MSWVRQAPGKGLEWV SAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCAK DGGSSPYYDSSGLLPW YFDLWGRGTLVTVSSA STKGPSVFPLAPCSRST SESTAALGCLVKDYFPE PVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSV VTVPSSNFGTQTYTCNV DHKPSNTKVDKTVERK CCVECPPCPAPPVAGP SVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEV QFNWYVDGVEVHNAKT KPREEQFNSTFRVVSVL TVVHQDWLNGKEYKCK VSNKGLPAPIEKTISKTK GQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFY PSDIAVEWESNGQPEN NYKTTPPMLDSDGSFFL YSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQ KSLSLSPGK	SEQ ID 2553	CAGGTGCAGCTGGTGCAGTCTGG GGGAGGCTTGGTACAGCCTGGGG GGTCCCTGAGACTCTCCTGTGCAG CCTCTGGATTCACCTTTAGCAGCT ATGCCATGAGCTGGGTCCGCCAG GCTCCAGGGAAGGGGCTGGAGTG GGTCTCAGCTATTAGTGGTAGTGG TGGTAGCACATACTACGCAGACTC CGTGAAGGGCCGGTTCACCATCT CCAGAGACAATTCCAAGAACACGC TGTATCTGCAAATGAACAGCCTGA GAGCCGAGGACACGGCCGTATAT TACTGTGCGAAAGATGGGGGGTC CAGCCCATACTATGATAGTAGTGG TTTACTACCCTGGTACTTCGATCTC TGGGGCCGTGGCACCCTGGTCAC CGTCTCCTCAGCAAGCACAAAAGG TCCTTCAGTGTTCCCTCTGGCACC TTGCTCACGCAGCACCTCTGAGAG TACAGCCGCCCTGGGCTGCCTGG TAAAGGACTACTTTCCCGAACCAG TCACTGTGTCCTGGAATAGCGGG GCCTTGACCTCTGGAGTGCACACA TTTCCAGCTGTACTGCAGTCATCT GGACTCTACAGCCTGTCCAGTGTG GTCACCGTACCTTCCTCCAACTTT GGCACTCAAACATATACATGTAAC GTGGATCATAAGCCCTCTAACACC AAAGTGGATAAAACTGTGGAGCGT AAGTGTTGTGTCGAGTGTCCTCCT TGTCCTGCTCCTCCTGTGGCAGGC CCATCTGTGTTTCTCTTTCCCCCAA AGCCAAAGGACACTTTGATGATAT CCCGGACCCCTGAGGTGACTTGC GTCGTCGTAGATGTTTCACACGAA GATCCAGAGGTGCAGTTCAACTGG TACGTGGATGGCGTGGAAGTGCA TAATGCCAAGACAAAGCCCCGCGA AGAGCAGTTTAATTCCACCTTCCG CGTGGTGTCTGTGCTGACCGTGG TACATCAGGATTGGCTTAACGGTA AGGAGTACAAGTGCAAGGTGAGTA ACAAGGGGCTGCCCGCCCCTATC GAGAAGACTATCAGTAAAACCAAG GGCCAGCCAAGGGAGCCACAGGT GTACACACTTCCACCATCTAGGGA GGAAATGACAAAGAACCAGGTGA GTTTGACCTGTCTCGTGAAAGGCT TTTATCCCAGTGATATAGCCGTGG AATGGGAAAGTAACGGGCAGCCC GAGAACAACTATAAGACCACACCA CCCATGCTGGACTCCGACGGTTCT TTCTTCCTTTATAGCAAGCTGACA GTGGATAAATCCAGGTGGCAGCA GGGTAACGTATTCAGTTGCAGTGT CATGCACGAGGCACTCCACAACCA

			CTATACTCAGAAAAGTCTTTCCCT GAGTCCAGGCAAG

SEQ ID 2446	QVQLQESGGGLVQPGG SLRLSCAASGFTFSSYA MHWVRQAPGKGLEYVS AISSNGGSTYYANSVKG RFTISRDNSKNTLYLQM GSLRAEDMAVYYCARA KFWTYYFDYWGQGTLV TVSSASTKGPSVFPLAP CSRSTSESTAALGCLVK DYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLY SLSSVVTVPSSNFGTQT YTCNVDHKPSNTKVDKT VERKCCVECPPCPAPP VAGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSH EDPEVQFNWYVDGVEV HNAKTKPREEQFNSTFR VVSVLTVVHQDWLNGK EYKCKVSNKGLPAPIEK TISKTKGQPREPQVYTL PPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNG QPENNYKTTPPMLDSD GSFFLYSKLTVDKSRW QQGNVFSCSVMHEALH NHYTQKSLSLSPGK	SEQ ID 2554	CAGGTGCAGCTGCAGGAGTCGGG GGGAGGCTTGGTCCAGCCTGGGG GGTCCCTGAGACTCTCCTGTGCAG CCTCTGGATTCACCTTCAGTAGCT ATGCTATGCACTGGGTCCGCCAG GCTCCAGGGAAGGGACTGGAATA TGTTTCAGCTATTAGTAGTAATGG GGGTAGCACATATTATGCAAACTC TGTGAAGGGCAGATTCACCATCTC CAGAGACAATTCCAAGAACACGCT GTATCTTCAAATGGGCAGCCTGAG AGCTGAGGACATGGCTGTGTATTA CTGTGCGAGAGCTAAGTTTTGGAC ATACTACTTTGACTACTGGGGCCA GGGAACCCTGGTGACCGTCTCCT CAGCAAGCACAAAAGGTCCTTCAG TGTTCCCTCTGGCACCTTGCTCAC GCAGCACCTCTGAGAGTACAGCC GCCCTGGGCTGCCTGGTAAAGGA CTACTTTCCCGAACCAGTCACTGT GTCCTGGAATAGCGGGGCCTTGA CCTCTGGAGTGCACACATTTCCAG CTGTACTGCAGTCATCTGGACTCT ACAGCCTGTCCAGTGTGGTCACC GTACCTTCCTCCAACTTTGGCACT CAAACATATACATGTAACGTGGAT CATAAGCCCTCTAACACCAAAGTG GATAAAACTGTGGAGCGTAAGTGT TGTGTCGAGTGTCCTCCTTGTCCT GCTCCTCCTGTGGCAGGCCCATCT GTGTTTCTCTTTCCCCCAAAGCCA AAGGACACTTTGATGATATCCCGG ACCCCTGAGGTGACTTGCGTCGTC GTAGATGTTTCACACGAAGATCCA GAGGTGCAGTTCAACTGGTACGTG GATGGCGTGGAAGTGCATAATGC CAAGACAAAGCCCCGCGAAGAGC AGTTTAATTCCACCTTCCGCGTGG TGTCTGTGCTGACCGTGGTACATC AGGATTGGCTTAACGGTAAGGAGT ACAAGTGCAAGGTGAGTAACAAGG GGCTGCCCGCCCCTATCGAGAAG ACTATCAGTAAAACCAAGGGCCAG CCAAGGGAGCCACAGGTGTACAC ACTTCCACCATCTAGGGAGGAAAT GACAAAGAACCAGGTGAGTTTGAC CTGTCTCGTGAAAGGCTTTTATCC CAGTGATATAGCCGTGGAATGGGA AAGTAACGGGCAGCCCGAGAACA ACTATAAGACCACACCACCCATGC TGGACTCCGACGGTTCTTTCTTCC TTTATAGCAAGCTGACAGTGGATA AATCCAGGTGGCAGCAGGGTAAC GTATTCAGTTGCAGTGTCATGCAC GAGGCACTCCACAACCACTATACT

			CAGAAAAGTCTTTCCCTGAGTCCA GGCAAG

SEQ ID 2447	QVQLQQWGAGLLKPSE TLSLTCAVYGGSFSGYY WSWIRQPPGKGLEWIG EINHSGSTNYNPSLKSR VTISVDTSKNQFSLKLSS VTAADTAVYYCARGGG SGSYYKRFFDYWGQGT LVTVSSASTKGPSVFPL APCSRSTSESTAALGCL VKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSG LYSLSSVVTVPSSNFGT QTYTCNVDHKPSNTKV DKTVERKCCVECPPCP APPVAGPSVFLFPPKPK DTLMISRTPEVTCVVVD VSHEDPEVQFNWYVDG VEVHNAKTKPREEQFN STFRVVSVLTVVHQDWL NGKEYKCKVSNKGLPA PIEKTISKTKGQPREPQV YTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWE SNGQPENNYKTTPPML DSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK	SEQ ID 2555	CAGGTGCAGCTACAGCAGTGGGG CGCAGGACTGTTGAAGCCTTCGG AGACCCTGTCCCTCACCTGCGCTG TCTATGGTGGGTCCTTCAGTGGTT ACTACTGGAGCTGGATCCGCCAG CCCCCAGGGAAGGGGCTGGAGTG GATTGGGGAAATCAATCATAGTGG AAGCACCAACTACAACCCGTCCCT CAAGAGTCGAGTCACCATATCAGT AGACACGTCCAAGAACCAGTTCTC CCTGAAGCTGAGCTCTGTGACCG CCGCGGACACGGCTGTGTATTACT GTGCGAGAGGCGGTGGTTCGGGG AGTTATTATAAGAGGTTCTTTGACT ACTGGGGCCAGGGAACCCTGGTC ACCGTCTCCTCAGCAAGCACAAAA GGTCCTTCAGTGTTCCCTCTGGCA CCTTGCTCACGCAGCACCTCTGAG AGTACAGCCGCCCTGGGCTGCCT GGTAAAGGACTACTTTCCCGAACC AGTCACTGTGTCCTGGAATAGCGG GGCCTTGACCTCTGGAGTGCACA CATTTCCAGCTGTACTGCAGTCAT CTGGACTCTACAGCCTGTCCAGTG TGGTCACCGTACCTTCCTCCAACT TTGGCACTCAAACATATACATGTAA CGTGGATCATAAGCCCTCTAACAC CAAAGTGGATAAAACTGTGGAGCG TAAGTGTTGTGTCGAGTGTCCTCC TTGTCCTGCTCCTCCTGTGGCAGG CCCATCTGTGTTTCTCTTTCCCCC AAAGCCAAAGGACACTTTGATGAT ATCCCGGACCCCTGAGGTGACTT GCGTCGTCGTAGATGTTTCACACG AAGATCCAGAGGTGCAGTTCAACT GGTACGTGGATGGCGTGGAAGTG CATAATGCCAAGACAAAGCCCCGC GAAGAGCAGTTTAATTCCACCTTC CGCGTGGTGTCTGTGCTGACCGT GGTACATCAGGATTGGCTTAACGG TAAGGAGTACAAGTGCAAGGTGAG TAACAAGGGGCTGCCCGCCCCTA TCGAGAAGACTATCAGTAAAACCA AGGGCCAGCCAAGGGAGCCACAG GTGTACACACTTCCACCATCTAGG GAGGAAATGACAAAGAACCAGGT GAGTTTGACCTGTCTCGTGAAAGG CTTTTATCCCAGTGATATAGCCGT GGAATGGGAAAGTAACGGGCAGC CCGAGAACAACTATAAGACCACAC CACCCATGCTGGACTCCGACGGTT CTTTCTTCCTTTATAGCAAGCTGAC AGTGGATAAATCCAGGTGGCAGCA GGGTAACGTATTCAGTTGCAGTGT CATGCACGAGGCACTCCACAACCA

			CTATACTCAGAAAAGTCTTTCCCT GAGTCCAGGCAAG

SEQ ID 2448	EVQLVQSGAEVRKPGA SVKVSCKASGYTFTSYA ISWVRQAPGQGLEWMG WISAYDGNTNYAQKLQ GRVTMTTDTSTSTAYM EVRSLRSDDTAVYYCAR DGTVRRVVGATTPGNF DYRGQGTLVTVSSASTK GPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVT VSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTV PSSNFGTQTYTCNVDH KPSNTKVDKTVERKCCV ECPPCPAPPVAGPSVFL FPPKPKDTLMISRTPEV TCVVVDVSHEDPEVQF NWYVDGVEVHNAKTKP REEQFNSTFRVVSVLTV VHQDWLNGKEYKCKVS NKGLPAPIEKTISKTKGQ PREPQVYTLPPSREEMT KNQVSLTCLVKGFYPSD IAVEWESNGQPENNYK TTPPMLDSDGSFFLYSK LTVDKSRWQQGNVFSC SVMHEALHNHYTQKSL SLSPGK	SEQ ID 2556	GAGGTGCAGCTGGTGCAGTCTGG AGCTGAGGTGAGGAAGCCTGGGG CCTCAGTGAAGGTCTCCTGCAAGG CTTCTGGTTACACATTTACCAGTTA TGCCATCAGCTGGGTGCGACAGG CCCCTGGACAAGGGCTTGAGTGG ATGGGGTGGATCAGCGCTTACGA CGGTAACACAAACTATGCACAGAA GCTCCAGGGCAGAGTCACCATGA CCACAGACACATCCACGAGCACA GCCTACATGGAGGTGAGGAGCCT GAGATCTGACGACACGGCCGTGT ATTACTGTGCGAGAGATGGTACGG TCCGAAGGGTAGTGGGAGCTACT ACCCCTGGAAACTTTGACTACAGG GGCCAGGGAACCCTGGTCACCGT CTCCTCAGCAAGCACAAAAGGTCC TTCAGTGTTCCCTCTGGCACCTTG CTCACGCAGCACCTCTGAGAGTAC AGCCGCCCTGGGCTGCCTGGTAA AGGACTACTTTCCCGAACCAGTCA CTGTGTCCTGGAATAGCGGGGCC TTGACCTCTGGAGTGCACACATTT CCAGCTGTACTGCAGTCATCTGGA CTCTACAGCCTGTCCAGTGTGGTC ACCGTACCTTCCTCCAACTTTGGC ACTCAAACATATACATGTAACGTG GATCATAAGCCCTCTAACACCAAA GTGGATAAAACTGTGGAGCGTAAG TGTTGTGTCGAGTGTCCTCCTTGT CCTGCTCCTCCTGTGGCAGGCCC ATCTGTGTTTCTCTTTCCCCCAAAG CCAAAGGACACTTTGATGATATCC CGGACCCCTGAGGTGACTTGCGT CGTCGTAGATGTTTCACACGAAGA TCCAGAGGTGCAGTTCAACTGGTA CGTGGATGGCGTGGAAGTGCATA ATGCCAAGACAAAGCCCCGCGAA GAGCAGTTTAATTCCACCTTCCGC GTGGTGTCTGTGCTGACCGTGGTA CATCAGGATTGGCTTAACGGTAAG GAGTACAAGTGCAAGGTGAGTAAC AAGGGGCTGCCCGCCCCTATCGA GAAGACTATCAGTAAAACCAAGGG CCAGCCAAGGGAGCCACAGGTGT ACACACTTCCACCATCTAGGGAGG AAATGACAAAGAACCAGGTGAGTT TGACCTGTCTCGTGAAAGGCTTTT ATCCCAGTGATATAGCCGTGGAAT GGGAAAGTAACGGGCAGCCCGAG AACAACTATAAGACCACACCACCC ATGCTGGACTCCGACGGTTCTTTC TTCCTTTATAGCAAGCTGACAGTG GATAAATCCAGGTGGCAGCAGGG TAACGTATTCAGTTGCAGTGTCAT GCACGAGGCACTCCACAACCACTA

			TACTCAGAAAAGTCTTTCCCTGAG TCCAGGCAAG

SEQ ID 2449	EVQLVQSGGGVVQPGR SLRLSCAASGFTFSSYG MHWVRQAPGKGLEWV AVIWYDGSNKYYADSVK GRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCAR DLNRGYCSGGSCFGYW GQGTLVTVSSASTKGPS VFPLAPCSRSTSESTAA LGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSN FGTQTYTCNVDHKPSN TKVDKTVERKCCVECPP CPAPPVAGPSVFLFPPK PKDTLMISRTPEVTCVV VDVSHEDPEVQFNWYV DGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQD WLNGKEYKCKVSNKGL PAPIEKTISKTKGQPREP QVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPP MLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVM HEALHNHYTQKSLSLSP GK	SEQ ID 2557	GAGGTGCAGCTGGTGCAGTCTGG GGGAGGCGTGGTCCAGCCTGGGA GGTCCCTGAGACTCTCCTGTGCAG CGTCTGGATTCACCTTCAGTAGCT ATGGCATGCACTGGGTCCGCCAG GCTCCAGGCAAGGGGCTGGAGTG GGTGGCAGTTATATGGTATGATGG AAGTAATAAATACTATGCAGACTC CGTGAAGGGCCGATTCACCATCTC CAGAGACAATTCCAAGAACACGCT GTATCTGCAAATGAACAGCCTGAG AGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATCTGAATCGAG GATATTGTAGTGGTGGTAGCTGCT TTGGCTACTGGGGCCAGGGAACC CTGGTCACCGTCTCCTCAGCAAGC ACAAAAGGTCCTTCAGTGTTCCCT CTGGCACCTTGCTCACGCAGCAC CTCTGAGAGTACAGCCGCCCTGG GCTGCCTGGTAAAGGACTACTTTC CCGAACCAGTCACTGTGTCCTGGA ATAGCGGGGCCTTGACCTCTGGA GTGCACACATTTCCAGCTGTACTG CAGTCATCTGGACTCTACAGCCTG TCCAGTGTGGTCACCGTACCTTCC TCCAACTTTGGCACTCAAACATATA CATGTAACGTGGATCATAAGCCCT CTAACACCAAAGTGGATAAAACTG TGGAGCGTAAGTGTTGTGTCGAGT GTCCTCCTTGTCCTGCTCCTCCTG TGGCAGGCCCATCTGTGTTTCTCT TTCCCCCAAAGCCAAAGGACACTT TGATGATATCCCGGACCCCTGAGG TGACTTGCGTCGTCGTAGATGTTT CACACGAAGATCCAGAGGTGCAG TTCAACTGGTACGTGGATGGCGTG GAAGTGCATAATGCCAAGACAAAG CCCCGCGAAGAGCAGTTTAATTCC ACCTTCCGCGTGGTGTCTGTGCTG ACCGTGGTACATCAGGATTGGCTT AACGGTAAGGAGTACAAGTGCAAG GTGAGTAACAAGGGGCTGCCCGC CCCTATCGAGAAGACTATCAGTAA AACCAAGGGCCAGCCAAGGGAGC CACAGGTGTACACACTTCCACCAT CTAGGGAGGAAATGACAAAGAACC AGGTGAGTTTGACCTGTCTCGTGA AAGGCTTTTATCCCAGTGATATAG CCGTGGAATGGGAAAGTAACGGG CAGCCCGAGAACAACTATAAGACC ACACCACCCATGCTGGACTCCGAC GGTTCTTTCTTCCTTTATAGCAAGC TGACAGTGGATAAATCCAGGTGGC AGCAGGGTAACGTATTCAGTTGCA GTGTCATGCACGAGGCACTCCACA

			ACCACTATACTCAGAAAAGTCTTTC CCTGAGTCCAGGCAAG

SEQ ID 2450	QVQLQESGGGLVQPGG SLRLSCAASGFTFSSYA MSWVRQAPGKGLEWV SYISSSGTTIYYADSVKG RFTVSRDNAKNSLYLQ MNSLRAEDTAVYYCAR DYSSSGECFDYWGQGT LVTVSSASTKGPSVFPL APCSRSTSESTAALGCL VKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSG LYSLSSVVTVPSSNFGT QTYTCNVDHKPSNTKV DKTVERKCCVECPPCP APPVAGPSVFLFPPKPK DTLMISRTPEVTCVVVD VSHEDPEVQFNWYVDG VEVHNAKTKPREEQFN STFRVVSVLTVVHQDWL NGKEYKCKVSNKGLPA PIEKTISKTKGQPREPQV YTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWE SNGQPENNYKTTPPML DSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK	SEQ ID 2558	CAGGTGCAGCTGCAGGAGTCTGG GGGAGGCTTGGTACAGCCGGGGG GGTCCCTGAGACTCTCCTGTGCAG CCTCTGGATTCACCTTTAGCAGCT ATGCCATGAGCTGGGTCCGCCAG GCTCCAGGGAAGGGGCTGGAGTG GGTTTCATACATTAGTAGTAGTGG TACTACCATATACTACGCAGACTC TGTGAAGGGCCGATTCACCGTCTC CAGAGACAATGCCAAGAACTCACT GTATCTGCAAATGAACAGCCTGAG AGCCGAGGACACGGCCGTGTATT ACTGTGCGAGGGATTATAGCAGCT CGGGGGAGTGCTTTGACTACTGG GGCCAGGGAACCCTGGTCACCGT CTCCTCAGCAAGCACAAAAGGTCC TTCAGTGTTCCCTCTGGCACCTTG CTCACGCAGCACCTCTGAGAGTAC AGCCGCCCTGGGCTGCCTGGTAA AGGACTACTTTCCCGAACCAGTCA CTGTGTCCTGGAATAGCGGGGCC TTGACCTCTGGAGTGCACACATTT CCAGCTGTACTGCAGTCATCTGGA CTCTACAGCCTGTCCAGTGTGGTC ACCGTACCTTCCTCCAACTTTGGC ACTCAAACATATACATGTAACGTG GATCATAAGCCCTCTAACACCAAA GTGGATAAAACTGTGGAGCGTAAG TGTTGTGTCGAGTGTCCTCCTTGT CCTGCTCCTCCTGTGGCAGGCCC ATCTGTGTTTCTCTTTCCCCCAAAG CCAAAGGACACTTTGATGATATCC CGGACCCCTGAGGTGACTTGCGT CGTCGTAGATGTTTCACACGAAGA TCCAGAGGTGCAGTTCAACTGGTA CGTGGATGGCGTGGAAGTGCATA ATGCCAAGACAAAGCCCCGCGAA GAGCAGTTTAATTCCACCTTCCGC GTGGTGTCTGTGCTGACCGTGGTA CATCAGGATTGGCTTAACGGTAAG GAGTACAAGTGCAAGGTGAGTAAC AAGGGGCTGCCCGCCCCTATCGA GAAGACTATCAGTAAAACCAAGGG CCAGCCAAGGGAGCCACAGGTGT ACACACTTCCACCATCTAGGGAGG AAATGACAAAGAACCAGGTGAGTT TGACCTGTCTCGTGAAAGGCTTTT ATCCCAGTGATATAGCCGTGGAAT GGGAAAGTAACGGGCAGCCCGAG AACAACTATAAGACCACACCACCC ATGCTGGACTCCGACGGTTCTTTC TTCCTTTATAGCAAGCTGACAGTG GATAAATCCAGGTGGCAGCAGGG TAACGTATTCAGTTGCAGTGTCAT GCACGAGGCACTCCACAACCACTA

			TACTCAGAAAAGTCTTTCCCTGAG TCCAGGCAAG

SEQ ID 2451	EVQLVQSGGGVVQPGR SLRLSCAASGFTFSSYG MHWVRQAPGKGLEWV AVIWYDGSNKYYADSVK GRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCAR DQAAMVGYFDYWGQG TLVTVSSASTKGPSVFP LAPCSRSTSESTAALGC LVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSS GLYSLSSVVTVPSSNFG TQTYTCNVDHKPSNTKV DKTVERKCCVECPPCP APPVAGPSVFLFPPKPK DTLMISRTPEVTCVVVD VSHEDPEVQFNWYVDG VEVHNAKTKPREEQFN STFRVVSVLTVVHQDWL NGKEYKCKVSNKGLPA PIEKTISKTKGQPREPQV YTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWE SNGQPENNYKTTPPML DSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK	SEQ ID 2559	GAGGTGCAGCTGGTGCAGTCTGG GGGAGGCGTGGTCCAGCCTGGGA GGTCCCTGAGACTCTCCTGTGCAG CGTCTGGATTCACCTTCAGTAGCT ATGGCATGCACTGGGTCCGCCAG GCTCCAGGCAAGGGGCTGGAGTG GGTGGCAGTTATATGGTATGATGG AAGTAATAAATACTATGCAGACTC CGTGAAGGGCCGATTCACCATCTC CAGAGACAATTCCAAGAACACGCT GTATCTGCAAATGAACAGCCTGAG AGCCGAGGACACGGCTGTGTATTA CTGTGCGAGAGATCAGGCAGCTAT GGTAGGCTACTTTGACTACTGGGG CCAGGGAACCCTGGTCACCGTCT CCTCAGCAAGCACAAAAGGTCCTT CAGTGTTCCCTCTGGCACCTTGCT CACGCAGCACCTCTGAGAGTACA GCCGCCCTGGGCTGCCTGGTAAA GGACTACTTTCCCGAACCAGTCAC TGTGTCCTGGAATAGCGGGGCCTT GACCTCTGGAGTGCACACATTTCC AGCTGTACTGCAGTCATCTGGACT CTACAGCCTGTCCAGTGTGGTCAC CGTACCTTCCTCCAACTTTGGCAC TCAAACATATACATGTAACGTGGA TCATAAGCCCTCTAACACCAAAGT GGATAAAACTGTGGAGCGTAAGTG TTGTGTCGAGTGTCCTCCTTGTCC TGCTCCTCCTGTGGCAGGCCCATC TGTGTTTCTCTTTCCCCCAAAGCC AAAGGACACTTTGATGATATCCCG GACCCCTGAGGTGACTTGCGTCG TCGTAGATGTTTCACACGAAGATC CAGAGGTGCAGTTCAACTGGTACG TGGATGGCGTGGAAGTGCATAATG CCAAGACAAAGCCCCGCGAAGAG CAGTTTAATTCCACCTTCCGCGTG GTGTCTGTGCTGACCGTGGTACAT CAGGATTGGCTTAACGGTAAGGAG TACAAGTGCAAGGTGAGTAACAAG GGGCTGCCCGCCCCTATCGAGAA GACTATCAGTAAAACCAAGGGCCA GCCAAGGGAGCCACAGGTGTACA CACTTCCACCATCTAGGGAGGAAA TGACAAAGAACCAGGTGAGTTTGA CCTGTCTCGTGAAAGGCTTTTATC CCAGTGATATAGCCGTGGAATGG GAAAGTAACGGGCAGCCCGAGAA CAACTATAAGACCACACCACCCAT GCTGGACTCCGACGGTTCTTTCTT CCTTTATAGCAAGCTGACAGTGGA TAAATCCAGGTGGCAGCAGGGTAA CGTATTCAGTTGCAGTGTCATGCA CGAGGCACTCCACAACCACTATAC

			TCAGAAAAGTCTTTCCCTGAGTCC AGGCAAG

SEQ ID 2452	QVTLKESGGGVVQPGR SLRLSCAASGFIFSNYAI HWVRQAPGKGLEWVA VISYDGSNKYYADSVKG RFTISRDNSKNTLYLQM NSLRAEDTAVYYCARTF AGYSSKLGYFDLWGRG TLVTVSSASTKGPSVFP LAPCSRSTSESTAALGC LVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSS GLYSLSSVVTVPSSNFG TQTYTCNVDHKPSNTKV DKTVERKCCVECPPCP APPVAGPSVFLFPPKPK DTLMISRTPEVTCVVVD VSHEDPEVQFNWYVDG VEVHNAKTKPREEQFN STFRVVSVLTVVHQDWL NGKEYKCKVSNKGLPA PIEKTISKTKGQPREPQV YTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWE SNGQPENNYKTTPPML DSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK	SEQ ID 2560	CAGGTCACCTTGAAGGAGTCTGG GGGAGGCGTGGTCCAGCCTGGGA GGTCCCTGAGACTCTCCTGTGCAG CCTCTGGATTCATCTTCAGTAACTA TGCTATACACTGGGTCCGCCAGG CTCCAGGCAAGGGGCTGGAGTGG GTGGCAGTTATATCATATGATGGA AGTAATAAATACTACGCAGACTCC GTGAAGGGCCGATTCACCATCTCC AGAGACAATTCCAAGAACACGCTG TATCTGCAAATGAACAGCCTGAGA GCTGAGGACACGGCTGTGTATTAC TGTGCGAGGACTTTTGCGGGGTAT AGCAGCAAACTGGGGTACTTCGAT CTCTGGGGCCGTGGCACCCTGGT CACCGTCTCCTCAGCAAGCACAAA AGGTCCTTCAGTGTTCCCTCTGGC ACCTTGCTCACGCAGCACCTCTGA GAGTACAGCCGCCCTGGGCTGCC TGGTAAAGGACTACTTTCCCGAAC CAGTCACTGTGTCCTGGAATAGCG GGGCCTTGACCTCTGGAGTGCAC ACATTTCCAGCTGTACTGCAGTCA TCTGGACTCTACAGCCTGTCCAGT GTGGTCACCGTACCTTCCTCCAAC TTTGGCACTCAAACATATACATGTA ACGTGGATCATAAGCCCTCTAACA CCAAAGTGGATAAAACTGTGGAGC GTAAGTGTTGTGTCGAGTGTCCTC CTTGTCCTGCTCCTCCTGTGGCAG GCCCATCTGTGTTTCTCTTTCCCC CAAAGCCAAAGGACACTTTGATGA TATCCCGGACCCCTGAGGTGACTT GCGTCGTCGTAGATGTTTCACACG AAGATCCAGAGGTGCAGTTCAACT GGTACGTGGATGGCGTGGAAGTG CATAATGCCAAGACAAAGCCCCGC GAAGAGCAGTTTAATTCCACCTTC CGCGTGGTGTCTGTGCTGACCGT GGTACATCAGGATTGGCTTAACGG TAAGGAGTACAAGTGCAAGGTGAG TAACAAGGGGCTGCCCGCCCCTA TCGAGAAGACTATCAGTAAAACCA AGGGCCAGCCAAGGGAGCCACAG GTGTACACACTTCCACCATCTAGG GAGGAAATGACAAAGAACCAGGT GAGTTTGACCTGTCTCGTGAAAGG CTTTTATCCCAGTGATATAGCCGT GGAATGGGAAAGTAACGGGCAGC CCGAGAACAACTATAAGACCACAC CACCCATGCTGGACTCCGACGGTT CTTTCTTCCTTTATAGCAAGCTGAC AGTGGATAAATCCAGGTGGCAGCA GGGTAACGTATTCAGTTGCAGTGT CATGCACGAGGCACTCCACAACCA

			CTATACTCAGAAAAGTCTTTCCCT GAGTCCAGGCAAG

[770] Antibody mediated Cytotoxicity

Post purification, anti CLEC2D antibody clones were assessed for cell surface binding on C4548 cells using flow cytometry. As can be seen from FIG. 19C, both clones with IgG4 isotype, exhibited binding towards surface expressed CLEC2D antigen with ~4-8 fold higher MFI when compared with control un-transfected CHO cell.

[771] In order to evaluate functionality of isotype variants, PC3 cells were labelled with Efluor as per the manufacturer's protocol and were seeded at a density of $0.04x10^6$ in 20% DMEM in 24 well plates. After 24 hours, freshly isolated PBMCs were added in T: E of 1:5 and novel monoclonal anti-CLEC2D antibodies C3276, C3256, C3452, and C4608 were added at 100 µg/ml in the assay reaction of 0.5ml and incubated for 14hours. Supernatant was collected from

24 well plate and adherent cells were trypsinized and collected in 1.5 ml tubes. Reaction mixture was incubated with sytox green (15nM) for 20min and fluorescence was detected in flow cytometer. Percent specific cell death was determined by subtracting the percent cell death of control from the test samples.

[772] As can be seen from FIG. 19D, for C3276, IgG4 variant and C4608 IgG1 variant exhibited similar percentage of cytotoxicity towards PC3 cells. Taken together, both IgG1 and IgG4 variants (treated at 100 μg/ml) showed anti-tumor activity towards PC3 cells signifying an engagement of both CD16 dependent target cell death and also killing of target cells via blocking of CLEC2D and CD161 interaction, in turn suggesting involvement of multiple pathways, probably functions independent of ADCC mechanism, to rapidly kill the tumour cells. In addition, different isotype format of the said antibody, could potentially pave new line of treatment for specific disease, not limiting to, prostate cancer.

[773] **Impact of Anti CLEC2D antibody with modified glycosylation on cytotoxicity**

[774] The monoclonal antibody based biotherapeutics function through effective recognition of the antigenic epitopes on target cells as well as the antibody effector functions, as an outcome of formation of immune complexes. In recent times, antibody effector function has gained considerable interest towards improving efficacy of the said class of biotherapeutics. Antibody dependent Cellular Cytotoxicity (ADCC) improves clinical efficacy of therapeutic antibodies, the effect is more pronounced in case of anticancer antibodies as exemplified in studies involving allelic polymorphism of leucocyte receptors (FcγR) in patients. Recently, an elegant study with homogeneous IgG glycoforms developed through chemo-enzymatic methods revealed antibody sialylation negatively impacts ADCC in the context of core fucosylation but not in case of nonfucosylated antibody. Multiple studies reported that completely nonfucosylated monoclonal antibody has significantly increased Fc affinity to FcγRIII and thereby improving antibody ADCC function by many folds, *in vitro* and *in vivo*.

[775] With the advent next generation monoclonal antibody drugs against immune oncology targets, where innate immune system is mobilized to tumor microenvironment, engaging NK cell effector functions becomes immensely important. Any such antibody with improved ADCC functionality recognizing epitopes on tumor cells has the potential to exert more inhibitory effects on tumor cell survival and hence tumor progression. In this context, controlling ADCC function

of monoclonal antibody therapeutics helps balancing the optimal effector function to deleterious cytokine release.

[776] Afucosylated anti CLEC2D antibody expression:

[777] Talen Fut8 gene knockout cell line was developed in GS negative CHO cell line. This cell line was sequence verified for FUT8 gene knock-out and was coded as C2899. C0694 (HC and LC vectors) and C2685 (HC and LC vectors) were transfected in this cell line. Antibiotic selection was performed, Minipools and single cell clones were developed from this cell line which expresses afucosylated anti CLEC2D antibody. Afucosylated antibodies were tested for cell surface antigen binding on C4548 cells by flow-cytometry and on target cells by confocal imaging.

[778] C2899 cell transfection to express novel anti-CLEC2D monoclonal antibody clones Transfection:

[779] C2899 cells were transfected with C0694 and C2685 heavy chain and light chain vectors. Cell count and viability data was collected using Vi-cell XR automated cell counter, Beckman coulter. Transfection was carried out as per manufacturer's protocol Lipofectamine® LTX Reagent with PLUS Reagent. Required volume of cell suspension was centrifuged at 1400 RPM for 4 mins and re-suspended in specified volume of OPTIMEM I in 125ml shake flask. Transfection mix was prepared as described before. C2899 cells transfected with C0694 HC and LC vectors were knwon as C3234 whereas C2899 cells transfected with C2685 HC and LC vectors were known as C4335.

[780] Generation of stable cell lines expressing afucosylated anti CLEC2D antibody:

[781] Antibiotic Selection:

[782] Antibiotic selection was initiated after transfection at >80% cell viability. Cell suspension was centrifuged at 1400 RPM for 4-5 mins. Pellet was re-suspended in complete Power CHO2 growth media and concentration of Puromycin Dihydrochloride was adjusted to 2µg /1X10^6 cells. Antibiotic selection was carried out on every 2nd or 3rd day.

[783] Repeat transfection of stable pool:

[784] Cell count was taken using Vi-cell XR. Cells were subcultured before the transfection. Two more sequential transfections were performed as mentioned previously. On completion of three rounds of transfection the pool was designated as R3 stable pool.

[785] Minipool plating:

[786] Minipools were generated by serial dilution method. Continuously growing culture of cell line was subcultured at 0.5 million cells/ml in 30ml complete PowerCHO 2 growth media with 2mM glutamax, 1 to 2 days before plating. Cell count and viability data was collected using Vi-cell XR. Serial dilution of the cell suspension was carried out in complete PowerCHO2 growth media at 1:10 ratio. Cells were seeded at a density of 10 cells/well in a 96 well plate in 200 µl volume per well in cloning media. These mini-pools were maintained at 37ºC Temperature in a humidified 5% CO2 incubator.

[787] Screening of mini-pools and amplification:

[788] Mini-pools were screened by flow cytometry wherein binding to C4548 cells was estimated. Minipools were ranked based on cell surface binding. Minipools selected from flow cytometry screening were amplified from 96 well plate to 24 well plate and maintained at 37 ºC, humidified condition in a 5% CO2 incubator. These were further amplified from 24 well plate to one well of 6 well plate. After cells were confluent mini-pools were amplified from one well of 6 well plate to a 50ml bioreactor tube or 125ml Erlenmeyer shake flask with 25-30 ml growth media and maintained at 37 ºC, humidified condition in a 5% CO2 incubator, 120-200RPM.

[789] Single cell cloning

[790] Single cells were generated by serial dilution method. Continuously growing culture of selected mini-pool was subcultured at 1 million cells/ml in 30ml complete PowerCHO 2 growth media with 2mM glutamax, 1-2 day before cloning. Cell count and viability data was collected using Vi-cell XR. Serial dilution of the cell suspension was carried out in complete powerCHO2 growth media at 1:10 ratio. Cells were seeded at a density of 0.5 cells/well in a 96 well plate and maintained at 37ºC Temperature in a humidified 5% CO2 static incubator. Plates were scanned by using CloneSelect Imager (Molecular Devices) for monoclonality report generation from day zero to day ten. The clonal population was confirmed from the day zero image of entire well and the monoclonality report generated by CloneSelect Imager. Passage number was P(x+0). Single cell clones were coded with four digit random numbers. The Single cell clones were amplified to 24 well plates after cells were confluent. Passage number was P(x+1).

[791] Screening of single cell clones and clone amplification:

[792] Cell surface binding assay was performed to estimate antibody in cell culture supernatant and to rank the clones. Single cell clones showing higher binding on C4548 cell surface expressed CLEC2D antigen were amplified from 24 to 6 well. Passage number was (x+2). This was followed

by amplification in 3 wells of 6 well plate. Passage number was (x+3). The clones were further amplified to bioreactor tubes or Erlenmeyer flasks. RCB vials were prepared for the clones.

[793] Culture harvest for protein purification:

[794] Cells were seeded at a density of approximately 0.3X10^6 cells/ml in 30-100ml Complete power CHO2 growth media and cultured for 6 days in 37°C, humidified condition in a 5% CO2 incubator with 120 RPM rotation. 20%v/v media top-up was given with complete power CHO2 growth media on 3rd or 4th day. Supernatants were harvested by centrifuging the entire cell suspension at 1400-2000 RPM for 10 mins. The supernatants were collected and subjected to purification by protein-A affinity chromatography.

[795] Cell surface binding assay by flow-cytometry:

[796] CHO cells were transiently transfected with CLEC2D surface expression vector. Surface expression was optimum on day 4 to day 5 on transfected cells. These cells were coded as C4548. Cell count was taken by Vi-cell XR automated cell counter. CHO and C4548 cells were centrifuged at 1000-1400rpm for 4-5 minutes. The pellet was re-suspended in 1ml DPBS. 50,000 cells were aliquoted in each well of a 96 well plate. 1-5µg of purified antibody samples and reference control was added to each well and incubated for 40-60 minutes at room temperature (25°C). The plate was centrifuged at 1000-1400 rpm for 4-5 minutes, the supernatant was aspirated and cells were washed with 0.1%BSA in DPBS. 2.5 ml of 2% BSA was diluted to 50ml with DPBS. Goat anti human IgG FITC conjugate was used as secondary antibody. 1:100 dilution of secondary antibody was prepared in DPBS and 100µl was added to each well. The plate was incubated for 30 minutes at room temperature (25°C) in dark. The cells were washed with 0.1% BSA and re-suspended in 100µl of 2% BSA. Samples were analyzed by flow-cytometry.

[797] Binding of test sample supernatant on un-transfected CHO cells was estimated and used for calculation of specific binding on C4548 cell surface using following formula:

$$\text{Fold change in MFI} = \frac{\text{Median FITC-A of test sample on CHO cells}}{\text{Median FITC-A of test sample on C4548 cells}}$$

[798] Purified anti CLEC2D antibody from stable cell clones were firstly assessed for cell surface binding on C4548 cells through flow cytometry, experimentation for flow cytometry based binding studies remains similar as described in section….. As can be seen from FIG. 19E, all clones as exemplified by C0613, C1301, C6268, C1699, C2437, C9832, C8900 and C7749, exhibited

differential binding towards surface expressed CLEC2D antigen with ~2-10 fold higher MFI when compared with control, which is un-transfected CHO cell.

[799] Cytotoxicity with Afucosylated anti CLEC2D antibody

[800] Confirmed afucosylated anti CLEC2D mono clonal antibodies were used subsequently for cytotoxicity experiments and effect of glycosylation was compared with fucosylated anti CLEC2D antibodies.

[801] Herein, PC3 cells were labelled with Efluor as per the manufacturer's protocol and were seeded at a density of $0.04x10^6$ in 20% DMEM in 24 well plates. After 24 hours, freshly isolated NK cell was added in T: E of 1:1. Novel monoclonal anti-CLEC2D antibody C5511 (100 µg/ml) and afucosylated mabs C7749, C8800 and C9832 were added at 20 µg/ml in the assay reaction of 0.5 ml and incubated for 14 hours. Supernatant was subsequently collected from 24 well plate followed by trypsinization of adherent cells. Reaction mixture was incubated with sytox green (15 nM) for 20 min and fluorescence signal was detected using flow cytometer. Percent specific cell death was determined by subtracting the percent cell death of control from the test samples.

[802] FIG. 19F depicts the impact of fucsylation on Anti CLEC2D antibody mediated cytotoxicity as assessed through killing of PC3 cells. As mentioned before, afucosylated anti CLEC2D antibodies were used at a concentration that is 5 times lower than fucosylated antibody i.e., C5511. Observed cytotoxicity suggests that afucosylated anti CLEC2D antibody is at least 5 times more effective when compared with the fucosylated anti CLEC2D antibody. Thereby, the said and described version i.e., afucosylated anti CLEC2D antibodies could be used as an efficient alternative treatment/therapy option to achieve increased clinical efficacy.

[803] Taken together, functional efficiency of anti CLEC2D monoclonal antibodies could be ADCC independent, as seen in functionality for said antibody in IgG4 isotype format, while afucosylated version of anti CLEC2D antibody elicits an efficient ADCC mediated target killing, which in turn elaborates/expands about/on the functional and application related versatility in therapeutic space.

[804] Complement dependent cytotoxicity

[805] Complement-dependent cytotoxicity, or CDC, is a well-known mechanism through which antibodies lyse the unwanted target by activating a cascade of complement-related reactions. Usually IgG1 and IgG3, elicits CDC killing effects via binding its Fc region to serum complement components, particularly C1q. Following complicated enzyme activations and

cleavage events, involving over 20 highly regulated elements, it will eventually lead to the formation of membrane attacking complex (MAC), thereby target cell destruction.

[806] Specific example details on experimentation wherein 50 µL of target cell suspension (PC3 and Ramos) containing 5×10^4 cells were added to each well of the 96-well assay plate. 50 µL of different concentrations of C5511 antibody (200, 40, 0.4, 0.04 µg/mL) dilution was added to the plate to start the reaction. The plate was shaken for 30 seconds. Baby rabbit complement was then diluted (1:20) in cell medium, and 50 µL was added to the appropriate wells. Following shaking for 30 seconds, the plate was incubated at 37°C, 5% CO2 for 120 minutes. The plate was then removed from the 37° C incubator and allowed to cool to room temperature (RT) for 15 minutes, and then add 25 µL of warm Risazurin solution and incubate overnight (16-20 hrs) at 37°C, 5% CO2 incubator. The plate was then removed from the 37° C incubator and allowed to cool to room temperature (RT) for 15 minutes, and then read plate in fluorescence mode (excitation 530 and emission 590) using the Synergy HT BIOTEK micro plate reader.

[807] The data obtained from both Ramos and PC3 cell line suggests that anti-CLEC2D antibody does not exhibits its cell killing mechanism through CDC pathway as shown in FIG. 19G.

[808] Example 7: In vivo mouse efficacy studies with anti-CLEC2D monoclonal antibody

[809] In vivo mouse efficacy studies

[810] During the development of therapeutic monoclonal antibodies (mAbs), a strategy for early identification of candidate mAbs with the greatest likelihood of success in the clinic is needed to avoid costly late-stage failures related to inadequate exposure, toxicity or lack of efficacy. Early screening and optimization of mAbs focus on characteristics such as affinity, potency and stability for selection of lead constructs, while confirmation on in vivo efficacy are typically required

[811] The anticancer activity of anti-CLEC2D monoclonal antibody was evaluated in huNOG-EXL mice bearing subcutaneous PC3 tumor xenografts (FIGS. 20A and 20B). The procedure relies on super immune-deficient hGM-CSF/hIL3 transgenic-NOG mice, which upon engraftment with human hematopoietic stem cells, results in human-like immune system (lymphoid & myeloid lineage of human origin). This model enabled an efficacy study of the key innate mechanisms involved in the function of immune-therapy agents. The study was conducted

for a period of 4-5 weeks with regular observation of tumor volume and body weight. The study was carried out in accordance with Institutional Animal Ethics Committee (IAEC).

[812] All animals were kept for acclimatization for a period of about 5–7 days before initiation of the experiment. Animals were housed group wise (5 animals per cage) in IVCs and autoclaved corncob was used as the bedding material. Animals were maintained in a controlled environment with 22±3°C temperature, 50±20% humidity, a light/dark cycle of 12 hours each and 15–20 fresh air changes per hour. The animals were fed, ad libitum, with certified Irradiated Laboratory Rodent Diet.

Species	*Mus musculus*
Strain	huNOGEXL
Source	Taconic Biosciences
Sex	Male
Age	5-6 weeks
Body weight	19-21g
Cancer cell line	PC3 (Human prostate adenocarcinoma)
Cell inoculation density	5 x 10^6 cells/animal
Study initiation	Tumor volume (≈100mm^3)
Duration of the study	4-5 weeks
Test item	Anti-CLEC2D antibody clones, IgG1 control monoclonal antibody, Check point monoclonal antibody
Dose & Dosing schedule	10mg/kg, 4 intraperitoneal dosing – once every 7 days
Route of dosing	Intraperitoneal
Tumor volume measurement	Once every three days
Body weight measurement	Once every three days

[813] All procedures were performed in a laminar flow hood following sterile techniques. PC-3 (Human prostate adenocarcinoma) cells with a viability of >90 % was chosen for the study. Around 5 x 10^6 cells were re-suspended in 200 µl of serum free media containing 50% of matrigel kept in ice. Male huNOG-EXL mice housed in Individually Ventilated Cages (IVCs) were used for the study. The PC-3 cell line was propagated into the animals by injecting the cells

subcutaneously in the right flank region of the animals. The implanted area was monitored for growth of tumor. Once the tumor attained palpable stage and required volume (Mean tumor volume 115 mm^3), animals were randomized and dosing was initiated with anti-CLEC2D monoclonal antibodies, the IgG1 control monoclonal antibody and check point monoclonal antibody. Antibodies were administered intraperitoneally. The dose of each individual animal was adjusted based on its body weight.

[814] The primary objective of the study was to evaluate the antitumor activity of anti-CLEC2D monoclonal antibodies. In addition to the efficacy of the anti-CLEC2D antibody clones alone, experiments were carried out for combination treatment with a check point monoclonal antibody against PDL1 antigen. In huNOG-EXL mice bearing PC-3 tumor xenograft, animal body weight, clinical signs and tumor volume were recorded once every three days throughout the experimental period. The study was constituted with following arms as described in Table 42:

Table 42

Sl No	Monoclonal antibody	Dosage	Frequency of treatment
Arm 1	Control human IgG1	10 mg/kg	Once a week
Arm 2	anti-CLEC2D mAb clone 1	10 mg/kg	Once a week
Arm 3	anti-CLEC2D clone 2	10 mg/kg	Once a week
Arm 4	Anti PDL1 mAb	10 mg/kg	Once a week
Arm 5	anti-CLEC2D clone 1 + Anti PDL1 mAb	5 mg/kg of anti-CLEC2D clone 1 + 5mg/kg of Anti PDL1 mAb	Once a week

[815] Animals in "Arm 1" revealed progressive tumor growth during the study period. Tumor growth inhibition was observed in all other experimental arms. Individual body weight was measured once every three days during the study period. The percentage change in body weight of individual mouse was calculated and recorded. Animals were observed for visible clinical signs every day during the study period. The tumor volume was determined by two-dimensional

measurement with a digital Vernier calliper on the day of randomization (Day 0) and then once every three days (i.e., on the same days when body weight was taken). Using a Vernier calliper the length (L) and width (W) of the tumor was measured. Tumor volume (TV) was calculated using the following formula:

TV = (L x W x W)/2; where L = Length (mm); W = Width (mm).

Mean, Standard Deviation (SD) or Standard Error of Mean (SEM) were calculated for individual groups. Antitumor activity was evaluated as maximum tumor volume inhibition versus the control IgG1 arm (Arm 1). Data evaluation was performed using statistical software Graph Pad Prism V 5.0. Tumor growth inhibition (TGI) was calculated using the following formula:

$$TGI = (1 - T/C) \times 100\ \%$$

where, T = (Mean Tumor volume (TV) of the test arm on Day X - Mean TV of the test arm on Day 0; C = (Mean TV of the control Human IgG (Arm 1) on Day X - Mean TV of the control Human IgG (Arm 1) on Day 0.

[816] The relative tumor volume (RTV) and tumor growth inhibition were calculated. Mean ± SEM was calculated for the RTV data and tumor growth inhibition was presented as a percentage. Two way ANOVA was utilized for statistical analysis and p value <0.05 between arms was considered significant. The results show significant tumor growth reduction with both monotherapy with anti-CLEC2D antibody and in combination with check point monoclonal antibody against PDL1.

[817] Significant tumor growth inhibition was observed in Arm 2, Arm 3, Arm 4 and Arm 5 compared to Arm 1, representing Control human IgG1. It was unexpected that significant tumor growth inhibition over entire study period was observed in animals treated with anti-CLEC2D monoclonal antibody clones, and anti-PDL1 antibody. More interestingly, a completely novel finding where tumor sizes were reduced by half in animals treated with a combination of anti-CLEC2D monoclonal antibody clone and anti-PDL1 monoclonal antibody was observed. This observation is very significant as the combination treatment with anti-CLEC2D antibody and anti-PDL1 antibody achieved this high level of tumor growth inhibition at a reduced dosage of 5 mg/kg. The data indicates significant anti tumor activity when anti-CLEC2D antibody was used alone and when it was used in combination with anti PDL1 antibody, showing that the antibody clones against CLEC2D antigen have great therapeutic potential for various disease indications.

[818] During the study period, monoclonal antibody dosages were well tolerated with mild body weight loss. Based on cage side observations there was no visible signs of abnormal behaviour or any adverse clinical symptoms in any of the groups during the experimental period. T cell infiltration to the tumor site was analysed using immunohistochemistry (IHC) of the excised tumor. The harvested tumor cells were subjected to different types of T cell markers to understand the infiltration. Histology processing was conducted for immunohistochemistry for FFPE tissue **(**Formalin-Fixed Paraffin-Embedded (*FFPE*) *tissue* specimens). Animals were euthanized and the tumors were harvested & fixed in 10% neutral buffer formalin for 24 hours. The tissues were subjected to tissue processing. Paraffin embedded tissue blocks were prepared after completion of tissue processing. Subsequently, sectioning blade holder angle was adjusted to the surface of tissue block in the microtome. Coarse trimming was carried out, and fine sections of 5 micron thickness were taken and transferred to the tissue water bath. Formalin-Fixed Paraffin-Embedded (*FFPE*) *tissue* specimens were processed for IHC staining with standard reagents.

[819] Samples were washed in washing buffer (PBST- 0.3% tritonX-100) for 10 min. Samples were incubated with blocking solution (10% Normal goat serum and 3% BSA in PBS) for 30-60 minutes in humidified environment. Primary antibodies were diluted in antibody dilution buffer (3% BSA in PBS). The tissues were incubated with primary antibody against CD3 antigen at 1:100 dilution and incubated overnight at 4^0C. Subsequently slides were washed three times in washing buffer for 10-30 minutes/wash. This was followed by incubation with secondary antibody Goat Anti-Rabbit IgG H&L (HRP) at room temperature. Slides were washed three times in washing buffer for 15-30 minutes for each wash. The DAB Chromogen was applied to develop proper intensity of tissue staining. Counterstaining was carried out with hematoxylin.

[820] The tumor samples were immunohistochemically stained with anti-CD3 antibody. CD3 cell (Pan T cell marker) infiltration was observed in the periphery of tumor tissues in human IgG control (Arm 1). However, in animals treated with anti-CLEC2D antibody, check point antibody alone, or a combination of anti-CLEC2D antibody with a check point antibody, the CD3 cell infiltration was observed heterogeneously in periphery and also around the tumor cells. CD3, a membranous immunohistochemical marker, revealed mild to moderate degree of staining of tumor samples harvested from animals treated with anti-CLEC2D antibody, check point

antibody, and a combination of anti-CLEC2D antibody with check point antibody. The data provides clear insights into the mechanisms of tumor mediated immune suppression

[821] Localization of labelled anti-CLEC2D antibody

[822] In a separate imaging experiment, anti-CLEC2D antibody labelled with Alexa 647 was administered at a single dose of 10 mg/kg intravenously. The fluorescently labelled antibody was administered to huNOG-EXL mice bearing subcutaneous PC-3 tumor (Mean Tumor volume ~213mm^3). *In-vivo* imaging was carried out at 0 min, 5 min, 15 min, 30 min, 1 hr, 3 hr, 6 hr, 12 hr, 24 hr, 48 hr, 72 hr and 96 hr post administration of Alexa 647 labelled antibody (FIGS. 20C). The monoclonal antibody against anti-CLEC2D antibody exhibited affinity (which was evident from tumor signal intensity) towards the target antigen of interest in huNOG-EXL mice bearing subcutaneous PC-3 tumor.

[823] The signal intensity from the tumor appeared as early as 5 minutes post injection of the antibody and gradually increased with time. The peak signal intensity was observed at 3hrs and the signal intensity from the tumor lasted until 96 hrs.

[824] ***In vivo* mouse efficacy with selected monoclonal antibody products**

[825] In a separate follow up xenograft mouse study, the monoclonal antibody drug products were tested to evaluate tumor growth reduction upon monoclonal antibody treatment.

[826] Origin of the animals: hGM-CSF/hIL3 NOG mice engrafted with human CD34+ hematopoietic stem cells (HSCs) stably develop extensive cell lineages as early as 6 to 8weeks post-injection. Both myeloid and lymphoid lineage cells are present in peripheral blood, bone marrow, thymus and spleen and non-lymphoid tissue including lung and liver. For the current study huNOG-EXL mice with greater than 25% hCD45+ in peripheral blood were used

[827] Rationale: The procedure relies on super immunodeficient the hGM-CSF/hIL3 transgenic-NOG mice which upon engraftment with human hematopoietic stem cells, results in a human-like immune system (lymphoid & myeloid lineage of human origin). This model enables to study the key innate mechanisms involved in the efficacy of immuno-therapy related agents and provide a suitable model for establishment of human xenografts.

Strain	huNOG-EXL
Sex	Male
Source	Taconic (USA)
Age at the start of experiment	13-14 weeks

Body Weight of animals 18-22 g

[828] **Animal Care**

[829] Animal Welfare

[830] Animals were taken care as per the regulations of Committee for the Purpose of Control and Supervision of Experiments on Animals (CPCSEA), Government of India and Association for Assessment and Accreditation of Laboratory Animal Care (AAALAC) guidelines.

[831] Housing and Feeding

[832] Animals were housed in individually ventilated cages maintained in a controlled environment with 22 + 3°C temperature, 50 + 20 % humidity, 12 h light/dark cycle and 15-20 fresh air changes per hour. Animals were housed group- wise and autoclaved corncob (Sparconn Life Sciences, Bangalore, India) was used as a bedding material. The animals were fed (NIH-31), ad libitum, with certified irradiated laboratory rodent diet during the study period.

[833] Drinking Water

[834] Fresh, potable water, filtered through RO, was provided ad libitum after autoclaving to all animals via bottle fitted with nozzle.

[835] Preparation of Animals

[836] The animals were kept under acclimatization in the experimental room for a period of 10 days. A thorough observation was performed before selecting the animals and only animals that were apparently healthy were used for the study.

[837] Animal Identification

[838] Animals were individually numbered and the cage cards indicating the experiment, study number, date of randomization, mouse strain, gender and individual mouse numbers were displayed to corresponding cages. After randomization group identity, treatment code, dosage, schedule and route of administration were included in the cage cards.

[839] **Experimental Procedure**

[840] Preparation of tumor cells

[841] All procedures were performed in a laminar flow hood following sterile techniques. PC-3 (Human prostate adenocarcinoma) cells with a viability of >90% was chosen for the study. Around 5 x 106 cells were re-suspended in 200 µL of serum free media containing 50% of matrigel kept in ice.

[842] Subcutaneous injection of cells

[843] Male huNOG-EXL mice housed in Individually Ventilated Cages (IVCs) were used for the study. PC-3 cell line was propagated into the animals by injecting the cells subcutaneously in the right flank region of the animals. The implanted area was monitored for growth of tumor. Four days post injection of cells animals were randomized based on tumor volume (Mean tumor volume ≈ 37mm3) and dosing was initiated.

[844] Route and mode of administration of the test substance:

[845] Required quantity of test antibodies were prepared and stored at 2-80C. The antibodies were administered intraperitoneally. The dose of individual animal was adjusted based on the body weight. For each antibody, unused new syringes and needles were used.

[846] Experimental design

- Monoclonal antibody products were used at 10mg/kg dosage
    a. C5511 mAb group;
    b. C6481 mAb group.
- Vehicle control IgG1 group – Control IgG1 was used at 10mg/kg dosage.
- 5 animals per treatment group.
- Antibody drug product was injected every 3 days for first 2 weeks and once weekly for remaining study period.
- Total study duration 36 days.
- Tumor volume measurement and animal body weight measurement was carried out every 3 days.

[847] Dose and route of administration

[848] Required quantity of test compounds (ready to use formulation) were used and it was stored at -200C. Test compounds were administered intraperitoneally to their respective groups. The dose of each individual animal was adjusted based on the body weight determined just before dosing and dose volume was maintained at 10mL/kg body weight. For each test compound, sterile new syringes and needles were used. The test compounds were freshly thawed on the day of drug administration.

[849] Observations

[850] Body weight - Individual body weight was measured once every three days during the study period. The % change in body weight of individual mouse was calculated and recorded.

[851] Clinical sign - Animals were observed for visible clinical signs and recorded once in every third day during the treatment period.

[852] Tumor volume measurement - The tumor volume was determined by two-dimensional measurement with a digital Vernier calliper on the day of randomization (Day 1). Second tumor volume measurement was on day 3, further every third day till the end of the experiment the tumor volume measurement was carried out (i.e. on the same days when body weight was taken). Using a Vernier calliper the length (L) and width (W) of the tumor was measured. Tumor volume (TV) was calculated using the following formula:

$$\text{Tumor volume (mm3)} = \frac{L \times W^2}{2}$$

Where, L = Length (mm); W = Width (mm).

Mean, Standard Deviation (SD) or Standard Error of Mean (SEM) were calculated for individual groups.

[853] Antitumor Activity

[854] Antitumor activity was evaluated as maximum tumor volume inhibition versus the vehicle control group. Data evaluation was performed using statistical software Graph Pad Prism V 5.0.

- Tumor growth inhibition (TGI)

TGI was calculated using the following formula:

$TGI = (1 - T/C) \times 100$

Where, T = (Mean TV of the test group on Day X - Mean TV of the test group on Day 1)

C = (Mean TV of the control group on Day X - Mean TV of the control group on Day 1)

- Relative tumor volume (RTV)

Relative Tumor volume (RTV) was calculated using the following formula:

$$RTV = \frac{\text{Tx (absolute tumor volume of the respective tumor on day x)}}{\text{T1 (absolute tumor volume of same tumor on day 1}}$$

[855] Statistical Analysis

[856] For the evaluation of the statistical significance of tumor inhibition, Two-way ANOVA followed by Bonferroni post hoc test was performed using Graph Pad Prism V 8.3.0. p values <0.05 indicate statistically significant differences between groups.

[857] Necropsy

[858] Tumor burden (TV>1500mm3) and tumor necrosis/ulceration were observed due to progressive tumor growth. Hence, based on tumor end points & ethical reasons (Day 36), all animals in all experimental groups were humanely euthanized & gross pathological observations were recorded. Prior to euthanasia, blood sampling was carried out, serum was separated and stored at -80°C. All live animals & excised tumor tissues were photographed with scale and whole tumor tissues were formalin-fixed.

[859] Results obtained from the in vivo studies

[860] Antitumor activity

[861] In this study, huNOG-EXL mice bearing PC-3 tumors were treated with test compounds at a dose of 10 mg/kg intraperitoneally (On day 1, 3, 6, 9, 12, 18, 24, 30 & 33). Under the present experimental condition, the vehicle control IgG1 group showed progressive tumor growth during the experimental period. Hence, other treatment groups were compared with this group for anticancer efficacy evaluation. Among the tested dose and regimen, two test arms revealed C5511 mAb group and C6481 mAb group showed significant tumor growth inhibition as $p<0.001$ and $p<0.05$ respectively when compared to vehicle control IgG1 on day 24. Whereas, on day 36 only C5511 mAb group exhibited significant tumor growth inhibition as $p<0.05$ when compared to vehicle control IgG1 group. The data is presented in Table 43.

Table 43. Effect of test compounds in humanized (huNOG-EXL) mice bearing subcutaneous PC-3 tumor xenografts

Test Compound	Number of animals/group	% TGI (Day 24)	Statistical Significance (Day 24)	% TGI (Day 36)	Statistical Significance (Day 36)	Mean % BWC (Day 36)
C5511 mAb group (10 mg/kg, i.p; On day 1, 3, 6, 9, 12, 18, 24, 30 & 33)	5	49	*** ($p < 0.001$)	35	* ($p < 0.05$)	-14

Vehicle Control IgG1 group (10 mg/kg, i.p; On day 1, 3, 6, 9, 12, 18, 24, 30 & 33)	5	-	-	-	-	-21
C6481 mAb group (10 mg/kg, i.p; On day 1, 3, 6, 9, 12, 18, 24, 30 & 33)	5	25	* ($p < 0.05$)	8	ns	-15

TGI – Tumor growth inhibition (TGI was calculated against vehicle control IgG1 group)
BWC – Body weight change
***$p<0.001$, * $p<0.05$ statistically significant when respective treatment groups were compared to vehicle control IgG1 group.
ns Statistically non-significant when respective treatment groups were compared to vehicle control IgG1 group.

[862] Tumor volume (TV) & Delta tumor volume (ΔTV) on day 24 and day 36

[863] On day 24, the mean Tumor volume (mm3) for C5511 mAb group, Vehicle control IgG1 group, & C6481 mAb group were 241 ± 31, 474 ± 38, and 355 ± 68, respectively. Further the mean delta tumor volume (ΔTV) on day 24 for C5511 mAb group, vehicle control IgG1 group, & C6481 mAb groups were 204 ± 32, 437 ± 38, and 318 ± 68 mm3, respectively. The treatment groups, C5511 mAb group and C6481 mAb group showed significant decrease ($p < 0.001$ & $p < 0.05$) in the tumor volume and delta tumor volume when compared to Vehicle control IgG1 group on day 24. The mean tumor volume on day 36 for C5511 mAb group, vehicle control IgG1 group, and C6481 mAb group were 690 ± 186, 1062 ± 157, and 977 ± 230 mm3 respectively. The mean delta tumor volume (ΔTV) on day 36 for C5511 mAb group, vehicle control IgG1 group, and C6481 mAb groups were 654 ± 187, 1025 ± 159, and 940 ± 231 mm3 respectively. The treatment groups, C5511 mAb group showed significant decrease ($p < 0.05$) in the tumor volume and delta tumor volume when compared to vehicle control IgG1 group. The

results of tumor volume (TV) & Delta tumor volume (ΔTV) for all treatment groups are summarized in table 44 and 45, and FIGS. 20D, 20E, 20F and 20G.

Table 44. Effect of test compounds on mean tumor volume of (huNOG-EXL) mice bearing subcutaneous PC-3 tumor xenograft

Groups	**Mean Tumor volume (mm^3)**													
	Days	**1**	**3**	**6**	**9**	**12**	**15**	**18**	**21**	**24**	**27**	**30**	**33**	**36**
C5511 mAb group (10 mg/kg, i.p; On day 1, 3, 6, 9, 12, 18, 24, 30 & 33)	Mean	37	58	78	97	112	152	179	213	241	356	508	621	690
	S.E.M	1	3	4	6	2	12	39	31	31	60	95	143	186
Vehicle control IgG1 group (10 mg/kg, i.p; On day 1, 3, 6, 9, 12, 18, 24, 30 & 33)	Mean	37	61	94	114	131	190	270	363	474	569	727	894	1062
	S.E.M	1	2	4	7	11	12	25	32	38	38	69	83	157
C6481 mAb group (10 mg/kg, i.p; On day 1, 3, 6, 9, 12, 18, 24, 30 & 33)	Mean	39	54	79	101	121	166	207	288	355	456	587	734	977
	S.E.M	2	2	6	11	15	21	33	60	68	102	108	125	230

Table 45. Effect of test compounds on Δ (Delta) mean tumor volume of (huNOG-EXL) mice bearing subcutaneous PC-3 tumor xenograft

Groups	**Δ (Delta) Mean Tumor Volume (mm^3)**													
	Days	**1**	**3**	**6**	**9**	**12**	**15**	**18**	**21**	**24**	**27**	**30**	**33**	**36**
C5511 mAb group	Mean	0	20	41	60	75	115	142	176	204	320	473	585	654

(10 mg/kg, i.p; On day 1, 3, 6, 9, 12, 18, 24, 30 & 33)	S.E.M	0	3	4	5	2	12	39	32	32	61	97	145	187
Vehicle control IgG1 group (10 mg/kg, i.p; On day 1, 3, 6, 9, 12, 18, 24, 30 & 33)	Mean	0	24	56	77	94	153	233	326	437	531	689	856	1025
	S.E.M	0	2	4	7	11	13	25	33	38	39	70	83	159
C6481 mAb group (10 mg/kg, i.p; On day 1, 3, 6, 9, 12, 18, 24, 30 & 33)	Mean	0	15	42	64	83	129	170	250	318	419	550	697	940
	S.E.M	0	1	5	11	15	21	33	60	68	102	108	125	231

[864] Percentage Tumor Growth Inhibition (%TGI) on day 24 and day 36

[865] The % Tumor Growth Inhibition (%TGI) for C5511 mAb group showed maximum value of 49% followed by C6481 mAb group with %TGI value of 25%, on day 24. Whereas, the %TGI on day 36, values for C5511 mAb group, and C6481 mAb groups were 35%, and 8% respectively on day 36 against Vehicle control IgG1 group. The individual animal Tumor Growth Inhibition are summarized in Table 46.

Table 46. % Tumor growth inhibition (% TGI) of test compounds against (huNOG-EXL) mice bearing PC-3 tumor xenograft

Groups				**% Tumor growth inhibition (%TGI) by Delta**									
	Day 1	**Day 3**	**Day 6**	**Day 9**	**Day 12**	**Day 15**	**Day 18**	**Day 21**	**Day 24**	**Day 27**	**Day 30**	**Day 33**	**Day 36**
C5511 mAb group (10 mg/kg, i.p; On day 1, 3, 6, 9, 12, 18, 24, 30 & 33)	0	6	17	15	14	20	34	41	49	37	30	31	35
Vehicle Control IgG1 group P3E (10 mg/kg, i.p; On day 1, 3, 6, 9, 12, 18, 24, 30 & 33)	-1	3	6	9	12	17	25	5	15	16	9	8	2
C6481 mAb group (10 mg/kg, i.p; On day 1, 3, 6, 9, 12, 18, 24, 30 & 33)	-4	12	16	11	8	13	24	21	25	20	19	18	8

[866] Relative Tumor volume (RTV) & Delta Relative tumor volume (ΔRTV) on day 24 and day 36

[867] On day 24, the mean relative tumor volume for C5511 mAb group vehicle control IgG1 group, and C6481 mAb group were 7 ± 1, 13 ± 1, and 10 ± 2 respectively. The delta relative tumor volume (ΔRTV) for C5511 mAb group, vehicle control IgG1 group, and C6481 mAb group were 6 ± 1, 12 ± 1, and 9 ± 2 respectively as shown in table 5. The treatment groups, C5511 mAb group showed significant decrease ($p < 0.001$) in the relative tumor volume and delta relative tumor volume when compared to vehicle control IgG1 group FIGS. 20H and 20I. The mean relative tumor volume on day 36, 20 ± 6 in C5511 mAb group, 29 ± 5 in vehicle control IgG1 group , and 27 ± 7 in C6481 mAb group. Whereas on day 36, the mean delta tumor volume (ΔRTV) for C5511 mAb group, vehicle control IgG1 group and C6481 mAb groups were 19 ± 6, 28 ± 5, and 26 ± 7 respectively as shown in Table 47 and FIGS 20J and 20K.

Table 47. Relative tumor volume (RTV) of test compounds against (hu NOG-EXL) mice bearing PC-3 tumor xenograft

Groups	**Relative Tumor Volume (mm^3)**													
	Days	**Day 1**	**Day 3**	**Day 6**	**Day 9**	**Day 12**	**Day 15**	**Day 18**	**Day 21**	**Day 24**	**Day 27**	**Day 30**	**Day 33**	**Day 36**
C5511 mAb group (10 mg/kg, i.p; On day 1, 3, 6, 9, 12, 18, 24, 30 & 33)	Mean	1	2	2	3	3	4	5	6	7	10	15	18	20
	S.E.M	0	0	0	0	0	0	1	1	1	2	3	5	6
Vehicle control IgG1 group (10 mg/kg, i.p; On day 1, 3, 6, 9, 12, 18, 24, 30 & 33)	Mean	1	2	3	3	4	5	7	10	13	15	20	24	29
	S.E.M	0	0	0	0	0	0	1	1	1	1	2	3	5
C6481 mAb group (10 mg/kg, i.p; On day 1, 3, 6, 9, 12, 18, 24, 30 & 33)	Mean	1	1	2	3	3	4	6	8	10	12	16	20	27
	S.E.M	0	0	0	0	0	1	1	2	2	3	3	4	7

Table 48. Delta relative tumor volume (ΔRTV) of test compounds against (hu NOG-EXL) mice bearing PC-3 tumor xenograft

Groups	**Delta Relative Tumor Volume (mm^3)**													
	Days	**Day 1**	**Day 3**	**Day 6**	**Day 9**	**Day 12**	**Day 15**	**Day 18**	**Day 21**	**Day 24**	**Day 27**	**Day 30**	**Day 33**	**Day 36**
	Mean	0	1	1	2	2	3	4	5	6	9	14	17	19

C5511 mAb group (10 mg/kg, i.p; On day 1, 3, 6, 9, 12, 18, 24, 30 & 33)	S.E.M	0	0	0	0	0	0	1	1	1	2	3	5	6
Vehicle control IgG1 group (10 mg/kg, i.p; On day 1, 3, 6, 9, 12, 18, 24, 30 & 33)	Mean	0	1	2	2	3	4	6	9	12	14	19	23	28
	S.E.M	0	0	0	0	0	0	1	1	1	1	2	3	5
C6481 mAb group (10 mg/kg, i.p; On day 1, 3, 6, 9, 12, 18, 24, 30 & 33)	Mean	0	0	1	2	2	3	5	7	9	11	15	19	26
	S.E.M	0	0	0	0	0	1	1	2	2	3	3	4	7

[868] The study revealed, under the test conditions, test compounds used in C5511 mAb group, vehicle control IgG1 group and C6481 mAb group at a dose of 10 mg/kg intraperitoneally (on day 1, 3, 6, 9, 12, 18, 24, 30 & 33) were tested to evaluate the anticancer efficacy against PC-3 tumor xenograft in huNOG-EXL mice. Efficacy evaluation was calculated against vehicle control IgG1 group. Among tested compounds, C5511 mAb group and C6481 mAb group exhibited significant anti-cancer efficacy when compared with vehicle control IgG1 group. Based on statistical analysis of tumor volume, tumor growth inhibition, relative tumor volume, treatment with C5511 mAb group showed better antitumor efficacy compared to test compound used in C6481 mAb group. Moderate body weight loss observed in all the treatment groups.

[869] In this context, it should be noted that the monoclonal antibody products tested in current HuNOG study, were utilized under sub optimal assay condition. The monoclonal antibody products used in this study require human NK cells for optimal function and till date no animal model is available where human NK cells could mimic the *in vivo* condition. Considering these constrains, HuNOG model was used rationally, wherein the human immune cells (including human NK cells) are established in mouse. However, the abundance of NK cells are significantly low. Therefore HuNOG mice model is justifiably provides a suitable experimental condition to test these novel Anti CLEC2D monoclonal antibody products. Moreover, it was observed that the overall number of human immune cells start to decline, as the animals become older, with progression of the study. These levels of tumor growth reduction in the HuNOG PC3 xenograft model is surprising, indicating highly superior efficacy of the novel Anti CLEC2D monoclonal antibodies of the present disclosure.

[870] Example 8: Characterization of anti-CLEC2D monoclonal antibody

[871] Purified anti-CLEC2D antibody was subjected various biophysical and biochemical characterization indicative of multiple inherent properties of antibody such as, mass, conformation, posttranslational modification, amongst others.

[872] In order to identify the confirmation of isolated fragments, SDS PAGE was carried out

Table 49. intact mass analysis

Sr. No.	Mass (Da)	Intensity (Counts)	Intensity (%)
1	149301	252629056	100
2	149131	228375856	90.4
3	149302	227410624	90.02
4	149132	222516864	88.08
5	149300	217502800	86.1
6	149466	200116976	79.21
7	149465	198714320	78.66
8	149130	186866464	73.97
9	149133	183556800	72.66
10	149303	170258512	67.39

under non-reducing conditions, where a single major band corresponding to a molecular weight (MW) of 150 kDa was observed for all the samples indicating the intact anti-CLEC2D antibody. While under reducing conditions, two bands were evident at 25kDa and 50kDa which were associated with light chain and heavy chains of the anti-CLEC2D antibody. SDS PAGE data has been shown in FIG. 21A).

[873] The intact mass experiment was carried out using methods based on ELISA, flow cytometry, Western blotting, BIACORE, Waters UPLC H-Class Bio with Xevo G2 XS QTOF with UNIFI. The Xevo G2 XS QTOF was run in positive sensitivity MS only mode. With no prior treatment, 1 µg sample was analyzed using the same chromatographic conditions (only gradient different from subunit mass analysis) and mass spectrometric conditions as subunit mass analysis as described above.

[874] The most abundant masses are close to generic glycosylated IgG1 monoclonal antibody as shown in FIG. 21B), and Table 49, thus confirming the molecular weight of anti-CLEC2D monoclonal antibody.

[875] Acidic, Basic and Main peak was resolved and the percentage of each variant along with main peak is tabulated in below shows the charge distribution determined by WCX-LC method in anti-CLEC2D antibody molecule. The relative abundance of acidic isoforms is generally attributed to oxidation, deamidation, and glycation process within the antibody. On the other hand, the presence of C-terminal Lysine and amidation are mainly responsible for forming basic isoforms in the antibody. The WCX chromatogram is shown in FIG. 21C).

Acidic Species: 10%

Main Species: 83%

Basic Species: 7%

[876] It is known that protein aggregation can induce immunogenicity; although a small amount of aggregates is expected, this amount is likely to increase due to stress conditions that a antibody may undergo during its manufacture, purification, formulation, and shelf-life. Aggregation can also induce production of anti-drug antibodies (ADAs) which can result in the loss of activity or cause adverse effects upon administration. Anti-CLEC2D antibody sample was analyzed by size exclusion chromatography (SEC) and typical chromatograms were shown in below. As observed in attached chromatogram in FIG. 21D), 100% monomer was observed thus confirming that sample is free from any aggregates and/or degradant.

[877] One of the important quality attribute for therapeutic monoclonal antibodies is their glycosylation profile. To check the glycan distributions of anti-CLEC2D antibody, the sample was analyzed by HILIC N-glycan profiling method. The major glycan such as G0F, G1F, G1F' and G2F were identified and total percentage of Galactosylated glycan was found to be around 46.44%.

[878] Binding studies against soluble CLEC2D antigen:

[879] Binding studies were carried out using anti CLEC2D antibody against purified soluble CLEC2D antigen while the measurements were made through both ELISA and SPR based methods.

[880] Besides, SPR was also employed to understand the interaction between anti CLEC2D antibody and FcRn, as Binding interactions with the neonatal Fc receptor (FcRn) are one determinant of pharmacokinetic properties of recombinant human monoclonal antibody

therapeutics, and a conserved binding motif in the crystallizable fragment (Fc) region of IgG molecules interacts with FcRn.

[881] ELISA;

[882] Soluble CLEC2D antigen was produced and purified using CHO cell culture system and Anti CLEC2D antibody C5511 were used for ELISA assay. The method was optimized using various ELISA formats, as exemplified by, direct ELISA, indirect ELISA and sandwich ELISA. Finally, the optimized ELISA assay was based on protein A coated plate wherein the antigen was labelled with biotin moiety. The Anti CLEC2D antibody dilutions ranging from 0.01 µg/mL to 62.5 µg/mL were made in dilution buffer 0.5% BSA in (DPBS with 0.05% tween20).

[883] The protein A coated wells were washed thrice with 200µL of wash buffer (DPBS with 0.1% Tween20). 100µL of each antibody dilution was added to well, and the plate was incubated for 90 minutes at room temperature on orbital shaker. Each well was rinsed four times with 200µL of wash buffer. 100µL of different concentration of biotinylated antigen, labelling was carried out as described before, was added to each well and plate was incubated for 60 minutes at room temperature on orbital shaker. Each well was rinsed four times with 200µL of wash buffer. 100µL of 1:5000 diluted HRP-labelled streptavidin was added and plate was incubated for 60 minutes at room temperature on orbital shaker. Each well was rinsed five times with 200µL of wash buffer. 100µl 1X TMB was added and the plate was incubated for 30min at RT in dark. After 30 minutes 100µl of stop solution was added and the plate was read at 450nm.

[884] Further to appropriate subtraction of blank, absorbance values were plotted and fit into binding model based on sigmoidal association, using Graphpad PRISM 6.0. The KD value as obtained from the fit is found to be 10-17 nM for anti CLEC2D antibody to purified CLEC2D antigen (FIG. 21F). The experiments were repeated at least 3 times independently in triplicates to achieve statistical confidence and variation was found to be less than 5%, while confidence interval resides within 95%.

[885] BIAcore binding studies with anti-CLEC2D antibody against soluble CLEC2D antigen

[886] CLEC2D antigen interaction with specific monoclonal antibody was monitored through surface plasmon resonance, using BIACORE. The kinetic parameters for the interaction of anti-CLEC2D antibodies with CLEC2D antigen were evaluated. This method was used to screen potential high affinity monoclonal antibodies against CLEC2D antigen.

Different monoclonal antibodies revealed differential affinities towards the CLEC2D antigen. The experiment revealed affinity constants ranging from less than 100 nM (e.g., ≤ 90 nM, ≤ 80 nM, ≤ 70 nM, ≤ 60 nM, ≤ 50 nM, ≤ 40 nM, ≤ 30 nM, ≤ 20 nM, ≤ 10 nM, ≤ 5 nM, or ≤ 1 nM).

[887] CLEC2D antigen binding kinetics and affinity studies between CLEC2D antigen and Anti CLEC2D antibody binding studies were carried out using Anti-His Antibody binding capture chemistry on BIACORE 3000 instrument. His Capture Kit (GE healthcare) was immobilized onto CM5 chip surface at an RU of ~1800. CLEC2D antigen was captured on Anti-His, coupled with CM5 chip, surface, at a concentration of ~200 µg/mL, wherein the dilution of antigen was made through running buffer comprising HBS-EP+ buffer (GE healthcare). Subsequently anti CLEC2D antibody C5511 was passed at concentrations ranging from 1 to 100 µg/mL, at association and dissociation time of 3 minutes and 25 minutes, respectively. Antibody dilutions were made in HBS-EP+ buffer (GE healthcare). Response curves (FIG. 21G) obtained were appropriately subtracted from reference flow cell signal and blanks, respectively and fit to a 1:1:1 Langmuir binding leading to estimated KD of ~10^9 M-1.

[888] FcRn binding

[889] Surface plasmon resonance (SPR) biosensor assays are often used to characterize interactions between FcRn and antibody therapeutics. Studies have shown that FcRn interacts with a binding motif in the crystallizable fragment (Fc) of IgG at the CH2-CH3 domain interface in a pH-dependent manner.6,8 The pH dependency of this interaction is essential for maintaining the long serum half-life of IgG molecules. Specifically, in the endosomes of endothelial cells (~pH 6.0), IgG internalized through pinocytosis binds to FcRn to form IgG-FcRn complexes; the IgG-FcRn complexes are then trafficked to the cell surface where IgG is released backcinto the circulation at physiological pH (~7.4). This prevents lysosomal degradation of the IgG. For recombinant human monoclonal antibody (rhumAb) therapeutics, the FcRn-rhumAb binding interaction is a critical determinant of pharmacokinetic (PK) properties and targeted engineering of the FcRn binding motif may enable less frequent dosing of antibody therapeutics in patients. Multiple studies have suggested that there is a correlation between FcRn binding affinity and antibody half-life, although the absence of such a correlation has also been reported.

[890] Binding kinetics and affinity studies between Human FcRn / FCGRT & B2M Heterodimer Protein and Anti CLEC2D antibody binding studies were carried out using BIACORE 3000 instrument. Human FcRn / FCGRT & B2M Heterodimer Protein (Acro

Biosystems) was immobilized onto CM5 chip surface at an RU of ~300. Human FcRn / FCGRT & B2M Heterodimer Protein was captured on CM5 chip surface through amine coupling, at a concentration of ~1 µg/mL, wherein the dilution of protein was made through running buffer comprising HBS-EP+ buffer (GE healthcare). Subsequently anti CLEC2D antibody C5511 was passed at concentrations ranging from 0.0315 to 0.5 µM, at both pH 5.9 and pH 7.4. Antibody dilutions were made in HBS-EP+ buffer (GE healthcare). As can be seen from the response curve that there was no binding observed at pH 7.4 (FIG. 21H) while response was monitored at pH 5.9 (FIG. 21I). Response curves obtained were appropriately subtracted from reference flow cell signal and blanks, respectively and fit to a 1:1:1 Langmuir binding leading to estimated KD of ~ 1.88X 10^6 M-1. As can be concluded that no binding at neutral pH may increase the possibility of the anti CLEC2D antibody to be released back into the blood stream.

[891] Example 9: Anti-CLEC2D monoclonal antibody as a diagnostic tool/ as prognostic marker against multiple disease indications

[892] All high binding anti-CLEC2D antibodies were screened to pick the top binder as diagnostic antibody. Among the 4 high binding anti-CLEC2D antibody, one was selected through antigen binding assay with PC3 tumor cell line.

[893] Tumor cells expressing CLEC2D antigen were harvested by trypsinization. Cell count was taken by Vi-cell XR automated cell counter. Cells were centrifuged at 1400-1500 rpm for 4-5 minutes. The pellet was re-suspended in 1ml DPBS. 50,000 cells were aliquoted in each well of a 96 well plate.1µg of C2779, C2438, C0949, C2543 were added to each well and incubated for 30-60 minutes at room temperature (25ºC). The plate was centrifuged at 1400-1500 rpm for 4-5 minutes, the supernatant was aspirated and cells were washed with 0.1%BSA in DPBS. 2.5 ml of 2% BSA was diluted to 50ml with DPBS. Goat anti human IgG FITC conjugate was used as secondary antibody. 1:100 dilution of secondary antibody was prepared in DPBS and 100µl was added to each well. The secondary antibody, Goat anti human IgG FITC conjugate, was used as control at 1:100 dilution for all relevant experimentation. The plate was incubated for 30 minutes at room temperature (25ºC) in dark. The cells were washed with 0.1% BSA and re-suspended in 100µl of 1% BSA. Samples were analyzed by flow-cytometry.

[894] C0949 was selected as diagnostic antibody reagent due to maximum percentage of binding observed against surface expressed CLEC2D on PC3 when compared with other anti

CLEC2D clones (FIG. 22A) and purposed further to detect CLEC2D antigen on various tumour cell lines.

[895] Among the prostate cancer cell lines, 22RV showed highest antigen expression with 5 fold increase as compared to secondary antibody control (FIG. 22B). Further, diagnostic anti-CLEC2D antibody, not limited to C0949, was used in antigen binding assay for multiple tumor cell lines of several disease indications shown in FIG. 22C.

[896] Efficient and sensitive binding as observed in multiple cancer cell lines including prostate cancer cell lines, using various anti CLEC2D antibody clones, strongly support the candidacy of the said molecules as diagnostic/prognostic reagent.

[897] Clinical prospect of Anti-CLEC2D monoclonal antibody

[898] Disease relevance: prostate cancer

[899] TCGA analysis

[900] The cancer genome atlas (TCGA) data was metastatic prostate cancer was analysed to improve on the current understanding of genes involved in the disease progression along with the expression level of CLEC2D in prostate cancer patients.

[901] The PRAD project is the TCGA's prostate cancer project and it contains data for 500 Cancer cases. The relevant sources of data that were analysed were limited to Gene Expression Quantification, which included HTSeq Count Data, miRNA Expression Quantification and Isoform Expression Quantification. Table 50 shows a case-wise breakdown of the occurrences of the above specified files in the data that was accessible for download from the data categories of interest.

Table 50. A breakdown of the cases based on the availability of different data files, such as tumor and normal files

Description	**Cases**	**Percentage**
Transcriptome Profiling		
No files	2	0.4
only miRNA+Isoform	3	0.6
only GEQ	4	0.8
all files, only Tumor	436	87.2

all files, Tumor+Normal	52	10.4
two different miRNA+Isoform Files	1	0.2
two different GEQ (tumor) files	2	0.4

[902] TCGA Data - Transcriptome profiling

[903] The transcriptome profiling data category contains counts of gene, miRNA and isoform expression. Of the 500 cases deposited in the TCGA, 498 have data associated with Primary Tumor tissue, while 52 cases have expression data related to the Normal Tissue. The files are a list of 60483 genes and their variants, denoted by their Ensembl IDs and their counts within each case.

[904] TCGA Data - Metastatic Cases Identification

[905] The 500 TCGA PRAD Project cases were parsed to identify cases which displayed characteristics that would lead to them being identified as cases of metastatic prostate cancers. A total of 289 cases were identified to be metastatic, this identification was made on the basis of key parameters, in other TCGA documentation which lists among other parameters Gleason Scores and prescribed Drugs. Of the 289, only 18 had relevant Normal Tissue data, as this analysis is concerned with the change in expression levels for before and after the disease, it was necessary to establish baseline values, Normal data, for the other genes as well. This was achieved by looking at all 52 Normal Tissue data, these were used to create a baseline file, by taking into account all 52 values from each case for each gene, removing outlier values, and calculating an 'normal baseline' value for the gene. For cases lacking a Normal Tissue counts, the baseline file was used for the comparative analysis.

[906] TCGA Data - Metastatic Cases Sub-groupings

[907] The same key parameters which served as the basis of the Metastatic case identification were also used to segregate the data into other sub-groupings such as stage of the cancer and current treatment regimen - this data was used to analyse the CLEC2D Expression levels among the sub-groups

[908] Subsequently expression of CLEC2D gene was monitored wherein all the associated FPKM files from the projects were downloaded and specifically queried for CLEC2D expression. The FPKM files were made up of Tumor expression files and in some cases Normal

Tissue Expression files. Both sets were separately used to calculate a range for CLEC2DCLEC2D Expression for each cancer among Normal and Tissue cases. Additionally outliers were omitted from the data by assuming a normal distribution of the Expression values and discarding values that were more than 2 standard deviations away from the mean.

[909] In order to better understand the role of CLEC2D in cancers the relative expression levels of the gene in normal tissue samples and tumor tissue samples was analysed. This was done by collecting all the case data for specific cancers/conditions and retrieving the CLEC2D expression value from each file before analysing the sets of values. For each subset the 'spread' of the CLEC2D expression profile was plotted by looking at the minimum, maximum and interquartile values. As can be seen from FIG. 23A, CLEC2D appears to conform remarkable existence in terms of expression level seen in different subsets conditions, such as, metastasis, tumor stage and treatment received, amongst others.

[910] Induction driven expression increase

[911] In order to determine the expression label of CLEC2D on the surface of different tumor cell lines, firstly surface expression of CLEC2D on the surface of CLEC2D transfected HDCHO, C4548, was looked at and distribution of same was observed on the transfected cells by using commercially available anti- CLEC2D (4C7) antibody. Assuming translation of CLEC2D could be heavily regulated upon various kind of inductions, various prostate cancer cell types were induced with multiple inducers such as effector cells (either whole PBMC or supernatant of PBMC) or activators of NK cells (e.g., LPS) on prostate tumor cell line (PC3) to monitor the impact on expression label of CLEC2D. Upon treatments with various inducers, an increased CLEC2D expression label was observed when compared to the untreated target cells.

[912] Among the prostate tumor cell lines under no induction, castrate-resistant prostate cancer (CRPC) cell lines i.e. PC3 and DU145 have high CLEC2D surface expression compare to Non-CRPC cell lines i.e. LNCap and 22RV1 wherein the CLEC2D was probed by using Novel anti-CLEC2D antibody as exemplified by, not limited to, C2685 clone (FIG. 23B). Extending the observation obtained in uninduced condition, the therapeutic anti CLEC2D antibody, such as C2685, not limited to, was used to understand the changes in expression level in the presence or absence of inducers. Next, in order to look into the changes in expression label of CLEC2D on all prostate tumor cell lines upon various treatments, prostate tumor cells were incubated with effector cells (either whole PBMC or supernatant of PBMC or isolated NK cells or isolated T

cells) or with activators/inducers of NK cells (either LPS or Poly I:C or IFN gamma), and examined the expression label of CLEC2D by using C2685 anti CLEC2D antibody. Upon treatment an increased expression label of CLEC2D was observed when compared with the untreated target cells (FIG. 23C). Among the prostate tumor cell lines, castrate-resistant prostate cancer (CRPC) cell lines i.e. PC3 and Non-CRPC cell line i.e., LNCap have shown further enhancement of CLEC2D surface expression upon treatment compare to DU145 and 22RV1 treated with said inducers (FIG. 23C).

[913] Considering all and having specific focus on prostate cancer, cell lines such as, castrate-resistant prostate cancer (CRPC) cell lines (such as PC3 and DU145) and Non-CRPC cell lines (such as LNCap and 22RV1), revealed significant expression level of CLEC2D antigen on tumor cell surface, which was further increased with various treatments, including multiple TLR treatments. The choice of cell lines were strategic, as all prostate cancer cell lines used herein signifies certain stage or condition of prostate cancer disease and can be associated with CLEC2D expression level. As described and shown in the present disclosure, prostate cancer cell lines, LNCaP, DU145, 22RV1 and PC3 have low, moderate and high metastatic potential wherein PC3, with high cell surface CLEC2D expression, is effectively killed by NK cells when the inhibitory signal through CLEC2D-CD161 axis is blocked using identified anti CLEC2D antibody, thereby, establishing CLEC2D as clinically relevant target for prostate cancer.

[914] Example 10: Expression of CLEC2D antigen in cancer tissue

[915] CLEC2D has been described as a multi-functional protein, and to fully elucidate the functional consequences of its interactions with its receptor, CD161, a comprehensive characterisation of CLEC2D distribution is needed. CLEC2D has been observed to be activated in different tumor cell lines and present on various immune cells in humans. CLEC2D can be detected in several healthy human tissues, and can be remarkably prevalent in immune-privileged sites. This information will be used to emphasize and postulate on the role of CLEC2D in cross talk between lymphocytes and immune tolerance.

[916] The tissue microarray (TMA) represents a high-throughput technology for the assessment of histology-based laboratory tests, including immunohistochemistry and fluorescent in-situ hybridization (FISH). For immune-fluorescent staining, anti-CLEC2D monoclonal antibody is used as primary antibody and either direct labelling or indirect labelling, with a labelled

secondary Ab, is used for detection. Thus, the role of CLEC2D is determined in various cancers and in the context of various stages of cancer.

[917] Additionally, 3D cell culture methodology is used to understand the interaction of tissue expressed CLEC2D antigen with human immune system to determine the cross-talk between CLEC2D antigen and interacting partners (including CD161) expressing on tumor cells, and immune cell types, such as B cells, T cells, monocytes and NK cells.

[918] Having described embodiments of this disclosure with reference to the accompanying drawings, it is to be understood that this disclosure is not limited to the precise embodiments, and that various changes and modifications may be effected therein by those skilled in the art without departing from the scope or spirit of this disclosure as defined in the appended claims.

[919] Human tissue microarray from US Biomax (cat number TP242d), top 4 types of cancer (colon, breast, lung and prostate) tissue array with normal tissue, including TNM and pathology grade, 24cases/ 24 cores were used to analyse reactivity of anti CLEC2D antibody clones C0694 and C2685. The prostate cancer samples are as follows.

Table 51

Patient Age	Patient sex	Cancer	Pathology Diagnosis	TNM	Grade	Stage	Type
71	M	Prostate	Adenocarcinoma Gleason 2 (2+2)	T2N0M0	1	I	Malignant
73	M	Prostate	Adenocarcinoma Gleason 4 (4+4)	T3N0M0	2	III	Malignant
60	M	Prostate	Adenocarcinoma Gleason 3 (3+3)	T3N1M0	2	IV	Malignant
64	M	Prostate	Adenocarcinoma Gleason 4 (4+3)	T3N0M0	2	III	Malignant
31	M	Prostate	Prostate tissue	-	-	-	Normal
35	M	Prostate	Prostate tissue	-	-	-	Normal

[920] The IHC staining followed both CC1 and CC2 protocols at different concentrations of antibody from 1:10 dilution to 1:30 dilution. The data suggests C2685 revealed strong reactivity and less interference from negative regions. Results are described in FIG. 23D.

[921] TCGA Data - All Cancers CLEC2D Expression

[922] A pan-cancer analysis was carried out by studying all the TCGA cancer projects. All the associated FPKM files from the projects were downloaded and specifically queried for CLEC2D

expression. The FPKM files were made up of Tumor expression files and in some cases Normal Tissue Expression files. Both sets were separately used to calculate a range for CLEC2D Expression for each cancer among Normal and Tissue cases. Additionally outliers were omitted from the data by assuming a normal distribution of the Expression values and discarding values that were more than 2 standard deviations away from the mean.

Table 52. A List of the Cancers analysed for CLEC2D Expression. * denotes projects whose CLEC2D expression levels differed significantly from the rest.

ACC	Adrenocortical Carcinoma
BLCA	Bladder Urothelial Carcinoma
BRCA	Breast Invasive Carcinoma
CESC	Cervical Squamous Cell Carcinoma and Endocervical Adenocarcinoma
CHOL	Cholangiocarcinoma
COAD	Colon Adenocarcinoma
DLBC*	Lymphoid Neoplasm Diffuse Large B-cell Lymphoma
ESCA	Esophageal Carcinoma
GBM	Glioblastoma Multiforme
HNSC	Head and Neck Squamous Cell Carcinoma
KICH	Kidney Chromophobe
KIRC	Kidney Renal Clear Cell Carcinoma
KIRP	Kidney Renal Papillary Cell Carcinoma
LAML	Acute Myeloid Leukemia
LGG	Brain Lower Grade Glioma
LIHC	Liver Hepatocellular Carcinoma
LUAD	Lung Adenocarcinoma
LUSC	Lung Squamous Cell Carcinoma
MESO	Mesothelioma

OV	Ovarian Serous Cystadenocarcinoma
PAAD*	Pancreatic Adenocarcinoma
PCPG	Pheochromocytoma and Paraganglioma
PRAD	Prostate Adenocarcinoma
READ	Rectum Adenocarcinoma
SARC	Sarcoma
SKCM	Skin Cutaneous Melanoma
STAD	Stomach Adenocarcinoma
TGCT*	Testicular Germ Cell Tumors
THCA	Thyroid Carcinoma
THYM*	Thymoma
UCEC	Uterine Corpus Endometrial Carcinoma
UCS	Uterine Carcinosarcoma
UVM	Uveal Melanoma

[923] For each subset the 'spread' of the CLEC2D expression profile was plotted by looking at the minimum, maximum and interquartile values. As can be seen from FIG. 24A CLEC2D appears to conform remarkable existence in terms of expression level seen in different cancer conditions as listed in above table, amongst others.

[924] Binding studies: Flow cytometry and Imaging

[925] As observed in prostate cancer cell lines, the observations were extended to other tumour cell lines as well, using identified anti CLEC2D antibody clones, as exemplified by C2685, C5511, amongst others. The binding was also monitored through both flow cytometry and confocal microscopy, wherein respective experimental conditions are similar to the description above.

[926] Using anti CLEC2D antibody C5511, flow cytometric observation have been summarized in the following Table 53.

Table 53. Bispecific antibody

Tumor cell line	Disease indication	Binding fold change against Control (C5511)
HepG2	Liver cancer	1.5
SKBR3	Breast cancer	1.8
SKOV3	Ovary cancer	1.2
BT474	Breast cancer	2.0
Ramos	Lymphoma	2.2
FADu	Head & Neck squamous cell carcinoma	1.2
LN229	Glioblastoma	7.5
SW620	Colon cancer	2.3
MDA-MB-361	Breast cancer	3
NCI-H1838	non-small cell lung cancer	2.3
Capan-1	Pancreatic cancer	1.8

[927] As can be understood, the expression level of CLEC2D on various cancer cell lines was found to be either low or moderate to high.

[928] Similarly, in order to determine the disease relevance for novel antibodies we have checked the expression label of CLEC2D on the surface of different tumor cell lines such as liver carcinoma cancer, Glioma, ovarian adenocarcinoma, lung carcinoma, myeloma, lymphoma and breast cancer tough confocal microscopy. There are varying labels of expression of CLEC2D observed across the cancer cell lines tested by using anti- CLEC2D antibody clone C2685 (FIG. 24B). Predominant expression of CLEC2D was observed on the surface of hepatocellular carcinoma (HepG2), breast cancer (BT474), and glioma (LN229) whereas a very low or no expression observed in ovarian adenocarcinoma (SkoV3), myeloma (NCI-H929) and lymphoma (Ramos) (FIG. 24B).

[929] To check the regulation on the translation of CLEC2D in these cancer cell lines were induced with various inducers such as effector cells (either whole PBMC or soup of PBMC) or activator of NK cells (e.g. LPS), IFN-γ, poly I:C to all tumor cell lines (HepG2, BT474, LN229, SkoV3, NCI-H929 and Ramos) similar to prostate tumor cell line and monitored expression label of CLEC2D. Upon treatments, increased expression label of CLEC2D was observed when compared to the untreated target cells (FIG. 24C). Interestingly, on the SkoV3, NCI-H929 and Ramos cells have observed increased expression of CLEC2D upon treatment whereas on untreated cells have no/less expression (FIG. 24C). These finding indicates that CLEC2D is induced upon specific TLR stimulations on these cells and could be a potential target on these cancer conditions which can be targeted using anti CLEC2D antibody.

[930] Cytotoxicity

[931] Tumour cell lines, as exemplified by SKOV3 (Ovarrian cancer cell line), HepG2 (hepatocellular carcinoma) cells were labelled with Efluor as per the manufacturer's protocol and were seeded at a density of $0.04x10^6$ in 20% DMEM in 24 well plates. After 24 hours, freshly isolated PBMCs were added in T: E of 1:5. Novel monoclonal anti-CLEC2D antibodies C5511 were added at 200µg/ml in the assay reaction of 0.5ml and incubated for 14 hours. Supernatant was collected from 24 well plate and adherent cells were trypsinized and collected in 1.5ml tubes. Reaction mixture was incubated with sytox green (15nM) for 20min and fluorescence was detected in flow cytometer. Percent specific cell death was determined by subtracting the percent cell death of control from the test samples and showed significant cytotoxicity in ovarian (SKOv3) and liver (HepG2) (FIG. 24D) cancer cell lines indicating antitumor activity of anti CLEC2D antibody against multiple diseases.

[932] As can be understood, isolated anti CLEC2D antibody that were used to monitor CLEC2D surface expression on several cell lines associated with diseases, such as breast cancer (BT474), lymphoma (ramos), liver cancer (HepG2), prostate cancer (PC3, DU145, LNCAP and 22RV1) glioma (LN229) ovarian adenocarcinoma (SkoV3), myeloma (NCI-H929), is first-in-class in the space. Moreover, cytotoxicity elicited by the said anti CLEC2D antibody reflects the fact that these anti CLEC2D antibody could be potentially used as therapeutic avenue against respective diseases. Taken together, this also signifies that CLEC2D antigen expression is linked with multiple cancer cell lines and could play an important role in cancer biology, as speculated the present disclosure.

[933] Risk mitigation studies done with Anti-CLEC2D monoclonal antibody

[934] Immunogenicity to protein based biotherapeutics is a complex process involving numerous factors specific to products, including critical feature such as quality of drug, and patients. These critical quality attributes may include: variations in the primary sequence, host-cell specific post-translational modifications, the presence of host cell proteins, formulation changes, aggregation, chemical modifications (oxidation, deamidation, or glycation), and changes in protein structure. Some critical quality attributes of antibody drug products have been suggested to affect patient safety through enhancing the sequence based risk of immunogenicity, although the exact contribution of specific types of attributes is not known. T-cell dependent responses are the primary drivers of the long-term affinity matured immune response to biologics in the clinic. These include assay systems using: whole blood, peripheral blood mononuclear cells (PBMC), CD8+-depleted PBMC, immortalized cell lines, dendritic cells/ monocytes/ macrophages co-cultured with autologous CD4+ Tcells, and artificial lymph node systems, to name a few. Various biological outcomes can be measured at different stages of immune cell activation in these in vitro assays including, cytokine secretion, expression of cell surface markers of activation, identification of HLA-DR bound peptides, signal transduction events, phagocytosis by antigen presenting cells (APC), and proliferation. The application of the designated assay to the development of biopharmaceuticals can range from candidate selection at the early development phase to the late stage evaluation of specific attributes that may impact the risk of immunogenicity. Present disclosure details on attempts to evaluate anti CLEC2D antibody associated risk towards immunogenicity or related attributes.

[935] Lymphocyte proliferation studies

[936] Proliferation of lymphocytes were tested by three independent experimental protocols such as, wet coating of antibodies, air dried coating of antibodies and high density PBMC pre-culture followed by induction with test antibodies, detailed as follows:

[937] Wet coating of antibodies

Different concentrations of test antibodies, not limited to C5511, ranging from 1µg/ml to 100 µg/ml and 1µg/ml of the positive control - anti CD3 antibody, anti OKT3 antibody, were added to the wells of a 96 well flat bottom plate and incubated in a 37^{0}C incubator for 2-3 hours. After that the wells were washed three times with 200µl of DPBS. PBMCs were labelled with Efluor 670 viable cell dye as per manufacturer's protocol. 30000 PBMC cells were seeded in each well

in total 200µl growth media (RPMI-1640 with 10% FBS). Day 0 samples were collected and analyzed by flow-cytometry. Cells were incubated at 37ºC in a 5% CO2 incubator for 4 days. On 4th day samples were collected, stained with anti CD4 antibody-FITC conjugate and analyzed by flow-cytometry.

[938] Air dried coating of antibodies

[939] Different concentrations of test antibodies ranging from 1µg/ml to 100 µg/ml and 1µg/ml of the positive control anti CD3 antibody OKT3 were added to the wells of a 96 well flat bottom plate and air dried in biosafety cabinet. Volume of antibodies were restricted to less than 50µl for optimum air drying. PBMCs were labelled with Efluor 670 viable cell dye as per manufacturer's protocol. Once the wells were dry, 30000 PBMC cells were seeded in each well in total 200µl growth media (RPMI-1640 with 10% FBS). Day 0 samples were collected and analyzed by flow-cytometry. Cells were incubated at 37ºC in a 5% CO2 incubator for 4 days. On 4th day samples were collected, stained with anti CD4 antibody-FITC conjugate and analyzed by flow-cytometry.

[940] High density pre-culture of PBMC for TCR priming followed by induction with antibodies in solution

[941] PBMC cells were pre-cultured at 1X10^6 cells/ml and 10X10^6 cells/ml density for 48hrs in growth media at 37ºC in a 5% CO2 incubator. After 48 hours PBMCs were labelled with Efluor 670 viable cell dye as per manufacturer's protocol. 1X10^6 PBMC cells/ml were seeded in each well in total 200µl growth media (RPMI-1640 with 10% FBS). Different concentrations of test antibodies ranging from 1µg/ml to 100 µg/ml and 1µg/ml of the positive control anti CD3 antibody OKT3 were added to the wells containing PBMCs. Day 0 samples were collected and analyzed by flow-cytometry. Cells were incubated at 37ºC in a 5% CO2 incubator for 4 days. On 4th day samples were collected, stained with anti CD4 antibody-FITC conjugate and analyzed by flow-cytometry.

[942] Sample processing for flow-cytometry

[943] PBMC samples were centrifuged at 200rpm for 5 minutes. Supernatants were discarded and the cells were re-suspended in 100µl of DPBS with 0.5%BSA along with anti CD4 antibody-FITC conjugate (1:100 dilution in final reaction). Cells were incubated for 30 minutes in dark. After that cells were centrifuged at 200rpm for 5 minutes, removed the supernatant and re-suspended in 100µl of DPBS with 0.5%BSA.

[944] As can be observed from FIGS. 25A, 25B and 25C, wherein anti CLEC2D antibody treatment was used as positive control, PBMC treated with anti OKT3 antibody showed lymphocyte proliferation as observed by partitioning of Efluor viability dye into multiple daughter populations (showed by the arrows on the histogram). Appearance of single population after 4 days of culture was observed in untreated PBMC control and 1µg/ml to 100 µg/ml anti CLEC2D antibody treated test samples, shows that anti CLEC2D antibodies did not induce any lymphocyte proliferation. This observation was consistent with three independent test protocols that are wet coating of antibodies (FIG. 25A), air dried coating of antibodies (FIG. 25B) and high density PBMC pre-culture (FIG. 25C) followed by induction with test antibodies. PBMC from multiple healthy donors were tested and the results obtained were consistent.

[945] Measurement of secreted cytokines: IFN-γ and IL2

[946] As described earlier in the current segment, apart from understanding lymphocyte proliferation assay, it is essential to confirm whether Anti CLEC2D antibody induces any cytokines, such as IFN-γ, IL2, or not. Measurement of secreted cytokines such as IFN-γ, IL2, not limited to, were performed through ELISA based detection method wherein supernatant collected from various experimental set up/conditions as detailed above e.g., high density, wet coating, was used at 24 hrs interval for subsequent quantitation. In all experiments concentration of respective antibodies used are anti OKT3 antibody (1ug/ml) and anti CLEC2D antibody clones such as C5511 C6481 C4608 at 100 ug/ml. Subsequently, supernatant obtained from anti OKT3 antibody treated sample was diluted in the ratio of 1:4 wherein 50 ul of supernatant was diluted by adding 150ul of 10%RPMI 1640, on the contrary, anti CLEC2D antibody treated samples were used directly without any further dilution of supernatant. Simultaneously, samples to measure cytokine IL2 was prepared by wet coating method. Herein anti OKT3 antibody treated sample was diluted in the ratio of 1:10 while 25 ul was diluted by adding 225 ul of 10%RPMI 1640, while supernatant collected from anti CLEC2D antibody treated samples were used directly. Supernatant obtained from PBMC without treatment was used as control against respective experimentation either for IFN-γ or IL2.

[947] As can be seen from FIG. 25D, wherein PBMC treated with anti OKT3 antibody exhibited highest level of IFN gamma secretion in supernatant at a concentration of 1155 pg/mL while tested anti CLEC2D antibodies did not elevate IFN gamma production beyond 30 pg/mL concentration, related to any anti CLEC2D antibody clones (FIG. 25D). Similarly, for IL2

measurement anti OKT3 antibody induced elevation in secretion was found to be 121.50 pg/mL while anti CLEC2D antibodies did not give rise to IL2 secretion more than 4.7 pg/mL (FIG. 25E). Taken together, identified therapeutic anti CLEC2D antibody poses low possibility on immunogenicity reaction as judged by the lack of any T lymphocyte daughter population seen when treated with anti CLEC2D antibody and also extremely low amount of cytokine secretion as observed with both IFN-γ and IL2.

[948] Safety study performed with Anti-CLEC2D monoclonal antibody in Rat/ non-human primate

[949] Toxicology studies with therapeutic monoclonal antibodies should be carried out in a species that are pharmacologically relevant, meaning one that both expresses the target antigen recognized by the monoclonal antibody and evokes a similar pharmacological response following antibody binding, similar to that expected in humans. It is required to demonstrate comparable effector function of monoclonal antibodies in animals that can be extended to humans, especially for antibodies with relatively strong effector function, such as, IgG1. Thereby, the most sensitive animal model available for predicting human safety is utilized. However, cross-reactivity, or lack in cross reactivity, can be predicted through a detailed *in silico* analysis of sequence and structural understanding between the human antigen protein or targeted epitopes and the equivalent proteins in conventional species used for toxicology studies. It is advisable that toxicology assessment should be performed in two relevant species if available, one rodent and one non-rodent, while non-human primates (NHP), such as, cynomolgus monkey, is celebrated as the most suitable species to ethically justify its use and strategies minimizing primate use.

[950] *In silico* understanding of comparative sequence analysis of CLEC2D antigens homologs from Human Rat, Mouse and Cynomolgus moneky, indicated that human CLEC2D antigen shares highest sequence homology (>90%) with cynomolgus monkey CLEC2D homolog while sequence homology against Rat and mouse homologs being less than ~70%. However, sequences were looked into in detail to identify the presence of the important residues which contacts antibody paratope sequence. The said exercise indicated that all species contain at least 70% of the contact points and interacting amino acid residues conserved and possibly available to interact with anti CLEC2D antibody. Therefore efforts towards understanding the binding of anti CLEC2D mono clonal antibodies was attempted through generating surface expressed

CLEC2D antigen homologs from Rat, Mouse and cynomolgus monkey species. Flow cytometry based method was employed to assess the binding between antibody and CLEC2D antigen homologs.

[951] As can be linked with SEQ IDs 886, 910, 911, 918, full length CLEC2D homologous sequences, from respective species were synthesized and cloned in pCDNA3.1, mammalian expression vector, which were transfected in CHO cells for binding studies through flow cytometry.

[952] Transfection with constructs of CLEC2D antigen variants for homology study

[953] CHO suspension cells at more than 90% viability were used for expression of CLEC2D antigen variants. For 100ml volume of transfection 1.25 X10^8 cells were taken. Cells were centrifuged at 1000-1400 rpm for 4-5 minutes, decanted the spent media and re-suspended in 25 ml of OptiMEM I media. DNA constructs were transfected using Lipofectamine LTX with PlusTM reagent. 50-100 µg of respective pCDNA 3.1, constructs, were used with 1:3 to 1:6 DNA to transfection reagent ratio and 50-100 µl PlusTM reagent was used. DNA and Lipofectamine LTX complex was prepared in 25ml OptiMEM I and incubated at 20-25°C for 5 minutes for complex formation. The transfection mix was added slowly to the cell suspension. The cells were incubated for 4-6 hours at 37°C in a 5% CO2 shaker Incubator at 100-120 RPM. 50ml of Power CHO2 CD growth media was added to the cells. The cells were incubated at 37°C in a 5% CO2 shaker Incubator at 100-120 RPM. 2-3 days post transfection 200 ml Power CHO2 CD growth media was added and Glutamax was added from 200mM stock to achieve final concentration of 2mM. The cells were incubated at 37°C in a 5% CO2 shaker Incubator at 100-120 RPM. Cells were analyzed for cell surface antigen binding by flow-cytometry on day 3 to day 6 after transfection.

[954] As can be seen in FIG. 26, Anti CLEC2D antibody clones C5511, C4608, not limited to, developed against human CLEC2D antigen, and exhibited similar binding ranging from 2-4 fold of MFI. This indicates a broad specificity of anti CLEC2D antibodies towards CLEC2D homologs in both rodent and non-human primate species.

Table 54. Amino acid sequence recognized by ant-CLEC2D antibody

SEQ ID NO	Amino acid sequence recognized by ant-CLEC2D antibody
2560	ARG175- XAA176- TYR177-XAA178-GLU179
2561	GLU150-XAA151- THR152- ARG153- GLN154

2562	ARG175-XAA176-TYR177-XAA178-GLU179
2563	ARG101-XAA102-XAA-103-XAA104-SER105-XAA106-ASP107
2564	GLU138-XAA139-XAA140-GLN141-XAA142-XAA143-LYS144
2565	GLU138-GLN139-XAA140-GLN141
2566	ARG175-XAA176-TYR177-XAA178-XAA179-ARG180
2567	TYR177-XAA179-XAA180-LYS181

CLAIMS

1. An isolated antibody or antigen-binding fragment thereof comprising a heavy chain and a light chain, wherein the heavy chain comprises a sequence selected from the group consisting of:
   a. a sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 46, SEQ ID NO: 65, SEQ ID NO: 59, and SEQ ID NO: 99;
   b. a sequence that is at least 80%, at least 81%, at least 82%, at least 83% , at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 57, SEQ ID NO: 91, SEQ ID NO: 98, SEQ ID NO: 84, SEQ ID NO: 58, SEQ ID NO: 88, SEQ ID NO: 96, SEQ ID NO: 47, SEQ ID NO: 17, and SEQ ID NO: 8;
   c. a sequence that is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 93, SEQ ID NO: 53, SEQ ID NO: 95, SEQ ID NO: 23, SEQ ID NO: 103, and SEQ ID NO: 7;
   d. a sequence that is at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 45, SEQ ID NO: 15, SEQ ID NO: 51, SEQ ID NO: 44, SEQ ID NO: 73, SEQ ID NO: 36, SEQ ID NO: 77, SEQ ID NO: 50, and SEQ ID NO: 6;
   e. a sequence that is at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5% or at least 99.9% identical or 100% identical to a sequence selected from SEQ ID NO: 97, SEQ ID NO: 16, SEQ ID NO: 76, SEQ ID NO: 9, SEQ ID NO: 89, SEQ ID NO: 107, SEQ ID NO: 68, SEQ ID NO: 29, SEQ ID NO:

67, SEQ ID NO: 74, SEQ ID NO: 32, SEQ ID NO: 81, SEQ ID NO: 106, SEQ ID NO: 31, SEQ ID NO: 62, SEQ ID NO: 48, SEQ ID NO: 75, SEQ ID NO: 12, SEQ ID NO: 102, SEQ ID NO: 54, SEQ ID NO: 80, SEQ ID NO: 26, SEQ ID NO: 30, SEQ ID NO: 92, SEQ ID NO: 108, and SEQ ID NO: 79;

f. a sequence that is at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5% or at least 99.9% identical or 100% identical to a sequence selected from SEQ ID NO: 105, SEQ ID NO: 101, SEQ ID NO: 4, SEQ ID NO: 72, SEQ ID NO: 28, SEQ ID NO: 64, SEQ ID NO: 25, SEQ ID NO: 60, SEQ ID NO: 55, SEQ ID NO: 52, SEQ ID NO: 27, SEQ ID NO: 43, SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 14, SEQ ID NO: 85, SEQ ID NO: 13, SEQ ID NO: 61, SEQ ID NO: 42, SEQ ID NO: 39, SEQ ID NO: 10, SEQ ID NO: 49, SEQ ID NO: 24, SEQ ID NO: 40, SEQ ID NO: 63, SEQ ID NO: 78, SEQ ID NO: 2, SEQ ID NO: 94, and SEQ ID NO: 5;

g. a sequence that is at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5% or at least 99.9% identical or 100% identical to a sequence selected from SEQ ID NO: 11, SEQ ID NO: 35, SEQ ID NO: 86, SEQ ID NO: 22, SEQ ID NO: 69, SEQ ID NO: 41, SEQ ID NO: 3, SEQ ID NO: 66, SEQ ID NO: 37, SEQ ID NO: 56, SEQ ID NO: 21, SEQ ID NO: 38, SEQ ID NO: 90, SEQ ID NO: 100, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 83, SEQ ID NO: 1, and SEQ ID NO: 19; and

h. a sequence that is at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5% or at least 99.9% identical or 100% identical to a sequence selected from SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 87, SEQ ID NO: 82, and SEQ ID NO: 104,

wherein the antibody or antigen-binding fragment thereof binds to C-Type Lectin Domain Family 2 Member D (CLEC2D).

2. An isolated antibody or antigen-binding fragment thereof comprising a heavy chain and a light chain, wherein the light chain comprises a sequence selected from the group consisting of:
   a. a sequence that is at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 218, SEQ ID NO: 249, SEQ ID NO: 230, SEQ ID NO: 279, SEQ ID NO: 316, SEQ ID NO: 237, SEQ ID NO: 322, SEQ ID NO: 225, SEQ ID NO: 318, SEQ ID NO: 233, SEQ ID NO: 305, SEQ ID NO: 280, SEQ ID NO: 283, SEQ ID NO: 242, SEQ ID NO: 286, SEQ ID NO: 297, SEQ ID NO: 309, and SEQ ID NO: 246;
   b. a sequence that is at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 222, SEQ ID NO: 258, SEQ ID NO: 219, SEQ ID NO: 313, SEQ ID NO: 294, SEQ ID NO: 303, SEQ ID NO: 317, SEQ ID NO: 273, SEQ ID NO: 266, SEQ ID NO: 315, SEQ ID NO: 257, SEQ ID NO: 288, SEQ ID NO: 301, SEQ ID NO: 221, SEQ ID NO: 240, SEQ ID NO: 299, SEQ ID NO: 247, SEQ ID NO: 263, and SEQ ID NO: 274;
   c. a sequence that is at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 231, SEQ ID NO: 250, SEQ ID NO: 260, SEQ ID NO: 226, SEQ ID NO: 271, SEQ ID NO: 256, SEQ ID NO: 272, SEQ ID NO: 278, SEQ ID NO: 302, SEQ ID NO: 320, SEQ ID NO: 295, SEQ ID NO: 292, SEQ ID NO: 229, SEQ ID NO: 264, SEQ ID NO: 252, SEQ ID NO: 267, SEQ ID NO: 304, SEQ ID NO: 300, SEQ ID NO: 311, and SEQ ID NO: 324;
   d. a sequence that is at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical

to a sequence selected from SEQ ID NO: 259, SEQ ID NO: 239, SEQ ID NO: 281, SEQ ID NO: 228, SEQ ID NO: 217, SEQ ID NO: 227, and SEQ ID NO: 251;

e. a sequence that is at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100%identical to a sequence selected from SEQ ID NO: 307, SEQ ID NO: 262, SEQ ID NO: 253, SEQ ID NO: 276, SEQ ID NO: 323, SEQ ID NO: 234, SEQ ID NO: 261, SEQ ID NO: 312, and SEQ ID NO: 290;

f. a sequence that is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 254, SEQ ID NO: 289, SEQ ID NO: 238, SEQ ID NO: 268, SEQ ID NO: 248, SEQ ID NO: 284, SEQ ID NO: 244, SEQ ID NO: 310, SEQ ID NO: 243, SEQ ID NO: 285, SEQ ID NO: 220, SEQ ID NO: 255, SEQ ID NO: 293, SEQ ID NO: 298, SEQ ID NO: 235, SEQ ID NO: 319, SEQ ID NO: 245, SEQ ID NO: 224, SEQ ID NO: 291, SEQ ID NO: 277, and SEQ ID NO: 232; and

g. a sequence that is at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 282, SEQ ID NO: 308, SEQ ID NO: 287, SEQ ID NO: 321, SEQ ID NO: 236, SEQ ID NO: 265, SEQ ID NO: 270, SEQ ID NO: 275, SEQ ID NO: 306, SEQ ID NO: 296, SEQ ID NO: 241, SEQ ID NO: 314, and SEQ ID NO: 223;

wherein the antibody or antigen-binding fragment thereof binds to CLEC2D.

3. An isolated antibody or antigen-binding fragment thereof, comprising:

a. a heavy chain comprising a sequence selected from:

i. a sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 46, SEQ ID NO: 65, SEQ ID NO: 59, and SEQ ID NO: 99;

ii. a sequence that is at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 57, SEQ ID NO: 91, SEQ ID NO: 98, SEQ ID NO: 84, SEQ ID NO: 58, SEQ ID NO: 88, SEQ ID NO: 96, SEQ ID NO: 47, SEQ ID NO: 17, and SEQ ID NO: 8;

iii. a sequence that is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 93, SEQ ID NO: 53, SEQ ID NO: 95, SEQ ID NO: 23, SEQ ID NO: 103, and SEQ ID NO: 7;

iv. a sequence that is at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 45, SEQ ID NO: 15, SEQ ID NO: 51, SEQ ID NO: 44, SEQ ID NO: 73, SEQ ID NO: 36, SEQ ID NO: 77, SEQ ID NO: 50, and SEQ ID NO: 6;

v. a sequence that is at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 97, SEQ ID NO: 16, SEQ ID NO: 76, SEQ ID NO: 9, SEQ ID NO: 89, SEQ ID NO: 107, SEQ ID NO: 68, SEQ ID NO: 29, SEQ ID NO: 67, SEQ ID NO: 74, SEQ ID NO: 32, SEQ ID NO: 81, SEQ ID NO: 106, SEQ ID NO: 31, SEQ ID NO: 62, SEQ ID NO: 48, SEQ ID NO: 75, SEQ ID NO: 12, SEQ ID NO: 102, SEQ ID NO: 54, SEQ ID NO: 80, SEQ ID NO: 26, SEQ ID NO: 30, SEQ ID NO: 92, SEQ ID NO: 108, and SEQ ID NO: 79;

vi. a sequence that is at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 105, SEQ ID NO: 101, SEQ ID NO: 4, SEQ ID NO: 72, SEQ ID NO: 28, SEQ ID NO: 64, SEQ ID NO: 25, SEQ ID NO: 60, SEQ ID NO: 55, SEQ ID NO: 52, SEQ ID NO: 27, SEQ ID NO: 43, SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 14, SEQ ID NO: 85, SEQ ID NO: 13, SEQ ID NO: 61, SEQ ID NO: 42, SEQ ID NO: 39, SEQ ID NO: 10, SEQ ID NO: 49, SEQ ID NO: 24, SEQ ID NO: 40, SEQ ID NO: 63, SEQ ID NO: 78, SEQ ID NO: 2, SEQ ID NO: 94, and SEQ ID NO: 5;

vii. a sequence that is at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 11, SEQ ID NO: 35, SEQ ID NO: 86, SEQ ID NO: 22, SEQ ID NO: 69, SEQ ID NO: 41, SEQ ID NO: 3, SEQ ID NO: 66, SEQ ID NO: 37, SEQ ID NO: 56, SEQ ID NO: 21, SEQ ID NO: 38, SEQ ID NO: 90, SEQ ID NO: 100, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 83, SEQ ID NO: 1, and SEQ ID NO: 19; and

viii. a sequence that is at least 35%, at least 40%,a t least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 87, SEQ ID NO: 82, and SEQ ID NO: 104; and

b. a light chain comprising a sequence selected from:

i. a sequence that is at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 218, SEQ ID NO: 249, SEQ ID NO: 230, SEQ ID NO: 279, SEQ ID NO: 316, SEQ ID NO: 237, SEQ ID NO: 322, SEQ ID NO: 225, SEQ ID NO: 318, SEQ ID NO: 233, SEQ ID NO: 305, SEQ ID NO: 280, SEQ ID NO: 283, SEQ ID NO: 242, SEQ ID NO: 286, SEQ ID NO: 297, SEQ ID NO: 309, and SEQ ID NO: 246;

ii. a sequence that is at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 222, SEQ ID NO: 258, SEQ ID NO: 219, SEQ ID NO: 313, SEQ ID NO: 294, SEQ ID NO: 303, SEQ ID NO: 317, SEQ ID NO: 273, SEQ ID NO: 266, SEQ ID NO: 315, SEQ ID NO: 257, SEQ ID NO: 288, SEQ ID NO: 301, SEQ ID NO: 221, SEQ ID NO: 240, SEQ ID NO: 299, SEQ ID NO: 247, SEQ ID NO: 263, and SEQ ID NO: 274;

iii. a sequence that is at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 231, SEQ ID NO: 250, SEQ ID NO: 260, SEQ ID NO: 226, SEQ ID NO: 271, SEQ ID NO: 256, SEQ ID NO: 272, SEQ ID NO: 278, SEQ ID NO: 302, SEQ ID NO: 320, SEQ ID NO: 295, SEQ ID NO: 292, SEQ ID NO: 229, SEQ ID NO: 264, SEQ ID NO: 252, SEQ ID NO: 267, SEQ ID NO: 304, SEQ ID NO: 300, SEQ ID NO: 311, and SEQ ID NO: 324;

iv. a sequence that is at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 259, SEQ ID NO: 239, SEQ ID NO: 281, SEQ ID NO: 228, SEQ ID NO: 217, SEQ ID NO: 227, and SEQ ID NO: 251;

v. a sequence that is at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 307, SEQ ID NO: 262, SEQ ID NO: 253, SEQ ID NO: 276, SEQ ID NO: 323, SEQ ID NO: 234, SEQ ID NO: 261, SEQ ID NO: 312, and SEQ ID NO: 290;

vi. a sequence that is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 254, SEQ ID NO: 289, SEQ ID NO: 238, SEQ ID NO: 268, SEQ ID NO: 248, SEQ ID NO: 284, SEQ ID NO: 244, SEQ ID NO: 310, SEQ ID NO: 243, SEQ ID NO: 285, SEQ ID NO: 220, SEQ ID NO: 255, SEQ ID NO: 293, SEQ ID NO: 298, SEQ ID NO: 235, SEQ ID NO: 319, SEQ ID NO: 245, SEQ ID NO: 224, SEQ ID NO: 291, SEQ ID NO: 277, and SEQ ID NO: 232; and

vii. a sequence that is at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% or 100% identical to a sequence selected from SEQ ID NO: 282, SEQ ID NO: 308, SEQ ID NO: 287, SEQ ID NO: 321, SEQ ID NO: 236, SEQ ID NO: 265, SEQ ID NO: 270, SEQ ID NO: 275, SEQ ID NO: 306, SEQ ID NO: 296, SEQ ID NO: 241, SEQ ID NO: 314, and SEQ ID NO: 223;

wherein the antibody or antigen-binding fragment thereof binds to CLEC2D.

4. An isolated antibody or antigen-binding fragment thereof comprising a heavy chain and a light chain, wherein the heavy chain comprises a sequence selected from any one of SEQ ID NOs: 1-108, wherein the antibody or antigen-binding fragment thereof binds to CLEC2D.

5. An isolated antibody or antigen-binding fragment thereof comprising a heavy chain and a light chain, wherein the light chain comprises a sequence selected from any one of SEQ ID NOs: 217-324, wherein the antibody or antigen-binding fragment thereof binds to CLEC2D.
6. An isolated antibody or antigen-binding fragment thereof comprising a heavy chain and a light chain, wherein the heavy chain comprises a sequence selected from any one of SEQ ID NOs: 1-108, and the light chain comprises a sequence selected from any one of SEQ ID NOs: 217-324, wherein the antibody or antigen-binding fragment thereof binds to CLEC2D.
7. An isolated antibody or antigen-binding fragment thereof comprising a heavy chain and a light chain, wherein the heavy chain comprises:

(i) a heavy chain (HC) CDR1 comprising a sequence selected from SEQ ID NOs: 433-485;

(ii) an HC CDR2 comprising a sequence selected from SEQ ID NOs: 486-546; and

(iii) an HC CDR3 comprising a sequence selected from SEQ ID NOs: 547-653,

wherein the antibody or antigen-binding fragment thereof binds to CLEC2D.
8. An isolated antibody or antigen-binding fragment thereof comprising a heavy chain and a light chain, wherein the light chain comprises:

(i) a light chain (LC) CDR1 comprising a sequence selected from SEQ ID NOs: 654-726;

(ii) an LC CDR2 comprising a sequence selected from SEQ ID NOs: 727-783; and

(iii) an LC CDR3 comprising a sequence selected from SEQ ID NOs: 784-885;

wherein the antibody or antigen-binding fragment thereof binds to CLEC2D.
9. An isolated antibody or antigen-binding fragment thereof, comprising:

a. a heavy chain comprising an HC CDR1 sequence selected from SEQ ID NOs: 433-485, an HC CDR2 sequence selected from SEQ ID NOs: 486-546, and an HC CDR3 sequence selected from SEQ ID NOs: 547-653;
b. a light chain comprising a LC CDR1 sequence selected from SEQ ID NOs: 654-726, a LC CDR2 sequence selected from SEQ ID NOs: 727-783, and a LC CDR3 sequence selected from SEQ ID NOs: 784-885; or
c. a combination thereof,

wherein the antibody or antigen-binding fragment thereof binds to CLEC2D.

10. The antibody or antigen-binding fragment thereof of any one of claims 1-9, wherein the antibody or antigen-binding fragment thereof binds to:
    a. a human CLEC2D polypeptide comprising a sequence selected from SEQ ID NOs: 886-909 and 930-1003;
    b. a cynomolgus CLEC2D polypeptide comprising a sequence selected from SEQ ID NOs: 918-920;
    c. a mouse CLEC2D polypeptide comprising a sequence selected from SEQ ID NOs: 911-915;
    d. a rat CLEC2D polypeptide comprising a sequence of SEQ ID NO: 910; and/or
    e. a dog CLEC2D polypeptide comprising a sequence selected from SEQ ID NOs: 916-917.
11. An isolated antibody or antigen-binding fragment thereof comprising a heavy chain and a light chain, wherein the heavy chain comprises a heavy chain complementarity determining region (CDRH) 1, CDRH2 and CDRH3 amino acid sequence of any one of the anti-CLEC2D antibody Nos. A1-N2 in Table 9A, and wherein the light chain comprises a light chain complementarity determining region (CDRL)1, CDRL2 and CDRL3 amino acid sequence of any one of the anti-CLEC2D antibody Nos. A1-N2 in Table 9A.
12. An isolated antibody or antigen-binding fragment thereof comprising a heavy chain and a light chain, wherein the heavy chain comprises a heavy chain amino acid sequence of any one of the anti-CLEC2D antibody Nos. A1-N2 in Table 9A, and wherein the light chain comprises a light chain amino acid sequence of any one of the anti-CLEC2D antibody Nos. A1-N2 in Table 9A.
13. An isolated antibody or antigen-binding fragment thereof comprising a heavy chain and a light chain, wherein the heavy chain comprises a heavy chain complementarity determining region (CDRH) 1, CDRH2 and CDRH3 amino acid sequence of an anti-CLEC2D antibody selected from the group consisting of: A1, B1, E1, P1, U1, Y1, E2, I2 and L2 in Table 9A, and wherein the light chain comprises a light chain complementarity determining region (CDRL)1, CDRL2 and CDRL3 amino acid sequence of an anti-CLEC2D antibody selected from the group consisting of: A1, B1, E1, P1, U1, Y1, E2, I2 and L2 in Table 9A.
14. An isolated antibody or antigen-binding fragment thereof comprising a heavy chain and a light chain, wherein the heavy chain comprises a variable heavy chain amino acid sequence

of an anti-CLEC2D antibody selected from the group consisting of: A1, B1, E1, P1, U1, Y1, E2, I2 and L2 in Table 9A, and wherein the light chain comprises a variable light chain amino acid sequence of an anti-CLEC2D antibody selected from the group consisting of: A1, B1, E1, P1, U1, Y1, E2, I2 and L2 in Table 9A.

15. An isolated antibody or antigen-binding fragment thereof comprising a heavy chain and a light chain, wherein the heavy chain comprises a heavy chain frame work region sequence of a Germline family of an anti-CLEC2D antibody selected from the group consisting of: A1, B1, E1, P1, U1, Y1, E2, I2 and L2 in Table 9B, and wherein the light chain comprises a frame work region sequence of a light chain Germline family of an anti-CLEC2D antibody selected from the group consisting of: A1, B1, E1, P1, U1, Y1, E2, I2 and L2 in Table 9B.
16. The isolated antibody or antigen-binding fragment thereof, of any one of claims 62 to 64, wherein the anti-CLEC2D antibody is anti-CLEC2D antibody No. A1 in Table 9A and 9B.
17. The isolated antibody or antigen-binding fragment thereof, of any one of claims 62 to 64, wherein the anti-CLEC2D antibody is anti-CLEC2D antibody No. B1 in Table 9A and 9B.
18. The isolated antibody or antigen-binding fragment thereof, of any one of claims 62 to 64, wherein the anti-CLEC2D antibody is anti-CLEC2D antibody No. E1 in Table 9A and 9B.
19. The isolated antibody or antigen-binding fragment thereof, of any one of claims 62 to 64, wherein the anti-CLEC2D antibody is anti-CLEC2D antibody No. P1 in Table 9A and 9B.
20. The isolated antibody or antigen-binding fragment thereof, of any one of claims 62 to 64, wherein the anti-CLEC2D antibody is anti-CLEC2D antibody No. U1 in Table 9A and 9B.
21. The isolated antibody or antigen-binding fragment thereof, of any one of claims 62 to 64, wherein the anti-CLEC2D antibody is anti-CLEC2D antibody No. Y1 in Table 9A and 9B.
22. The isolated antibody or antigen-binding fragment thereof, of any one of claims 62 to 64, wherein the anti-CLEC2D antibody is anti-CLEC2D antibody No. E2 in Table 9A and 9B.
23. The isolated antibody or antigen-binding fragment thereof, of any one of claims 62 to 64, wherein the anti-CLEC2D antibody is anti-CLEC2D antibody No. I2 in Table 9A and 9B.
24. The isolated antibody or antigen-binding fragment thereof, of any one of claims 62 to 64, wherein the anti-CLEC2D antibody is anti-CLEC2D antibody No. L2 in Table 9A and 9B.
25. The antibody or antigen-binding fragment thereof of any one of claims 1-24, wherein antibody or antigen-binding fragment thereof is a monoclonal antibody.

26. The antibody or antigen-binding fragment thereof of any one of claims 1-24, wherein the antibody or antigen-binding fragment thereof modulates or blocks binding of CLEC2D to a receptor.
27. The antibody or antigen-binding fragment thereof of claim 26, wherein the receptor comprises a CD161 receptor, and wherein the CD161 receptor comprises a sequence selected from SEQ ID NOs: 921-929.
28. The antibody or antigen-binding fragment thereof of any one of claims 1-27, wherein the antibody or antigen binding fragment thereof is human, murine or chimeric.
29. The antibody or antigen-binding fragment thereof of any one of claims 1-28, wherein the antigen-binding fragment is selected from the group consisting of Fv, Fav, F(ab')2, Fab', dsFv, scFv, sc(Fv)2, scFv-CH3, scFv-Fc, and diabody fragments.
30. The isolated antibody or antigen-binding fragment thereof, of any one of claims 1-29, wherein the antibody is afucosylated.
31. The isolated antibody or antigen-binding fragment thereof, of any one of claims 1-30, wherein the antibody or antigen-binding fragment thereof is afucosylated.
32. The isolated antibody or antigen-binding fragment thereof, of any one of claims 1-31, wherein the antibody or antigen-binding fragment thereof is afucocsylated at the antibody region.
33. The isolated antibody or antigen-binding fragment thereof, of any one of claims 1-32, wherein the antibody or antigen-binding fragment thereof comprises an IgG1 Fc region.
34. The isolated antibody or antigen-binding fragment thereof, of any one of claims 1-32, wherein the antibody or antigen-binding fragment thereof comprises an IgG4 Fc region.
35. The isolated antibody or antigen-binding fragment thereof, of any one of claims 1-32, wherein the antibody or antigen-binding fragment thereof comprises an IgG1 N to A Fc region.
36. The isolated antibody or antigen-binding fragment thereof, of any one of claims 1-32, wherein the antibody or antigen-binding fragment thereof comprises an IgG2 Fc region.
37. The antibody or antigen-binding fragment thereof of any one of claims 1-35, wherein the antibody or antigen-binding fragment thereof binds to human CLEC2D with an affinity (KD) of less than 100 nM.

38. The antibody or antigen-binding fragment thereof of any one of claims 1-37, wherein the antibody or antigen-binding fragment thereof, recognizes and binds to conformational epitope of CLEC2D antigen, comprised of amino acids positions overlapping and/or non-overlapping with CD161 receptor interacting amino acid residues.
39. The antibody or antigen-binding fragment thereof of any one of claims 1-37, wherein the antibody or antigen-binding fragment thereof, comprises a variable heavy chain sequence and a variable light chain sequence, that inhibit or abrogate or compete with another antibody that recognizes and binds to conformational epitope of CLEC2D antigen, comprised of amino acids positions either overlapping and/or non-overlapping with CD161 receptor interacting amino acid residues.
40. The antibody or antigen-binding fragment thereof of any one of claims 1-37, wherein the antibody or antigen-binding fragment thereof, comprises a variable heavy chain sequence and a variable light chain sequence that bind to conformational epitope of CLEC2D antigen comprising any of the amino acid positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95 or a combination thereof.
41. The antibody or antigen-binding fragment thereof of any one of claims 1-37, wherein the antibody or antigen-binding fragment thereof, comprises a variable heavy chain sequence and a variable light chain sequence that inhibit or abrogate or competes with, the binding of another antibody to conformational epitope of CLEC2D antigen comprising any of the amino acid positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95 or a combination thereof.
42. The antibody or antigen-binding fragment thereof of any one of claims 1-37, wherein the antibody or antigen-binding fragment thereof, a variable heavy chain sequence and a variable light chain sequence that bind to conformational epitope of CLEC2D antigen comprising at least one of the amino acids positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180;

SER187; LYS181; PHE116; ASN95 of SEQ ID No: 886-920 and 930-1003, constituting non-linear scaffolds for CD161 receptor interacting amino acid residues, thereby blocking the interaction between CLEC2D and CD161 receptors.

43. The antibody or antigen-binding fragment thereof of any one of claims 1-37, wherein the antibody or antigen-binding fragment thereof, comprises a variable heavy chain sequence and a variable light chain sequence that bind to conformational epitope of CLEC2D antigen comprising at least one of the amino acids positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95 of SEQ ID No: 886-920 and 930-1003, constituting allosteric and non-linear scaffolds for CD161 receptor non-interacting amino acid residues, thereby blocking the interaction between CLEC2D and CD161 receptors.

44. The antibody or antigen-binding fragment thereof of any one of claims 1-43, wherein the antibody or antigen-binding fragment thereof, comprises a variable heavy chain sequence and a variable light chain sequence that when bound to CLEC2D selected from SEQ ID Nos: 886-920 and 930-1003, bind to at least one of the amino acids positions ARG175; TYR177; GLU179; ARG153; ARG84; HIS190; ARG101; GLU150; GLN154; THR152; GLN141; SER105; ASP107; ASP92; THR93; LYS94; LYS144; GLU138; CYS176; GLN139; ARG180; SER187; LYS181; PHE116; ASN95, independently or in combination to induce tumour killing or cytotoxicity.

45. The antibody or antigen-binding fragment thereof of claim 44, wherein the antibody or antigen-binding fragment thereof, induces cytotoxicity in at least 5%, at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90% or at least 95%, of the total number of cells treated with the antibody or antigen binding fragment thereof.

46. A pharmaceutical composition comprising the antibody or antigen-binding fragment thereof of any one of claims 1-45.

47. The pharmaceutical composition of claim 46, further comprising at least one of a buffer, a pharmaceutically acceptable diluent, a carrier, a solubilizer, an emulsifier, and a preservative.

48. An isolated nucleic acid comprising a polynucleotide sequence that encodes an amino acid heavy chain sequence selected from SEQ ID NOs: 109-216.
49. An isolated nucleic acid comprising a polynucleotide sequence that encodes an amino acid light chain sequence selected from SEQ ID NOs: 325-432.
50. An isolated nucleic acid comprising a polynucleotide sequence that encodes a heavy chain amino acid sequence of any one of claims 1, 3, 4, 6, 7, and 9-37.
51. An isolated nucleic acid comprising a polynucleotide sequence that encodes a light chain amino acid sequence of any one of claims 2, 3, 5, 6, 8, and 9-37.
52. A composition comprising a first nucleic acid that encodes a polypeptide selected from SEQ ID NOs: 109-216 and a second nucleic acid that encodes a polypeptide selected from SEQ ID NOs: 325-432.
53. A vector comprising the nucleic acid of any one of claims 48-51.
54. A cell comprising the nucleic acid of any one of claims 48-51, the composition of claim 52 or the vector of claim 53, wherein the cell is a eukaryotic cell.
55. The cell of claim 54, wherein the eukaryotic cell is a mammalian cell.
56. The cell of claim 55, wherein the mammalian cell is selected from the group consisting of a CHO cell, a 293 cell, an NSO cell, a PER.C6 cell, and a B cell.
57. The cell of claim 56, wherein the mammalian cell is a 293-6E cell or a DG44 cell.
58. A cell producing the antibody or antigen-binding fragment thereof of any one of claims 1-45.
59. A method of treating a disease in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of the antibody or antigen-binding fragment thereof of any one of claims 1-45.
60. The method of claim 59, wherein the disease or disorder is associated with differential or aberrant expression of CLEC2D on various cell surfaces of the subject in need thereof.
61. The method of claim 59, wherein the disease or disorder is associated with increased expression of CLEC2D on various cell surfaces of the subject in need thereof.
62. The method of any one of claims 60-61, wherein the cell is an immune cell.
63. The method of claim 62, wherein the immune cell is a NK cell.
64. The method of any one of claims 60-61, wherein the wherein the cell is a cancer cell.
65. The method of any one of claims 60-61, wherein the cell is a cell infected with microorganism.

66. The method of claim 65, wherein the microorganism is a bacteria, a virus, a fungus, a parasitic microorganism or a protozoa.
67. The method of claim 66, wherein the microorganism is an intracellular bacteria.
68. The method of any one of claims 59-67, wherein the disease is rheumatoid arthritis.
69. The method of claim 68, wherein the subject exhibits bone loss as a result of having rheumatoid arthritis.
70. The method of claim 69, wherein administration of a therapeutically effective amount of the antibody or antigen-binding fragment thereof slows or reverses the bone loss in the subject.
71. The method of any one of claims 59-67, wherein the disease is a cancer.
72. The method of claim 71, wherein the cancer is selected from the group consisting of breast cancer, prostate cancer, endometrial cancer, bladder cancer, kidney cancer, esophageal cancer, squamous cell carcinoma, uveal melanoma, follicular lymphoma, renal cell carcinoma, cendcal cancer, ovarian cancer, lung cancer, colorectal cancer, brain cancer, pancreatic cancer, head and neck cancer, liver cancer, leukemia, lymphoma, Hodgkin's disease, multiple myeloma, melanoma, astrocytoma, stomach cancer, and pulmonary adenocarcinoma.
73. The method of claim 71, wherein the cancer is selected from the group consisting of Adrenocortical Carcinoma, Bladder Urothelial Carcinoma, Breast Invasive Carcinoma, Cervical Squamous Cell Carcinoma and Endocervical Adenocarcinoma, Cholangiocarcinoma, Colon Adenocarcinoma, Lymphoid Neoplasm Diffuse Large B-cell Lymphoma, Esophageal Carcinoma, Glioblastoma Multiforme, Head and Neck Squamous Cell Carcinoma, Kidney Chromophobe, Kidney Renal Clear Cell Carcinoma, Kidney Renal Papillary Cell Carcinoma, Acute Myeloid Leukemia, Brain Lower Grade Glioma, Liver Hepatocellular Carcinoma, Lung Adenocarcinoma, Lung Squamous Cell Carcinoma, Mesothelioma, Ovarian Serous Cystadenocarcinoma, Pancreatic Adenocarcinoma, Pheochromocytoma and Paraganglioma, Prostate Adenocarcinoma, Rectum Adenocarcinoma, Sarcoma, Skin Cutaneous Melanoma, Stomach Adenocarcinoma, Testicular Germ Cell Tumors, Thyroid Carcinoma, Thymoma, Uterine Corpus Endometrial Carcinoma, Uterine Carcinosarcoma, and Uveal Melanoma.

74. The method of any one of claims 71-73, wherein administration of a therapeutically effective amount of the antibody or antigen-binding fragment thereof results in an anti-tumor response in the subject.
75. The method of any one of claims 59-74, wherein administration of a therapeutically effective amount of the antibody or antigen-binding fragment thereof alleviates a sign or a symptom of the disease.
76. The method of any one of claims 59-75, wherein the therapeutically effective amount of the antibody or antigen-binding fragment thereof of any one of claims 1-45 modulates or inhibits the interaction of CLEC2D with its cognate receptor CD161.
77. A method of modulating the activation of an immune response in a subject in need thereof in response to a disease, disorder or an infection caused by a microorgaism, comprising administering to the subject a therapeutically effective amount of the antibody or antigen-binding fragment thereof of any one of claims 1-45, wherein the immune response is an innate immune response or an adaptive immune response or a combination thereof.
78. A method of increasing the cytotoxicity of a natural killer cell in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of the antibody or antigen-binding fragment thereof of any one of claims 1-45.
79. An antibody library comprising at least about 108 unique monoclonal antibody clones, wherein at least about 80% of the antibody clones detectably and specifically bind a CLEC2D antigen.
80. The antibody library of claim 79, wherein the CLEC2D antigen comprises an amino acid sequence selected from SEQ ID NOs: 886-920 and 930-1003.
81. The antibody library of claim 79 or 80, wherein the CLEC2D antigen comprises a CLEC2D antigen expressed on a tumor cell surface, a variant of the CLEC2D antigen, or a homolog of the CLEC2D antigen.
82. The antibody library of claim 81, wherein the variant of the CLEC2D antigen comprises a fragment of the CLEC2D protein.
83. The antibody library of claim 82, wherein the homolog of the CLEC2D antigen comprises a human, a mouse, a dog, a rat or a cynomolgus CLEC2D.
84. A method of screening a high diversity antibody gene library for antibodies that bind to a CLEC2D antigen, comprising:

a) Inserting a library of antibody genes into a phage protein gene and transforming a plurality of phages to produce a phage library, wherein the phages in the phage library display the library of antibody genes on the surface of the phages;
b) Panning the phage library with a CLEC2D antigen for individual phages that bind to the CLEC2D antigen, thereby producing an enriched phage library that is enriched for antibody genes that encode antibodies that bind to the CLEC2D antigen;
c) Repeating step (b) at least once or at least twice;
d) Transferring the antibody genes from the enriched phage library to a yeast surface display library;
e) Isolating individual yeast cells that bind to the CLEC2D antigen from the yeast surface display library;
f) Culturing the isolated individual yeast cells that bind to the CLEC2D antigen to produce yeast surface display library clones; and
g) Sequencing the yeast surface display library clones;
thereby isolating antibody genes that bind to the CLEC2D antigen.

85. The method of claim 84, wherein the panning step (b) comprises panning the phage library with CLEC2D coated magnetic beads.

86. The method of claim 84, wherein the transferring step (d) comprises cloning the antibody genes into a yeast expression vector.

87. The method of claim 86, further comprising analyzing the surface expression of the antibody genes with a FLAG tag, a c-Myc tag, a polyhistidine tag or a V5 tag.

88. The method of claim 84, wherein the testing step (e) comprises isolating yeast cells expressing antibody genes that bind to the CLEC2D antigen with flow cytometry.

89. The method of claim 88, further comprising repeating the flow cytometry isolation at least 1x, at least 2x, at least 3x, at least 4x or at least 5x.

90. The method of any one of claims 84-89, further comprising cloning the antibody genes that bind to the CLEC2D antigen into a mammalian expression vector.

91. A method of making a composition comprising an anti-CLEC2D antibody or antigen-binding fragment thereof, comprising

a) Transforming mammalian cells with a vector comprising a sequence encoding a promoter and a sequence encoding an anti-CLEC2D antibody or antigen-binding fragment thereof,

wherein the sequence encoding the promoter and the anti-CLEC2D antibody or antigen-binding fragment thereof are operably linked;

b) Culturing the mammalian cells under conditions suitable for the expression of the anti-CLEC2D antibody or antigen-binding fragment thereof; and

c) Obtaining the anti-CLEC2D antibody or antigen-binding fragment thereof from the cultured mammalian cells to produce a supernatant.

92. The method of claim 91, wherein step (c) comprises collecting the supernatant of the cultured mammalian cells.

93. The method of claim 91 or 92, further comprising step (d) filtering the supernatant after step (c).

94. The method of any one of claims 91-93, further comprising step (e) purifying the filtered supernatant.

95. A method of treating a disease in a subject in need thereof, comprising:

a. determining the level of CLEC2D protein in the subject; and

b. administering a therapeutically effective amount of a CLEC2D antibody to the subject.

96. The method of claim 95, wherein the disease is a cancer.

97. The method of claim 96, wherein a cancer cell of the subject has an elevated level of CLEC2D protein when compared to a normal cell that does not have cancer.

98. The method of claim 95, wherein an increased level of CLEC2D is associated with a poor prognostic outcome.

99. The method of claim 95, wherein the disease is an autoimmune or inflammatory disorder.