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(54) **Title:**
**ANTIBODIES AGAINST HUMAN IL-22 AND USES
THEREFOR**

(57) **Abstract:**
ABSTRACT ANTIBODIES AGAINST HUMAN IL-22 AND USES THEREFOR The present application provides human antibodies and antigen binding fragments thereof that specifically bind to the human interleukin-22 (IL-22). The antibodies can act as antagonists of IL-22 activity, thereby modulating immune responses in general, and those mediated by IL-22 in particular. The disclosed compositions and methods may be used for example, in diagnosing, treating or preventing inflammatory disorders, autoimmune diseases, allergies, septic shock, infectious disorders, transplant rejection, cancer, and other immune system disorders. Fig. 1 *G00002*

ABSTRACT

ANTIBODIES AGAINST HUMAN IL-22 AND USES THEREFOR

The present application provides human antibodies and antigen binding fragments thereof that specifically bind to the human interleukin-22 (IL-22). The antibodies can act as antagonists of IL-22 activity, thereby modulating immune responses in general, and those mediated by IL-22 in particular. The disclosed compositions and methods may be used for example, in diagnosing, treating or preventing inflammatory disorders, autoimmune diseases, allergies, septic shock, infectious disorders, transplant rejection, cancer, and other immune system disorders.

Fig. 1



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ANTIBODIES AGAINST HUMAN IL-22 AND USES THEREFOR
CROSS REFERENCE TO RELATED APPLICATIONS

TECHNICAL FIELD

[0001] This invention relates to antibodies, e.g., human antibodies, and antigen-binding fragments thereof that bind interleukin-22 (IL-22), in particular, human IL-22, and their use in regulating IL-22-associated activities. The antibodies disclosed herein are useful in diagnosing, preventing, and/or treating IL-22 associated disorders, e.g., autoimmune disorders, including arthritis.

BACKGROUND OF THE INVENTION

[0002] Antigens initiate immune responses and activate the two largest populations of lymphocytes: T cells and B cells. After encountering antigen, T cells proliferate and differentiate into effector cells, while B cells proliferate and differentiate into antibody-secreting plasma cells. These effector cells secrete and/or respond to cytokines, which are small proteins (< about 30 kDa) secreted by lymphocytes and other cell types.

[0003] Interleukin-22 (IL-22) is a class II cytokine that shows sequence homology to IL-10. Its expression is up-regulated in T cells by IL-9 or ConA (Dumoutier L. et al. (2000) *Proc Natl Acad Sci USA* 97(18):10144-9). Further studies have shown that expression of IL-22 mRNA is induced *in vivo* in response to LPS administration, and that IL-22 modulates parameters indicative of an acute phase response (Dumoutier L. et al. (2000); Pittman D. et al. (2001) *Genes and Immunity* 2:172). In addition, IL-22 enhances the expression of antimicrobial peptides associated with host defense, including β -defensin, S100A7, S100A8, and S100A. Wolk et al., *Immunity*, 21:241-54 (2004); Boniface et al., *J. Immunol.* 174:3695-3702 (2005); Liang et al., *J. Exp. Med.*, 203(10):2271-79 (2006). Taken together, these observations indicate that IL-22 plays a role in inflammation (Kotenko S.V. (2002) *Cytokine & Growth Factor Reviews* 13(3):223-40).

[0004] IL-22 is believed to bind to a receptor complex consisting of IL-22R and IL-10R2, two members of the type II cytokine receptor family (CRF2) (Xie M.H. et al. (2000) *J Biol Chem* 275(40):31335-9; Kotenko S.V. et al. (2001) *J Biol Chem* 276(4):2725-32). Both chains of the IL-22 receptor are expressed constitutively in a number of organs. Epithelial cell lines derived from these organs are responsive



to IL-22 *in vitro* (Kotenko S.V. (2002) *Cytokine & Growth Factor Reviews* 13(3):223-40). IL-22 induces activation of the JAK/STAT3 and ERK pathways, as well as intermediates of other MAPK pathways (Dumoutier L. et al. (2000) *supra*; Xie M.H. et al. (2000) *supra*; Dumoutier L. et al. (2000) *J Immunol* 164(4):1814-9; Kotenko S.V. et al. (2001) *J Biol Chem* 276(4):2725-32; Lejeune, D. et al. (2002) *J Biol Chem* 277(37):33676-82).

[0005]CRF2 members are receptors for IFN α/β , IFN γ , coagulation factor VIIa, IL-10 and the IL-10 related proteins IL-19, IL-20, IL-22, IL-24, IL-26, as well as the recently identified IFN-like cytokines, IL-28 and IL-29 (Kotenko S.V. (2002) *Cytokine & Growth Factor Reviews* 13(3):223-40; Kotenko, S.V. et al. (2000) *Oncogene* 19(21):2557-65; Sheppard, P. et al. (2003) *Nature Immunology* 4(1):63-8; Kotenko, S.V. et al. (2003) *Nature Immunology* 4(1):69-77). In addition to these membrane receptors, the CRF2 family also includes a soluble protein, IL-22 binding protein (IL-22BP), which is specific for IL-22 and blocks its activity (Dumoutier, L. et al. (2001) *J Immunol* 166(12):7090-5; Kotenko, S.V. et al. (2001) *J Immunol* 166(12):7096-103; Xu, W. et al. (2001) *Proc Natl Acad Sci USA* 98(17):9511-6; Gruenberg, B.H. et al. (2001) *Genes & Immunity* 2(6):329-34; Wei C-C et al. (2003) *Genes & Immunity* 4:204-211). While the IL-22 receptor complex is unique for IL-22, each chain (i.e., IL-22R and IL-10R2) is shared with other CRF2 members to define functional receptors for other cytokines, including IL-20, IL-24 (IL-22R/IL-20R2), IL-28, IL-29 (IFN- λ R1/IL-10R2) and IL-10 (IL-10R1/IL-10R2) (Dumoutier, L. et al. (2001) *J. Immunol.* 167(7):3545-9; Wang, M. et al. (2002) *J Biol Chem* 277(9):7341-7; Parrish-Novak, J. et al. (2002) *J Biol Chem* 277(49):47517-23; Kotenko, S.V. et al. (1997) *EMBO J.* 16(19):5894-903; Spencer, S.D. et al. (1998) *J Exp Med* 187(4):571-8).

[0006]Both chains of the CRF2-composed receptor are necessary for signal transduction. One chain of the composed receptor has been historically defined as a ligand binding chain (e.g., IFN γ R1) based on its high affinity for the cytokine. The other chain (e.g., IFN γ R2) has been characterized as a helper or accessory chain, and shows minimal affinity for the cytokine alone (Kotenko, S.V. et al. (2000) *Oncogene* 19(21):2557-65). For IL-22, IL-22R is the high affinity receptor subunit with IL-10R2 subsequently binding to the IL-22/IL-22R complex (Li, J. et al. (2004)

Int. Immunopharmacol. 4(5):673-708; Logsdon, N. J. et al. (2002) *J. Interferon Cytokine Res* 22(11):1099-1112).

SUMMARY OF THE INVENTION

[0007] The present application provides, at least in part, IL-22 binding agents such as antibodies and antigen-binding fragments thereof that bind to interleukin-22 ("IL-22"), in particular, human IL-22, with high affinity and specificity. The antibodies and antigen-binding fragments thereof of the present invention are also referred to herein as "anti-IL-22 antibodies" and "fragments thereof," respectively. In one embodiment, the antibody or fragment thereof reduces, inhibits, or antagonizes IL-22 activity. Such antibodies can be used to regulate immune responses or IL-22-associated disorders by antagonizing IL-22 activity. In other embodiments, the anti-IL-22 antibody can be used diagnostically, or as a targeting antibody to deliver a therapeutic or a cytotoxic agent to an IL-22-expressing cell. Thus, the anti-IL-22 antibodies of the invention are useful in diagnosing, treating, and/or preventing IL-22-associated disorders, e.g., autoimmune disorders, e.g., arthritis (including rheumatoid arthritis, juvenile rheumatoid arthritis, osteoarthritis, psoriatic arthritis, lupus-associated arthritis or ankylosing spondylitis), scleroderma, systemic lupus erythematosus, HIV, Sjogren's syndrome, vasculitis, multiple sclerosis, autoimmune thyroiditis, dermatitis (including atopic dermatitis and eczematous dermatitis), myasthenia gravis, inflammatory bowel disease (IBD), Crohn's disease, colitis, diabetes mellitus (type I); inflammatory conditions of, e.g., the skin (e.g., psoriasis), cardiovascular system (e.g., atherosclerosis), nervous system (e.g., Alzheimer's disease); liver (e.g., hepatitis), kidney (e.g., nephritis) and pancreas (e.g., pancreatitis); cardiovascular disorders, e.g., cholesterol metabolic disorders, oxygen free radical injury, ischemia; disorders associated with wound healing; respiratory disorders, e.g., asthma and COPD (e.g., cystic fibrosis); acute inflammatory conditions (e.g., endotoxemia, sepsis and septicaemia, toxic shock syndrome and infectious disease); transplant rejection and allergy. In one embodiment, the IL-22-associated disorder is, an arthritic disorder, e.g., a disorder chosen from one or more of rheumatoid arthritis, juvenile rheumatoid arthritis, osteoarthritis, psoriatic arthritis, or ankylosing spondylitis; a respiratory disorder (e.g., asthma, chronic obstructive pulmonary disease (COPD)); or an inflammatory condition of, e.g., the skin (e.g., psoriasis), cardiovascular system (e.g.,

atherosclerosis), nervous system (e.g., Alzheimer's disease), liver (e.g., hepatitis), kidney (e.g., nephritis), pancreas (e.g., pancreatitis), and gastrointestinal organs, e.g., colitis, Crohn's disease and IBD.

[0008] Accordingly, in one aspect, the invention features an isolated antibody that binds to IL-22, in particular, human IL-22. In certain embodiments, the anti-IL-22 antibody may have at least one of the following characteristics: (1) it is a monoclonal or single specificity antibody; (2) it is a human antibody; (3) it is an *in vitro* generated antibody; (4) it is an *in vivo* generated antibody (e.g., transgenic mouse system); (5) it binds to IL-22 with an association constant of at least 10^{12} M^{-1} ; (6) it binds to IL-22 with an association constant of at least 10^{11} M^{-1} ; (7) it binds to IL-22 with an association constant of at least 10^{10} M^{-1} ; (8) it binds to IL-22 with an association constant of at least 10^9 M^{-1} ; (9) it binds to IL-22 with an association constant of at least 10^6 M^{-1} ; (10) it binds to IL-22 with a dissociation constant of 500 nM or less; (11) it binds to IL-22 with a dissociation constant of 10 nM or less; (12) it binds to IL-22 with a dissociation constant of 150 pM or less; (13) it binds to IL-22 with a dissociation constant of 60 pM or less; (14) it inhibits binding of IL-22 to IL-22R or a receptor complex of IL-22R and IL-10R2 with an IC_{50} of 10 nM or less; (15) it blocks IL-22 mediated proliferation of IL-22 receptor engineered BaF3 cells with an IC_{50} of 1 nM or less in one embodiment, with an IC_{50} of 150 pM or less in another embodiment, with an IC_{50} of 100 pM or less in another embodiment, and with an IC_{50} of 10 pM or less in another embodiment; and (16) it blocks IL-22 mediated GRO α secretion from HT29 cells with an IC_{50} of 1 nM or less in one embodiment, with an IC_{50} of 150 pM or less in another embodiment, and with an IC_{50} of 10 pM or less in another embodiment. IL-22 mediated BaF3 cell proliferation and IL-22 mediated GRO α secretion from HT29 cells can be measured as described in the examples.

[0009] Nonlimiting illustrative embodiments of the antibodies of the invention are referred to herein as "GIL01," "GIL16," "GIL45," "GIL60," "GIL68," "GIL92," "097D09," "062A09," "062G05," "087B03," "367D04," "368D04," "166B06," "166G05," "375G06," "376B10," "354A08," "355B06," "355E04," and "356A11." These antibodies can be germlined or non-germlined. In another embodiment, the antibody is chosen from 356A11, 354A08, 087B03, and 368D04. The antibodies of the invention may specifically bind to the same IL-22 epitope or a similar epitope

(e.g., an overlapping epitope) that GIL01, GIL16, GIL45, GIL60, GIL68, GIL92, 097D09, 062A09, 062G05, 087B03, 367D04, 368D04, 166B06, 166G05, 375G06, 376B10, 354A08, 355B06, 355E04, or 356A11 binds to. In other embodiments, the antibodies specifically bind to a fragment of an IL-22, e.g., a fragment of at least 10, 20, 50, 75, 100, 150, or 200 amino acids contiguous to the amino acid sequence set forth in SEQ ID NO:1, or a sequence that is at least 85%, 90%, 95%, 96%, 97%, 98%, 99% or more identical thereto. In other embodiments, the antibody competitively inhibits the binding of at least one of GIL01, GIL16, GIL45, GIL60, GIL68, GIL92, 097D09, 062A09, 062G05, 087B03, 367D04, 368D04, 166B06, 166G05, 375G06, 376B10, 354A08, 355B06, 355E04, or 356A11 to its target epitope.

[0010] In one embodiment, the antibody of the present invention includes a V_H domain, V_L domain, or combination thereof, of the F_v fragment of GIL01, GIL16, GIL45, GIL60, GIL68, GIL92, 097D09, 062A09, 062G05, 087B03, 367D04, 368D04, 166B06, 166G05, 375G06, 376B10, 354A08, 355B06, 355E04, or 356A11. For example, the antibody includes a V_H and/or a V_L domain having amino acid sequence as set forth in Tables 1 and 7 (SEQ ID NO:5, 23, 41, 59, 77, 95, 113, 131, 149, 167, 185, 203, 221, 239, 257, 275, 293, 311, 329, 347, 365, 383, 401, 419, 437, 455, 473, 491, 509, 527, 545, 563, 581, 599, or 617 for V_H and SEQ ID NO:6, 24, 42, 60, 78, 96, 114, 132, 150, 168, 186, 204, 222, 240, 258, 276, 294, 312, 330, 348, 366, 384, 402, 420, 438, 456, 474, 492, 510, 528, 546, 564, 582, 600, or 618 for V_L), or a sequence substantially identical thereto (e.g., a sequence at least about 85%, 90%, 95%, 96%, 97%, 98%, 99% or more identical thereto, or which differs by no more than 1, 2, 5, 10 or 15 amino acid residues from SEQ ID NO:5, 6, 23, 24, 41, 42, 59, 60, 77, 78, 95, 96, 113, 114, 131, 132, 149, 150, 167, 168, 185, 186, 203, 204, 221, 222, 239, 240, 257, 258, 275, 276, 293, 294, 311, 312, 329, 330, 347, 348, 365, 366, 383, 384, 401, 402, 419, 420, 437, 438, 455, 456, 473, 474, 491, 492, 509, 510, 527, 528, 545, 546, 563, 564, 581, 582, 599, 600, 617, or 618).

[0011] In another embodiment, the antibody of the present invention includes a V_H domain, V_L domain, or combination thereof, of the F_v fragment of an antibody chosen from 356A11, 354A08, 087B03, and 368D04. In this embodiment, the antibody, or antigen-binding fragment thereof, comprises:

[0012] a V_H domain comprising the amino acid sequence set out in SEQ ID NO:167 or 491 and/or a V_L domain comprising the amino acid sequence set out in SEQ ID NO:168 or 492 (087B03);

[0013] a V_H domain comprising the amino acid sequence set out in SEQ ID NO:293 or 545 and/or a V_L domain having the amino acid sequence set out in SEQ ID NO:294 or 546 (354A08);

[0014] a V_H domain comprising the amino acid sequence set out in SEQ ID NO:203 or 617 and/or a V_L domain comprising the amino acid sequence set out in SEQ ID NO:204 or 618 (368D04); or

[0015] a V_H domain comprising the amino acid sequence set out in SEQ ID NO:347 or 599 and/or a V_L domain comprising the amino acid sequence set out in SEQ ID NO:348 or 600 (356A11).

[0016] In another embodiment, the antibody includes a V_H and/or V_L domain encoded by a nucleic acid having a nucleotide sequence as set forth in Tables 1 and 7 (SEQ ID NO:14, 32, 50, 68, 86, 104, 122, 140, 158, 176, 194, 212, 230, 248, 266, 284, 302, 320, 338, 356, 374, 392, 410, 428, 446, 464, 482, 500, 518, 536, 554, 572, 590, 608, or 626 for V_H and SEQ ID NO:15, 33, 51, 69, 87, 105, 123, 141, 159, 177, 195, 213, 231, 249, 267, 285, 303, 321, 339, 357, 375, 393, 411, 429, 447, 465, 483, 501, 519, 537, 555, 573, 591, 609, or 627 for V_L), or a sequence substantially identical thereto (e.g., a sequence at least about 85%, 90%, 95%, 96%, 97%, 98%, 99% or more identical thereto, or which differs by no more than 1, 2, 3, 6, 15, 30 or 45 nucleotides from SEQ ID NO: 14, 15, 32, 33, 50, 51, 68, 69, 86, 87, 104, 105, 122, 123, 140, 141, 158, 159, 176, 177, 194, 195, 212, 213, 230, 231, 248, 249, 266, 267, 284, 285, 302, 303, 320, 321, 338, 339, 356, 357, 374, 375, 392, 393, 410, 411, 428, 429, 446, 447, 464, 465, 482, 483, 500, 501, 518, 519, 536, 537, 554, 555, 572, 573, 590, 591, 608, 609, 626, or 627).

[0017] In other embodiments, the antibody includes an Fv domain having an amino acid sequence as set forth in Tables 1 and 7 (SEQ ID NO:7, 25, 43, 61, 79, 97, 115, 133, 151, 169, 187, 205, 223, 241, 259, 277, 295, 313, 331, 349, 367, 385, 403, 421, 439, 457, 475, 493, 511, 529, 547, 565, 583, 601, or 619), or a sequence substantially identical thereto (e.g., a sequence at least about 85%, 90%, 95%, 96%, 97%, 98%, 99% or more identical thereto, or which differs by no more than 1, 2, 5, 10, 15, 20, 30 or 35 amino acid residues from SEQ ID NO:7, 25, 43,

61, 79, 97, 115, 133, 151, 169, 187, 205, 223, 241, 259, 277, 295, 313, 331, 349, 367, 385, 403, 421, 439, 457, 475, 493, 511, 529, 547, 565, 583, 601, or 619). In another embodiment, the antibody of the present invention includes an Fv domain of an antibody chosen from 356A11 (SEQ ID NO:349 or 601), 354A08 (SEQ ID NO:295 or 547), 087B03 (SEQ ID NO:169 or 493), and 368D04 (SEQ ID NO:205 or 619). In another embodiment, the antibody includes an Fv domain encoded by a nucleic acid having a nucleotide sequence as set forth in Tables 1 and 7 (SEQ ID NO:16, 34, 52, 70, 88, 106, 124, 142, 160, 178, 196, 214, 232, 250, 268, 286, 304, 322, 340, 358, 376, 394, 412, 430, 448, 466, 484, 502, 520, 538, 556, 574, 592, 610, or 628), or a sequence substantially identical thereto (e.g., a sequence at least about 85%, 90%, 95%, 96%, 97%, 98%, 99% or more identical thereto, or which differs by no more than 1, 2, 3, 6, 15, 30, 45, 60, 90 or 105 nucleotides from SEQ ID NO: 16, 34, 52, 70, 88, 106, 124, 142, 160, 178, 196, 214, 232, 250, 268, 286, 304, 322, 340, 358, 376, 394, 412, 430, 448, 466, 484, 502, 520, 538, 556, 574, 592, 610, or 628). In yet other embodiments, the antibody comprises at least one complementarity determining region (CDR) of these V_H and V_L domains. For example, the antibody can include one, two, or three CDR's of the V_H domain having an amino acid sequence as set forth in or included within the sequences in Tables 1 and 7 (SEQ ID NO:5, 7, 8, 9, 10, 23, 25, 26, 27, 28, 41, 43, 44, 45, 46, 59, 61, 62, 63, 64, 77, 79, 80, 81, 82, 95, 97, 98, 99, 100, 113, 115, 116, 117, 118, 131, 133, 134, 135, 136, 149, 151, 152, 153, 154, 167, 169, 170, 171, 172, 185, 187, 188, 189, 190, 203, 205, 206, 207, 208, 221, 223, 224, 225, 226, 239, 241, 242, 243, 244, 257, 259, 260, 261, 262, 275, 277, 278, 279, 280, 293, 295, 296, 297, 298, 311, 313, 314, 315, 316, 329, 331, 332, 333, 334, 347, 349, 350, 351, 352, 365, 367, 368, 369, 370, 383, 385, 386, 387, 388, 401, 403, 404, 405, 406, 419, 421, 422, 423, 424, 437, 439, 440, 441, 442, 455, 457, 458, 459, 460, 473, 475, 476, 477, 478, 491, 493, 494, 495, 496, 509, 511, 512, 513, 514, 527, 529, 530, 531, 532, 545, 547, 548, 549, 550, 563, 565, 566, 567, 568, 581, 583, 584, 585, 586, 599, 601, 602, 603, 604, 617, 619, 620, 621, or 622), or a sequence substantially homologous thereto (e.g., a sequence at least about 85%, 90%, 95%, 96%, 97%, 98%, 99% or more identical thereto). In another embodiment, the antibody of the present invention includes one, two, or three CDR's of the V_H domain of an antibody chosen from 356A11, 354A08, 087B03, and 368D04. In this

embodiment, the antibody, or antigen-binding fragment thereof, comprises a heavy chain variable region comprising:

[0018]a) SEQ ID NO:170 or 494; b) SEQ ID NO: 171 or 495; and/or c) SEQ ID NO: 172 or 496 (087B03);

[0019]a) SEQ ID NO:296 or 548; b) SEQ ID NO:297 or 549; and/or c) SEQ ID NO:298 or 550 (354A08);

[0020]a) SEQ ID NO:206 or 620; b) SEQ ID NO:207 or 621; and/or c) SEQ ID NO:208 or 622 (368D04); or

[0021]a) SEQ ID NO:350 or 602; b) SEQ ID NO:351 or 603; and/or c) SEQ ID NO:352 or 604 (356A11).

[0022]In another embodiment, the antibody can include one, two, or three CDR's of the V_L domain having an amino acid sequence as set forth in or included within the sequences in Tables 1 and 7 (SEQ ID NO:6, 7, 11, 12, 13, 24, 25, 29, 30, 31, 42, 43, 47, 48, 49, 60, 61, 65, 66, 67, 78, 79, 83, 84, 85, 96, 97, 101, 102, 103, 114, 115, 119, 120, 121, 132, 133, 137, 138, 139, 150, 151, 155, 156, 157, 168, 169, 173, 174, 175, 186, 187, 191, 192, 193, 204, 205, 209, 210, 211, 222, 223, 227, 228, 229, 240, 241, 245, 246, 247, 258, 259, 263, 264, 265, 276, 277, 281, 282, 283, 294, 295, 299, 300, 301, 312, 313, 317, 318, 319, 330, 331, 335, 336, 337, 348, 349, 353, 354, 355, 366, 367, 371, 372, 373, 384, 385, 389, 390, 391, 402, 403, 407, 408, 409, 420, 421, 425, 426, 427, 438, 439, 443, 444, 445, 456, 457, 461, 462, 463, 474, 475, 479, 480, 481, 492, 493, 497, 498, 499, 510, 511, 515, 516, 517, 528, 529, 533, 534, 535, 546, 547, 551, 552, 553, 564, 565, 569, 570, 571, 582, 583, 587, 588, 589, 600, 601, 605, 606, 607, 618, 619, 623, 624, or 625), or a sequence substantially identical thereto (e.g., a sequence at least about 85%, 90%, 95%, 96%, 97%, 98%, 99% or more identical thereto). In another embodiment, the antibody of the present invention includes one, two, or three CDR's of the V_L domain of an antibody chosen from 356A11, 354A08, 087B03, and 368D04. In this embodiment, the antibody, or antigen-binding fragment thereof, comprises a light chain variable region comprising:

[0023]a) SEQ ID NO:173 or 497; b) SEQ ID NO: 174 or 498; and/or c) SEQ ID NO:175 or 499 (087B03);

[0024]a) SEQ ID NO:299 or 551; b) SEQ ID NO:300 or 552; and/or c) SEQ ID NO:301 or 553 (354A08);

[0025]a) SEQ ID NO:209 or 623; b) SEQ ID NO:210 or 624; and/or c) SEQ ID NO:211 or 625 (368D04); or

[0026]a) SEQ ID NO:353 or 605; b) SEQ ID NO:354 or 606; and/or c) SEQ ID NO:355 or 607 (356A11).

[0027]In a still further embodiment, the antibody comprises an H3 fragment of the V_H domain of GIL01, GIL16, GIL45, GIL60, GIL68, GIL92, 097D09, 062A09, 062G05, 087B03, 367D04, 368D04, 166B06, 166G05, 375G06, 376B10, 354A08, 355B06, 355E04, or 356A11, e.g., an H3 fragment having the amino acid sequence as set forth in Tables 1 and 7 (SEQ ID NO:10, 28, 46, 64, 82, 100, 118, 136, 154, 172, 190, 208, 226, 244, 262, 280, 298, 316, 334, 352, 370, 388, 406, 424, 442, 460, 478, 496, 514, 532, 550, 568, 586, 604, or 622), or a sequence substantially identical thereto (e.g., a sequence at least about 85%, 90%, 95%, 96%, 97%, 98%, 99% or more identical thereto).

[0028]The antibody of the invention can be full-length (e.g., include at least one complete heavy chain and at least one complete light chain) or can include only an antigen-binding fragment (e.g., a Fab, F(ab')₂, Fv, a single chain Fv fragment, a Fd fragment, or a dAb fragment). The antibody can include a constant region, or a portion thereof, chosen from any of: the kappa, lambda, alpha, gamma, delta, epsilon and mu constant region genes. For example, heavy chain constant regions of the various isotypes can be used, including: IgG₁, IgG₂, IgG₃, IgG₄, IgM, IgA₁, IgA₂, IgD, and IgE. The light chain constant region can be chosen from kappa or lambda. The antibody may be an IgG, or it may also be IgG_{1κ} or IgG_{1γ}.

[0029] The anti-IL-22 antibody described herein can be derivatized or linked to another functional molecule (such as another peptide or protein (e.g., a Fab fragment)). For example, an antibody of the invention can be functionally linked (e.g., by chemical coupling, genetic fusion, non-covalent association or otherwise) to at least one other molecular entity, such as another antibody (e.g., a bispecific or a multispecific antibody), toxin, radioisotope, cytotoxic or cytostatic agent, among others.

[0030]In another aspect, the invention features a pharmaceutical composition containing at least one anti-IL-22 antibody and a pharmaceutically acceptable carrier. The pharmaceutical composition can further include a

combination of at least one anti-IL-22 antibody and at least one therapeutic agent (e.g., cytokine and growth factor inhibitors, immunosuppressants, anti-inflammatory agents, metabolic inhibitors, enzyme inhibitors, cytotoxic agents, cytostatic agents, or combinations thereof, as described in more detail herein). Combinations of the anti-IL-22 antibody and a therapeutic agent are also within the scope of the invention. The compositions and combinations of the invention can be used to regulate IL-22-associated inflammatory conditions, e.g., by modulating IL-22 signaling through its receptors located on epithelial cells of a variety of tissues, including, but not limited to, those of the pancreas, skin, lung, gut, liver, kidney, salivary gland, and vascular endothelia, in addition to potentially activated and tissue localized immune cells.

[0031] In another aspect, the invention features a method of treating a subject with an IL-22-associated disorder. The method includes administering to the subject an anti-IL-22 antibody in an amount sufficient to inhibit at least one IL-22 activity of immune cells, thereby treating the IL-22-associated disorder.

[0032] The anti-IL-22 antibody can be administered to the subject, alone or in combination, with other therapeutic agents as described herein. The subject may be a mammal, e.g. human. For example, the method can be used to treat a subject with an IL-22-associated disorder such as autoimmune disorders, e.g., arthritis (including rheumatoid arthritis, juvenile rheumatoid arthritis, osteoarthritis, psoriatic arthritis, lupus-associated arthritis or ankylosing spondylitis), scleroderma, systemic lupus erythematosus, HIV, Sjogren's syndrome, vasculitis, multiple sclerosis, autoimmune thyroiditis, dermatitis (including atopic dermatitis and eczematous dermatitis), myasthenia gravis, inflammatory bowel disease (IBD), Crohn's disease, colitis, diabetes mellitus (type I); inflammatory conditions of, e.g., the skin (e.g., psoriasis), cardiovascular system (e.g., atherosclerosis), nervous system (e.g., Alzheimer's disease), liver (e.g., hepatitis), kidney (e.g., nephritis) and pancreas (e.g., pancreatitis); cardiovascular disorders, e.g., cholesterol metabolic disorders, oxygen free radical injury, ischemia; disorders associated with wound healing; respiratory disorders, e.g., asthma and COPD (e.g., cystic fibrosis); acute inflammatory conditions (e.g., endotoxemia, sepsis and septicaemia, toxic shock syndrome and infectious disease); transplant rejection and allergy. In one embodiment, the IL-22-associated disorder is, an arthritic disorder, e.g., a disorder

chosen from one or more of rheumatoid arthritis, juvenile rheumatoid arthritis, osteoarthritis, psoriatic arthritis, or ankylosing spondylitis; a respiratory disorder (e.g., asthma, chronic obstructive pulmonary disease (COPD); or an inflammatory condition of, e.g., the skin (e.g., psoriasis), cardiovascular system (e.g., atherosclerosis), nervous system (e.g., Alzheimer's disease), liver (e.g., hepatitis), kidney (e.g., nephritis), pancreas (e.g., pancreatitis), and gastrointestinal organs, e.g., colitis, Crohn's disease and IBD.

[0033] In another aspect, the invention features a method of decreasing, inhibiting or reducing an acute phase response in a subject. The method includes administering to the subject an IL-22 binding agent, e.g., an IL-22 antagonist, (e.g., an anti-IL-22 antibody or fragment thereof as described herein), in an amount sufficient to decrease, inhibit or reduce the acute phase response in the subject. In one embodiment, the subject is a mammal, e.g., a human suffering from an IL-22-associated disorder, including, e.g., respiratory disorders, inflammatory disorders and autoimmune disorders. In one embodiment, the IL-22 binding agent is administered locally, e.g., topically, subcutaneously, or other administrations that are not in the general circulation.

[0034] In another aspect, an IL-22 binding agent can be used to alter the type of immune response and/or increase the efficacy of a vaccine formulation used to immunize a subject. For example, an anti-IL-22 antibody of the present invention can be administered before, during and/or after an immunization to increase vaccine efficacy. In one embodiment, the vaccine formulation contains one or more IL-22 antagonists and an antigen, i.e., an immunogen, including, for example, viral, bacterial, or tumor antigens. In another embodiment, the IL-22 antagonist and the immunogen are administered separately, e.g., within one hour, three hours, one day or two days of each other.

[0035] In another aspect, the invention provides a method for detecting the presence of IL-22 in a sample *in vitro*. Samples may include biological samples such as serum, plasma, tissue and biopsy. The subject method can be used to diagnose a disorder, such as an IL-22-associated disorder as described herein. The method includes: (1) contacting the sample or a control sample with an anti-IL-22 antibody, and (2) detecting formation of a complex between the anti-IL-22 antibody and the sample or the control sample, wherein a statistically significant

change in the formation of the complex in the sample relative to a control sample, is indicative of the presence of the IL-22 in the sample.

[0036] In another aspect, the invention provides a method for detecting the presence of IL-22 *in vivo* (e.g., *in vivo* imaging in a subject). The method can be used to diagnose a disorder, e.g., an IL-22-associated disorder as described herein. The method includes: (1) administering an anti-IL-22 antibody to a subject or a control subject under conditions that allow binding of the antibody to IL-22, and (2) detecting formation of a complex between the antibody and IL-22, wherein a statistically significant change in the formation of the complex in the subject relative to a control, e.g., a control subject, is indicative of the presence of IL-22.

[0037] The antibody may be directly or indirectly labeled with a detectable substance to facilitate detection of the bound or unbound antibody. Suitable detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials and radioactive materials.

[0038] In another aspect, the invention provides a method for delivering or targeting an agent, e.g., a therapeutic or a cytotoxic agent, to an IL-22-expressing cell *in vivo*. The method includes administering an anti-IL-22 antibody to a subject under conditions that allow binding of the antibody to IL-22. The antibody may be coupled to a second therapeutic moiety, such as a toxin.

[0039] The disclosure provides nucleic acid sequences from the V_H and V_L domains of GIL01, GIL16, GIL45, GIL60, GIL68, GIL92, 097D09, 062A09, 062G05, 087B03, 367D04, 368D04, 166B06, 166G05, 375G06, 376B10, 354A08, 355B06, 355E04, and 356A11. Also provided are nucleic acid sequences that comprise at least one CDR from GIL01, GIL16, GIL45, GIL60, GIL68, GIL92, 097D09, 062A09, 062G05, 087B03, 367D04, 368D04, 166B06, 166G05, 375G06, 376B10, 354A08, 355B06, 355E04, and 356A11. The disclosure also provides vectors and host cells comprising such nucleic acids.

[0040] The disclosure further provides methods of producing new V_H and V_L domains and functional antibodies comprising all or a portion of such domains derived from the V_H or V_L domains of GIL01, GIL16, GIL45, GIL60, GIL68, GIL92, 097D09, 062A09, 062G05, 087B03, 367D04, 368D04, 166B06, 166G05, 375G06, 376B10, 354A08, 355B06, 355E04, or 356A11.

[0041]Additional aspects of the disclosure will be set forth in part in the description, and in part will be obvious from the description, or may be learned by practicing the invention. The invention is set forth and particularly pointed out in the claims, and the disclosure should not be construed as limiting the scope of the claims. The following detailed description includes exemplary representations of various embodiments of the invention, which are not restrictive of the invention as claimed. The accompanying figures constitute a part of this specification and, together with the description, serve only to illustrate embodiments and not limit the invention.

BRIEF DESCRIPTION OF THE FIGURES

[0042]Figure 1. Potency of parent anti-IL-22 scFv clones in the IL-22 receptor complex assay: bio.IL-22 binding IL-22 receptor complex DELFIA competition assay.

[0043]Figure 2. Profiling of lead scFv clones in IL-22 receptor complex assay: bio.IL-22 binding IL-22 receptor complex DELFIA competition assay. (A) GIL 1 derived. (B) GIL 16 derived. (C) GIL 16, GIL 60, and GIL 68 derived. (D) GIL 60 derived. (E) GIL 68 derived. (F) GIL 68 derived. (G) GIL 92 derived.

[0044]Figure 3. IgG potency in GROa cell based assays. Optimized GIL-IgGs in huIL-22 GROa assay. (A) Germlined IgG. (B) Non-germlined IgG.

[0045]Figure 4. Cross species reactivity of IL-22 antibodies by ELISA. Optimized GIL-IgGs specifically bind to IL-22. (A) Germlined IgG. (B) Non-germlined IgG.

[0046]Figure 5. Amino acid and nucleotide sequences of human IL-22. The nucleotide sequence of human IL-22 is SEQ ID NO:2 and includes a poly (A) tail. The disclosed nucleotide sequence includes an open reading frame and the amino acid sequence of full-length IL-22 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:1. The amino acid sequence of mature IL-22 corresponds to about amino acids 34-179 of SEQ ID NO:1.

[0047]Figure 6. Amino acid and nucleotide sequences of mouse IL-22.

[0048]Figure 7. Amino acid and nucleotide sequences of non-germlined GIL01, GIL16, GIL45, GIL60, GIL68, GIL92, 097D09, 062A09, 062G05, 087B03, 367D04, 368D04, 166B06, 166G05, 375G06, 376B10, 354A08, 355B06, 355E04,

and 356A11, including V_H and V_L domains, and CDRs (H1, H2, H3, L1, L2, and L3).

[0049]Figure 8. Amino acid and nucleotide sequences of germlined GIL01, GIL16, GIL45, GIL60, GIL68, GIL92, 062A09, 087B03, 166B06, 166G05, 354A08, 355B06, 355E04, 356A11, and 368D04, including V_H and V_L domains, and CDRs (H1, H2, H3, L1, L2, and L3).

[0050]Figure 9. Amino acid and nucleotide sequences of scFv's for non-germlined GIL01, GIL16, GIL45, GIL60, GIL68, GIL92, 097D09, 062A09, 062G05, 087B03, 367D04, 368D04, 166B06, 166G05, 375G06, 376B10, 354A08, 355B06, 355E04, and 356A11, with CDRs underlined (H1, H2, H3, L1, L2, and L3).

[0051]Figure 10. Amino acid and nucleotide sequences of scFv's for germlined GIL01, GIL16, GIL45, GIL60, GIL68, GIL92, 062A09, 087B03, 166B06, 166G05, 354A08, 355B06, 355E04, 356A11, and 368D04 with CDRs underlined (H1, H2, H3, L1, L2, and L3).

DETAILED DESCRIPTION

I. Definitions

[0052]In order that the present invention may be more readily understood, certain terms are first defined. Additional definitions are set forth throughout the detailed description.

[0053]The term “**antibody**” refers to an immunoglobulin or fragment thereof, and encompasses any polypeptide comprising an antigen-binding fragment or an antigen-binding domain. The term includes but is not limited to polyclonal, monoclonal, monospecific, polyspecific, non-specific, humanized, human, single-chain, chimeric, synthetic, recombinant, hybrid, mutated, grafted, and *in vitro* generated antibodies. Unless preceded by the word “intact”, the term “antibody” includes antibody fragments such as Fab, F(ab')₂, Fv, scFv, Fd, dAb, and other antibody fragments that retain antigen-binding function. Typically, such fragments would comprise an antigen-binding domain.

[0054]The terms “**antigen-binding domain**” and “**antigen-binding fragment**” refer to a part of an antibody molecule that comprises amino acids responsible for the specific binding between antibody and antigen. The part of the antigen that is specifically recognized and bound by the antibody is referred to as the “**epitope**.” An antigen-binding domain may comprise an antibody light chain

variable region (V_L) and an antibody heavy chain variable region (V_H); however, it does not have to comprise both. Fd fragments, for example, have two V_H regions and often retain some antigen-binding function of the intact antigen-binding domain. Examples of antigen-binding fragments of an antibody include (1) a Fab fragment, a monovalent fragment having the V_L , V_H , C_L and C_{H1} domains; (2) a $F(ab')_2$ fragment, a bivalent fragment having two Fab fragments linked by a disulfide bridge at the hinge region; (3) a Fd fragment having the two V_H and C_{H1} domains; (4) a Fv fragment having the V_L and V_H domains of a single arm of an antibody, (5) a dAb fragment (Ward et al., (1989) *Nature* 341:544-546), which has a V_H domain; (6) an isolated complementarity determining region (CDR), and (7) a single chain Fv (scFv). Although the two domains of the Fv fragment, V_L and V_H , are coded for by separate genes, they can be joined, using recombinant methods, by a synthetic linker that enables them to be made as a single protein chain in which the V_L and V_H regions pair to form monovalent molecules (known as single chain Fv (scFv); see e.g., Bird et al. (1988) *Science* 242:423-426; and Huston et al. (1988) *Proc. Natl. Acad. Sci. USA* 85:5879-5883). These antibody fragments are obtained using conventional techniques known to those with skill in the art, and the fragments are evaluated for function in the same manner as are intact antibodies.

[0055]The term “**effective amount**” refers to a dosage or amount that is sufficient to regulate IL-22 activity to ameliorate clinical symptoms or achieve a desired biological outcome, e.g., decreased T cell and/or B cell activity, suppression of autoimmunity, suppression of transplant rejection, etc.

[0056]The term “**human antibody**” includes antibodies having variable and constant regions corresponding substantially to human germline immunoglobulin sequences known in the art, including, for example, those described by Kabat et al. (See Kabat, et al. (1991) *Sequences of Proteins of Immunological Interest*, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242). The human antibodies of the invention may include amino acid residues not encoded by human germline immunoglobulin sequences (e.g., mutations introduced by random or site-specific mutagenesis *in vitro* or by somatic mutation *in vivo*), for example in the CDRs, and in particular, CDR3. The human antibody can have at least one, two, three, four, five, or more positions replaced with an

amino acid residue that is not encoded by the human germline immunoglobulin sequence.

[0057]The phrase "**inhibit**" or "**antagonize**" IL-22 activity and its cognates refer to a reduction, inhibition, or otherwise diminution of at least one activity of IL-22 due to binding an anti-IL-22 antibody, wherein the reduction is relative to the activity of IL-22 in the absence of the same antibody. The activity can be measured using any technique known in the art, including, for example, as described in Examples 7 and 9. Inhibition or antagonism does not necessarily indicate a total elimination of the IL-22 polypeptide biological activity. A reduction in activity may be about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or more.

[0058]The term "**interleukin-22**" or "**IL-22**" refers to a class II cytokine (which may be mammalian) capable of binding to IL-22R and/or a receptor complex of IL-22R and IL-10R2, and has at least one of the following features: (1) an amino acid sequence of a naturally occurring mammalian IL-22 polypeptide (full length or mature form) or a fragment thereof, e.g., an amino acid sequence shown as SEQ ID NO:1 (human) or SEQ ID NO:3 (murine) or a fragment thereof; (2) an amino acid sequence substantially identical to, e.g., at least 85%, 90%, 95%, 96%, 97%, 98%, 99% identical to, an amino acid sequence shown as SEQ ID NO:1 or amino acids 34-179 thereof (human) or SEQ ID NO:3 (murine) or a fragment thereof; (3) an amino acid sequence which is encoded by a naturally occurring mammalian IL-22 nucleotide sequence or a fragment thereof (e.g., SEQ ID NO:2 or nucleotides 71 to 610 (human) or SEQ ID NO:4 (murine) or a fragment thereof); (4) an amino acid sequence encoded by a nucleotide sequence which is substantially identical to, e.g., at least 85%, 90%, 95%, 96%, 97%, 98%, 99% identical to, a nucleotide sequence shown as SEQ ID NO:2 or nucleotides 71 to 610 thereof (human) or SEQ ID NO:4 (murine) or a fragment thereof; (5) an amino acid sequence encoded by a nucleotide sequence degenerate to a naturally occurring IL-22 nucleotide sequence or a fragment thereof, e.g., SEQ ID NO:2 (human) or SEQ ID NO:4 (murine) or a fragment thereof; or (6) a nucleotide sequence that hybridizes to one of the foregoing nucleotide sequences under stringent conditions, e.g., highly stringent conditions. The IL-22 may bind to IL-22R and/or a receptor complex of IL-22R and IL-10R2 of mammalian origin, e.g., human or mouse.

[0059]The nucleotide sequence and the predicted amino acid sequence of human IL-22 are shown in SEQ ID NO:2 and SEQ ID NO:1, respectively. The amino acid sequence of mature human IL-22 corresponds to amino acids 34-179 of SEQ ID NO:1. Analysis of recombinant human IL-22 reveals many structural domains. (Nagem et al. (2002) Structure, 10:1051-62; U.S. Patent Application No. US 2002/0187512 A1).

[0060]The term “**IL-22 activity**” refers to at least one cellular process initiated or interrupted as a result of IL-22 binding to a receptor complex consisting of IL-22R and IL-10R2 on the cell. IL-22 activities include at least one of, but are not limited to: (1) binding IL-22R or a receptor complex of IL-22R and IL-10R2 (e.g., human IL-22R with or without human IL-10R2); (2) associating with signal transduction molecules (e.g., JAK-1); (3) stimulating phosphorylation of STAT proteins (e.g., STAT5, STAT3, or combination thereof); (4) activating STAT proteins; and (5) modulating (e.g., increasing or decreasing) proliferation, differentiation, effector cell function, cytolytic activity, cytokine secretion, survival, or combinations thereof, of epithelial cells, fibroblasts, or immune cells. Epithelial cells include, but are not limited to, cells of the skin, gut, liver, and kidney, as well as endothelial cells. Fibroblasts include, but are not limited to, synovial fibroblasts. Immune cells may include CD8+ and CD4+ T cells, NK cells, B cells, macrophages, and megakaryocytes. IL-22 activity can be determined *in vitro*, for example, using the IL-22 receptor inhibition assay as described in Examples 2 and 6, the GROa secretion assay in Example 9, or the BAF3 proliferation assay of Example 7. IL-22 activity can also be determined *in vivo*, for example, by scoring progression of an immune response or disorder as described in Example 13.

[0061]As used herein, “***in vitro* generated antibody**” refers to an antibody where all or part of the variable region (e.g., at least one CDR) is generated in a non-immune cell selection (e.g., an *in vitro* phage display, protein chip or any other method in which candidate sequences can be tested for their ability to bind to an antigen). This term excludes sequences generated by genomic rearrangement in an immune cell.

[0062]The term “**isolated**” refers to a molecule that is substantially free of its natural environment. For instance, an isolated protein is substantially free of cellular material or other proteins from the cell or tissue source from which it was

derived. The term also refers to preparations where the isolated protein is sufficiently pure for pharmaceutical compositions; or at least 70-80% (w/w) pure; or at least 80-90% (w/w) pure; or at least 90-95% pure; or at least 95%, 96%, 97%, 98%, 99%, or 100% (w/w) pure.

[0063] The phrase “**percent identical**” or “**percent identity**” refers to the similarity between at least two different sequences. This percent identity can be determined by standard alignment algorithms, for example, the Basic Local Alignment Tool (BLAST) described by Altshul et al. ((1990) J. Mol. Biol., 215: 403-410); the algorithm of Needleman et al. ((1970) J. Mol. Biol., 48: 444-453); or the algorithm of Meyers et al. ((1988) Comput. Appl. Biosci., 4: 11-17). A set of parameters may be the Blosum 62 scoring matrix with a gap penalty of 12, a gap extend penalty of 4, and a frameshift gap penalty of 5. The percent identity between two amino acid or nucleotide sequences can also be determined using the algorithm of E. Meyers and W. Miller ((1989) CABIOS, 4:11-17) which has been incorporated into the ALIGN program (version 2.0), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4. The percent identity is usually calculated by comparing sequences of similar length.

[0064] The term “**repertoire**” refers to at least one nucleotide sequence derived wholly or partially from at least one sequence encoding at least one immunoglobulin. The sequence(s) may be generated by rearrangement *in vivo* of the V, D, and J segments of heavy chains, and the V and J segments of light chains. Alternatively, the sequence(s) can be generated from a cell in response to which rearrangement occurs, e.g., *in vitro* stimulation. Alternatively, part or all of the sequence(s) may be obtained by DNA splicing, nucleotide synthesis, mutagenesis, and other methods, see, e.g., U.S. Patent 5,565,332. A repertoire may include only one sequence or may include a plurality of sequences, including ones in a genetically diverse collection.

[0065] The terms “**specific binding**” or “**specifically binds**” refers to two molecules forming a complex that is relatively stable under physiologic conditions. Specific binding is characterized by a high affinity and a low to moderate capacity as distinguished from nonspecific binding which usually has a low affinity with a moderate to high capacity. Typically, binding is considered specific when the association constant K_A is higher than $10^6 M^{-1}$. If necessary, nonspecific binding

can be reduced without substantially affecting specific binding by varying the binding conditions. The appropriate binding conditions, such as concentration of antibodies, ionic strength of the solution, temperature, time allowed for binding, concentration of a blocking agent (e.g., serum albumin, milk casein), etc., may be optimized by a skilled artisan using routine techniques. Illustrative conditions are set forth in Example 3, but other conditions known to the person of ordinary skill in the art fall within the scope of this invention.

[0066]As used herein, the term **"stringent"** describes conditions for hybridization and washing. Stringent conditions are known to those skilled in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. Aqueous and nonaqueous methods are described in that reference and either can be used. One example of stringent hybridization conditions is hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by at least one wash in 0.2X SSC, 0.1% SDS at 50°C. A second example of stringent hybridization conditions is hybridization in 6X SSC at about 45°C, followed by at least one wash in 0.2X SSC, 0.1% SDS at 55°C. Another example of stringent hybridization conditions is hybridization in 6X SSC at about 45°C, followed by at least one wash in 0.2X SSC, 0.1% SDS at 60°C. A further example of stringent hybridization conditions is hybridization in 6X SSC at about 45°C, followed by at least one wash in 0.2X SSC, 0.1% SDS at 65°C. High stringent conditions include hybridization in 0.5M sodium phosphate, 7% SDS at 65°C, followed by at least one wash at 0.2X SSC, 1% SDS at 65°C.

[0067]The phrase **"substantially as set out," "substantially identical"** or **"substantially homologous"** means that the relevant amino acid or nucleotide sequence (e.g., CDR(s), V_H, or V_L domain) will be identical to or have insubstantial differences (through conserved amino acid substitutions) in comparison to the sequences which are set out. Insubstantial differences include minor amino acid changes, such as 1 or 2 substitutions in a 5 amino acid sequence of a specified region. In the case of antibodies, the second antibody has the same specificity and has at least 50% of the affinity of the first antibody.

[0068]Sequences substantially identical or homologous (e.g., at least about 85% sequence identity) to the sequences disclosed herein are also part of this application. In some embodiment, the sequence identity can be about 85%, 90%,

95%, 96%, 97%, 98%, 99% or higher. Alternatively, substantial identity or homology exists when the nucleic acid segments will hybridize under selective hybridization conditions (e.g., highly stringent hybridization conditions), to the complement of the strand. The nucleic acids may be present in whole cells, in a cell lysate, or in a partially purified or substantially pure form.

[0069]The term **"therapeutic agent"** is a substance that treats or assists in treating a medical disorder. Therapeutic agents may include, but are not limited to, substances that modulate immune cells or immune responses in a manner that complements the IL-22 activity of anti-IL-22 antibodies. Non-limiting examples and uses of therapeutic agents are described herein.

[0070]As used herein, a **"therapeutically effective amount"** of an anti-IL-22 antibody refers to an amount of an antibody which is effective, upon single or multiple dose administration to a subject (such as a human patient) at treating, preventing, curing, delaying, reducing the severity of, and/or ameliorating at least one symptom of a disorder or recurring disorder, or prolonging the survival of the subject beyond that expected in the absence of such treatment.

[0071]The term **"treatment"** refers to a therapeutic or preventative measure. The treatment may be administered to a subject having a medical disorder or who ultimately may acquire the disorder, in order to prevent, cure, delay, reduce the severity of, and/or ameliorate one or more symptoms of a disorder or recurring disorder, or in order to prolong the survival of a subject beyond that expected in the absence of such treatment.

II. Anti-IL-22 Antibodies

[0072]The disclosure provides novel anti-IL-22 antibodies that comprise novel antigen-binding fragments.

[0073]Numerous methods known to those skilled in the art are available for obtaining antibodies or antigen-binding fragments thereof. For example, antibodies can be produced using recombinant DNA methods (U.S. Patent 4,816,567). Monoclonal antibodies may also be produced by generation of hybridomas (see e.g., Kohler and Milstein (1975) *Nature*, 256: 495-499) in accordance with known methods. Hybridomas formed in this manner are then screened using standard methods, such as enzyme-linked immunosorbent assay (ELISA) and surface plasmon resonance (BIAcore™) analysis, to identify one or more hybridomas

that produce an antibody that specifically binds with a specified antigen. Any form of the specified antigen may be used as the immunogen, e.g., recombinant antigen, naturally occurring forms, any variants or fragments thereof, as well as antigenic peptide thereof.

[0074]One exemplary method of making antibodies includes screening protein expression libraries, e.g., phage or ribosome display libraries. Phage display is described, for example, in Ladner *et al.*, U.S. Patent No. 5,223,409; Smith (1985) *Science* 228:1315-1317; Clackson *et al.* (1991) *Nature*, 352: 624-628; Marks *et al.* (1991) *J. Mol. Biol.*, 222: 581-597; WO 92/18619; WO 91/17271; WO 92/20791; WO 92/15679; WO 93/01288; WO 92/01047; WO 92/09690; and WO 90/02809.

[0075]In addition to the use of display libraries, the specified antigen can be used to immunize a non-human animal, e.g., a rodent, e.g., a mouse, hamster, or rat. In one embodiment, the non-human animal includes at least a part of a human immunoglobulin gene. For example, it is possible to engineer mouse strains deficient in mouse antibody production with large fragments of the human Ig loci. Using the hybridoma technology, antigen-specific monoclonal antibodies derived from the genes with the desired specificity may be produced and selected. See, e.g., XENOMOUSE™, Green *et al.* (1994) *Nature Genetics* 7:13-21, US 2003-0070185, WO 96/34096, published Oct. 31, 1996, and PCT Application No. PCT/US96/05928, filed Apr. 29, 1996.

[0076]In another embodiment, a monoclonal antibody is obtained from the non-human animal, and then modified, e.g., humanized, deimmunized, chimeric, may be produced using recombinant DNA techniques known in the art. A variety of approaches for making chimeric antibodies have been described. See e.g., Morrison *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* 81:6851, 1985; Takeda *et al.*, *Nature* 314:452, 1985, Cabilly *et al.*, U.S. Patent No. 4,816,567; Boss *et al.*, U.S. Patent No. 4,816,397; Tanaguchi *et al.*, European Patent Publication EP171496; European Patent Publication 0173494, United Kingdom Patent GB 2177096B. Humanized antibodies may also be produced, for example, using transgenic mice that express human heavy and light chain genes, but are incapable of expressing the endogenous mouse immunoglobulin heavy and light chain genes. Winter describes an exemplary CDR-grafting method that may be used to prepare the

humanized antibodies described herein (U.S. Patent No. 5,225,539). All of the CDRs of a particular human antibody may be replaced with at least a portion of a non-human CDR, or only some of the CDRs may be replaced with non-human CDRs. It is only necessary to replace the number of CDRs required for binding of the humanized antibody to a predetermined antigen.

[0077] Humanized antibodies or fragments thereof can be generated by replacing sequences of the Fv variable domain that are not directly involved in antigen binding with equivalent sequences from human Fv variable domains. Exemplary methods for generating humanized antibodies or fragments thereof are provided by Morrison (1985) *Science* 229:1202-1207; by Oi *et al.* (1986) *BioTechniques* 4:214; and by US 5,585,089; US 5,693,761; US 5,693,762; US 5,859,205; and US 6,407,213. Those methods include isolating, manipulating, and expressing the nucleic acid sequences that encode all or part of immunoglobulin Fv variable domains from at least one of a heavy or light chain. Such nucleic acids may be obtained from a hybridoma producing an antibody against a predetermined target, as described above, as well as from other sources. The recombinant DNA encoding the humanized antibody molecule can then be cloned into an appropriate expression vector.

[0078] In certain embodiments, a humanized antibody is optimized by the introduction of conservative substitutions, consensus sequence substitutions, germline substitutions and/or backmutations. Such altered immunoglobulin molecules can be made by any of several techniques known in the art, (e.g., Teng *et al.*, *Proc. Natl. Acad. Sci. U.S.A.*, 80: 7308-7312, 1983; Kozbor *et al.*, *Immunology Today*, 4: 7279, 1983; Olsson *et al.*, *Meth. Enzymol.*, 92: 3-16, 1982), and may be made according to the teachings of PCT Publication WO92/06193 or EP 0239400).

[0079] An antibody or fragment thereof may also be modified by specific deletion of human T cell epitopes or "deimmunization" by the methods disclosed in WO 98/52976 and WO 00/34317. Briefly, the heavy and light chain variable domains of an antibody can be analyzed for peptides that bind to MHC Class II; these peptides represent potential T-cell epitopes (as defined in WO 98/52976 and WO 00/34317). For detection of potential T-cell epitopes, a computer modeling approach termed "peptide threading" can be applied, and in addition a database of

human MHC class II binding peptides can be searched for motifs present in the V_H and V_L sequences, as described in WO 98/52976 and WO 00/34317. These motifs bind to any of the 18 major MHC class II DR allotypes, and thus constitute potential T cell epitopes. Potential T-cell epitopes detected can be eliminated by substituting small numbers of amino acid residues in the variable domains, or preferably, by single amino acid substitutions. Typically, conservative substitutions are made. Often, but not exclusively, an amino acid common to a position in human germline antibody sequences may be used. Human germline sequences, e.g., are disclosed in Tomlinson, *et al.* (1992) *J. Mol. Biol.* 227:776-798; Cook, G. P. *et al.* (1995) *Immunol. Today* Vol. 16 (5): 237-242; Chothia, D. *et al.* (1992) *J. Mol. Biol.* 227:799-817; and Tomlinson *et al.* (1995) *EMBO J.* 14:4628-4638. The V BASE directory provides a comprehensive directory of human immunoglobulin variable region sequences (compiled by Tomlinson, I.A. *et al.* MRC Centre for Protein Engineering, Cambridge, UK). These sequences can be used as a source of human sequence, e.g., for framework regions and CDRs. Consensus human framework regions can also be used, e.g., as described in U.S. Patent No. 6,300,064.

[0080] In certain embodiments, an antibody can contain an altered immunoglobulin constant or Fc region. For example, an antibody produced in accordance with the teachings herein may bind more strongly or with more specificity to effector molecules such as complement and/or Fc receptors, which can control several immune functions of the antibody such as effector cell activity, lysis, complement-mediated activity, antibody clearance, and antibody half-life. Typical Fc receptors that bind to an Fc region of an antibody (e.g., an IgG antibody) include, but are not limited to, receptors of the FcγRI, FcγRII, and FcγRIII and FcRn subclasses, including allelic variants and alternatively spliced forms of these receptors. Fc receptors are reviewed in Ravetch and Kinet, *Annu. Rev. Immunol.* 9:457-92, 1991; Capel *et al.*, *Immunomethods* 4:25-34, 1994; and de Haas *et al.*, *J. Lab. Clin. Med.* 126:330-41, 1995).

[0081] For additional antibody production techniques, see *Antibodies: A Laboratory Manual*, eds. Harlow *et al.*, Cold Spring Harbor Laboratory, 1988. The present invention is not necessarily limited to any particular source, method of production, or other special characteristics of an antibody.

[0082]Antibodies, also known as immunoglobulins, are typically tetrameric glycosylated proteins composed of two light (L) chains of approximately 25 kDa each and two heavy (H) chains of approximately 50 kDa each. Two types of light chain, termed lambda and kappa, may be found in antibodies. Depending on the amino acid sequence of the constant domain of heavy chains, immunoglobulins can be assigned to five major classes: A, D, E, G, and M, and several of these may be further divided into subclasses (isotypes), e.g., IgG₁, IgG₂, IgG₃, IgG₄, IgA₁, and IgA₂. Each light chain includes an N-terminal variable (V) domain (VL) and a constant (C) domain (CL). Each heavy chain includes an N-terminal V domain (VH), three or four C domains (CHs), and a hinge region. The CH domain most proximal to VH is designated as CH1. The VH and VL domains consist of four regions of relatively conserved sequences called framework regions (FR1, FR2, FR3, and FR4), which form a scaffold for three regions of hypervariable sequences (complementarity determining regions, CDRs). The CDRs contain most of the residues responsible for specific interactions of the antibody with the antigen. CDRs are referred to as CDR1, CDR2, and CDR3. Accordingly, CDR constituents on the heavy chain are referred to as H1, H2, and H3, while CDR constituents on the light chain are referred to as L1, L2, and L3.

[0083]CDR3 is typically the greatest source of molecular diversity within the antibody-binding site. H3, for example, can be as short as two amino acid residues or greater than 26 amino acids. The subunit structures and three-dimensional configurations of different classes of immunoglobulins are well known in the art. For a review of the antibody structure, see *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, eds. Harlow et al., 1988. One of skill in the art will recognize that each subunit structure, e.g., a CH, VH, CL, VL, CDR, FR structure, comprises active fragments, e.g., the portion of the VH, VL, or CDR subunit the binds to the antigen, i.e., the antigen-binding fragment, or, e.g., the portion of the CH subunit that binds to and/or activates, e.g., an Fc receptor and/or complement. The CDRs typically refer to the Kabat CDRs, as described in *Sequences of Proteins of Immunological Interest*, US Department of Health and Human Services (1991), eds. Kabat et al. Another standard for characterizing the antigen binding site is to refer to the hypervariable loops as described by Chothia. See, e.g., Chothia, D. et al. (1992) *J. Mol. Biol.* 227:799-817; and Tomlinson et al. (1995)

EMBO J. 14:4628-4638. Still another standard is the AbM definition used by Oxford Molecular's AbM antibody modelling software. See, generally, e.g., *Protein Sequence and Structure Analysis of Antibody Variable Domains*. In: *Antibody Engineering Lab Manual* (Ed.: Duebel, S. and Kontermann, R., Springer-Verlag, Heidelberg). Embodiments described with respect to Kabat CDRs can alternatively be implemented using similar described relationships with respect to Chothia hypervariable loops or to the AbM-defined loops.

[0084]The Fab fragment (Fragment antigen-binding) consists of V_H - C_H1 and V_L - C_L domains covalently linked by a disulfide bond between the constant regions. The F_v fragment is smaller and consists of V_H and V_L domains non-covalently linked. To overcome the tendency of non-covalently linked domains to dissociate, a single chain F_v fragment (sc F_v) can be constructed. The sc F_v contains a flexible polypeptide that links (1) the C-terminus of V_H to the N-terminus of V_L , or (2) the C-terminus of V_L to the N-terminus of V_H . A 15-mer (Gly₄Ser)₃ peptide may be used as a linker, but other linkers are known in the art.

[0085]The sequence of antibody genes after assembly and somatic mutation is highly varied, and these varied genes are estimated to encode 10^{10} different antibody molecules (Immunoglobulin Genes, 2nd ed., eds. Jonio et al., Academic Press, San Diego, CA, 1995).

[0086]A "bispecific" or "bifunctional antibody" is an artificial hybrid antibody having two different heavy/light chain pairs and two different binding sites. Bispecific antibodies can be produced by a variety of methods including fusion of hybridomas or linking of Fab' fragments. See, e.g., Songsivilai & Lachmann, *Clin. Exp. Immunol.* 79:315-321 (1990); Kostelny et al., *J. Immunol.* 148, 1547-1553 (1992). In one embodiment, the bispecific antibody comprises a first binding domain polypeptide, such as a Fab' fragment, linked via an immunoglobulin constant region to a second binding domain polypeptide.

[0087]Small Modular ImmunoPharmaceuticals (SMIP™) provide an example of a variant molecule comprising a binding domain polypeptide. SMIPs and their uses and applications are disclosed in, e.g., U.S. Published Patent Application. Nos. 2003/0118592, 2003/0133939, 2004/0058445, 2005/0136049, 2005/0175614, 2005/0180970, 2005/0186216, 2005/0202012, 2005/0202023, 2005/0202028, 2005/0202534, and 2005/0238646, and related patent family

members thereof, all of which are hereby incorporated by reference herein in their entireties.

[0088]A SMIPTM typically refers to a binding domain-immunoglobulin fusion protein that includes a binding domain polypeptide that is fused or otherwise connected to an immunoglobulin hinge or hinge-acting region polypeptide, which in turn is fused or otherwise connected to a region comprising one or more native or engineered constant regions from an immunoglobulin heavy chain, other than CH1, for example, the CH2 and CH3 regions of IgG and IgA, or the CH3 and CH4 regions of IgE (*see e.g.*, U.S. 2005/0136049 by Ledbetter, J. *et al.*, which is incorporated by reference, for a more complete description). The binding domain-immunoglobulin fusion protein can further include a region that includes a native or engineered immunoglobulin heavy chain CH2 constant region polypeptide (or CH3 in the case of a construct derived in whole or in part from IgE) that is fused or otherwise connected to the hinge region polypeptide and a native or engineered immunoglobulin heavy chain CH3 constant region polypeptide (or CH4 in the case of a construct derived in whole or in part from IgE) that is fused or otherwise connected to the CH2 constant region polypeptide (or CH3 in the case of a construct derived in whole or in part from IgE). Typically, such binding domain-immunoglobulin fusion proteins are capable of at least one immunological activity selected from the group consisting of antibody dependent cell-mediated cytotoxicity, complement fixation, and/or binding to a target, for example, a target antigen, such as human IL-22.

[0089]Therapeutic proteins, i.e., a protein or peptide that has a biological effect on a region in the body on which it acts or on a region of the body on which it remotely acts via intermediates, are also useful for practicing the invention. A therapeutic protein can include peptide mimetics. Mimetics are peptide-containing molecules that mimic elements of protein secondary structure. See, for example, Johnson *et al.*, "Peptide Turn Mimetics" in BIOTECHNOLOGY AND PHARMACY, Pezzuto *et al.*, Eds., Chapman and Hall, New York (1993), incorporated herein by reference. The underlying rationale behind the use of peptide mimetics is that the peptide backbone of proteins exists chiefly to orient amino acid side chains in such a way as to facilitate molecular interactions, such as those of antibody and antigen. A peptide mimetic is expected to permit molecular interactions similar to the natural

molecule. These principles may be used to engineer second generation molecules having many of the natural properties of the targeting peptides disclosed herein, but with altered and potentially improved characteristics.

[0090] Other embodiments of therapeutic proteins include fusion proteins. These molecules generally have all or a substantial portion of a targeting peptide, for example, IL-22 or an anti IL-22 antibody, linked at the N- or C-terminus, to all or a portion of a second polypeptide or protein. For example, fusions may employ leader sequences from other species to permit the recombinant expression of a protein in a heterologous host. Another useful fusion includes the addition of an immunologically active domain, such as an antibody epitope, to facilitate purification of the fusion protein. Inclusion of a cleavage site at or near the fusion junction will facilitate removal of the extraneous polypeptide after purification. Other useful fusions include linking of functional domains, such as active sites from enzymes, glycosylation domains, cellular targeting signals or transmembrane regions. Examples of proteins or peptides that may be incorporated into a fusion protein include cytostatic proteins, cytotoxic proteins, pro-apoptosis agents, anti-angiogenic agents, hormones, cytokines, growth factors, peptide drugs, antibodies, Fab fragments of antibodies, antigens, receptor proteins, enzymes, lectins, MHC proteins, cell adhesion proteins and binding proteins. Methods of generating fusion proteins are well known to those of skill in the art. Such proteins can be produced, for example, by chemical attachment using bifunctional cross-linking reagents, by de novo synthesis of the complete fusion protein, or by attachment of a DNA sequence encoding the targeting peptide to a DNA sequence encoding the second peptide or protein, followed by expression of the intact fusion protein.

[0091] In one embodiment, the targeting peptide, for example, IL-22 or an anti IL-22 antibody, is fused with an immunoglobulin heavy chain constant region, such as an Fc fragment, which contains two constant region domains and a hinge region but lacks the variable region (See, U.S. Pat. Nos. 6,018,026 and 5,750,375, incorporated herein by reference). The Fc region may be a naturally occurring Fc region, or may be altered to improve certain qualities, such as therapeutic qualities, circulation time, reduced aggregation, etc. Peptides and proteins fused to an Fc region typically exhibit a greater half-life *in vivo* than the unfused counterpart. Also,

a fusion to an Fc region permits dimerization/multimerization of the fusion polypeptide.

[0092] VHH molecules (or nanobodies), as known to the skilled artisan, are heavy chain variable domains derived from immunoglobulins naturally devoid of light chains, such as those derived from Camelidae as described in WO9404678, incorporated herein by reference. Such a VHH molecule can be derived from antibodies raised in Camelidae species, for example in camel, llama, dromedary, alpaca and guanaco and is sometimes called a camelid or camelized variable domain. See e.g., Muyldermans., *J. Biotechnology* (2001) 74(4):277-302, incorporated herein by reference. Other species besides Camelidae may produce heavy chain antibodies naturally devoid of light chain. VHH molecules are about 10 times smaller than IgG molecules. They are single polypeptides and very stable, resisting extreme pH and temperature conditions. Moreover, they are resistant to the action of proteases which is not the case for conventional antibodies. Furthermore, *in vitro* expression of VHHs produces high yield, properly folded functional VHHs. In addition, antibodies generated in Camelids will recognize epitopes other than those recognized by antibodies generated *in vitro* through the use of antibody libraries or via immunization of mammals other than Camelids (see WO 9749805, which is incorporated herein by reference).

[0093] One aspect of the present invention comprises antibodies and antigen binding fragments that bind IL-22. The disclosure provides novel CDRs derived from human immunoglobulin gene libraries. The structure for carrying a CDR is generally an antibody heavy or light chain or portion thereof, where the CDR is located to a naturally occurring CDR region. The structures and locations of variable domains may be determined as described in Kabat et al., *Sequences of Proteins of Immunological Interest*, No. 91-3242, National Institutes of Health Publications, Bethesda, MD (1991).

[0094] DNA and amino acid (AA) sequences of illustrative embodiments of the anti-IL-22 antibodies of this invention, including their scF_v fragments, V_H and V_L domains, and CDRs, are set forth in Figures 7-10 and enumerated in Tables 1 and 7. Twenty specific embodiments of the non-germlined antibodies are identified as GIL01, GIL16, GIL45, GIL60, GIL68, GIL92, 097D09, 062A09, 062G05, 087B03, 367D04, 368D04, 166B06, 166G05, 375G06, 376B10, 354A08, 355B06, 355E04,

and 356A11. The CDR positions in the V_H and V_L domains of the non-germlined antibodies are listed in Table 2. Fifteen specific embodiments of the germlined antibodies are identified as GIL01, GIL16, GIL45, GIL60, GIL68, GIL92, 062A09, 087B03, 166B06, 166G05, 354A08, 355B06, 355E04, 356A11, and 368D04.

Table 1A: Amino acid and Nucleotide Sequences of V_H and V_L Domains, F_v, and CDRs of Non-germlined

Antibodies

Region	Type	GIL01 SEQ ID	GIL16 SEQ ID	GIL45 SEQ ID	GIL60 SEQ ID	GIL68 SEQ ID	GIL92 SEQ ID	097D09 SEQ ID	062A09 SEQ ID	062G05 SEQ ID	087B03 SEQ ID
V _H	AA	NO:5	NO:23	NO:41	NO:59	NO:77	NO:95	NO:113	NO:131	NO:149	NO:167
V _L	AA	NO:6	NO:24	NO:42	NO:60	NO:78	NO:96	NO:114	NO:132	NO:150	NO:168
scFv	AA	NO:7	NO:25	NO:43	NO:61	NO:79	NO:97	NO:115	NO:133	NO:151	NO:169
H1	AA	NO:8	NO:26	NO:44	NO:62	NO:80	NO:98	NO:116	NO:134	NO:152	NO:170
H2	AA	NO:9	NO:27	NO:45	NO:63	NO:81	NO:99	NO:117	NO:135	NO:153	NO:171
H3	AA	NO:10	NO:28	NO:46	NO:64	NO:82	NO:100	NO:118	NO:136	NO:154	NO:172
L1	AA	NO:11	NO:29	NO:47	NO:65	NO:83	NO:101	NO:119	NO:137	NO:155	NO:173
L2	AA	NO:12	NO:30	NO:48	NO:66	NO:84	NO:102	NO:120	NO:138	NO:156	NO:174
L3	AA	NO:13	NO:31	NO:49	NO:67	NO:85	NO:103	NO:121	NO:139	NO:157	NO:175
V _H	DNA	NO:14	NO:32	NO:50	NO:68	NO:86	NO:104	NO:122	NO:140	NO:158	NO:176
V _L	DNA	NO:15	NO:33	NO:51	NO:69	NO:87	NO:105	NO:123	NO:141	NO:159	NO:177
scF _v	DNA	NO:16	NO:34	NO:52	NO:70	NO:88	NO:106	NO:124	NO:142	NO:160	NO:178
H1	DNA	NO:17	NO:35	NO:53	NO:71	NO:89	NO:107	NO:125	NO:143	NO:161	NO:179
H2	DNA	NO:18	NO:36	NO:54	NO:72	NO:90	NO:108	NO:126	NO:144	NO:162	NO:180
H3	DNA	NO:19	NO:37	NO:55	NO:73	NO:91	NO:109	NO:127	NO:145	NO:163	NO:181
L1	DNA	NO:20	NO:38	NO:56	NO:74	NO:92	NO:110	NO:128	NO:146	NO:164	NO:182
L2	DNA	NO:21	NO:39	NO:57	NO:75	NO:93	NO:111	NO:129	NO:147	NO:165	NO:183
L3	DNA	NO:22	NO:40	NO:58	NO:76	NO:94	NO:112	NO:130	NO:148	NO:166	NO:184

Table 1B: Amino acid and Nucleotide Sequences of V_H and V_L Domains, Fv, and CDRs of Non-germlined Antibodies

Region	Type	367D04 SEQ ID	368D04 SEQ ID	166B06 SEQ ID	166G05 SEQ ID	375G05 SEQ ID	376B10 SEQ ID	354A08 SEQ ID	355B06 SEQ ID	355E04 SEQ ID	356A11 SEQ ID
V _H	AA	NO:185	NO:203	NO:221	NO:239	NO:257	NO:275	NO:293	NO:311	NO:329	NO:347
V _L	AA	NO:186	NO:204	NO:222	NO:240	NO:258	NO:276	NO:294	NO:312	NO:330	NO:348
scF _v	AA	NO:187	NO:205	NO:223	NO:241	NO:259	NO:277	NO:295	NO:313	NO:331	NO:349
H1	AA	NO:188	NO:206	NO:224	NO:242	NO:260	NO:278	NO:296	NO:314	NO:332	NO:350
H2	AA	NO:189	NO:207	NO:225	NO:243	NO:261	NO:279	NO:297	NO:315	NO:333	NO:351
H3	AA	NO:190	NO:208	NO:226	NO:244	NO:262	NO:280	NO:298	NO:316	NO:334	NO:352
L1	AA	NO:191	NO:209	NO:227	NO:245	NO:263	NO:281	NO:299	NO:317	NO:335	NO:353
L2	AA	NO:192	NO:210	NO:228	NO:246	NO:264	NO:282	NO:300	NO:318	NO:336	NO:354
L3	AA	NO:193	NO:211	NO:229	NO:247	NO:265	NO:283	NO:301	NO:319	NO:337	NO:355
V _H	DNA	NO:194	NO:212	NO:230	NO:248	NO:266	NO:284	NO:302	NO:320	NO:338	NO:356
V _L	DNA	NO:195	NO:213	NO:231	NO:249	NO:267	NO:285	NO:303	NO:321	NO:339	NO:357
scF _v	DNA	NO:196	NO:214	NO:232	NO:250	NO:268	NO:286	NO:304	NO:322	NO:340	NO:358
H1	DNA	NO:197	NO:215	NO:233	NO:251	NO:269	NO:287	NO:305	NO:323	NO:341	NO:359
H2	DNA	NO:198	NO:216	NO:234	NO:252	NO:270	NO:288	NO:306	NO:324	NO:342	NO:360
H3	DNA	NO:199	NO:217	NO:235	NO:253	NO:271	NO:289	NO:307	NO:325	NO:343	NO:361
L1	DNA	NO:200	NO:218	NO:236	NO:254	NO:272	NO:290	NO:308	NO:326	NO:344	NO:362
L2	DNA	NO:201	NO:219	NO:237	NO:255	NO:273	NO:291	NO:309	NO:327	NO:345	NO:363
L3	DNA	NO:202	NO:220	NO:238	NO:256	NO:274	NO:292	NO:310	NO:328	NO:346	NO:364

Table 2: Positions of CDRs within Non-germlined Antibody Amino Acid Sequences of V_H and V_L Domains

CDR	GIL01	GIL16	GIL45	GIL60	GIL68	GIL92	097D09	062A09	062G05	087B03
H1	31-35	31-35	31-35	31-35	31-35	31-35	31-35	31-35	31-35	31-35
H2	50-66	50-66	50-66	50-66	50-66	50-66	50-66	50-66	50-66	50-66
H3	99-108	99-108	99-108	99-110	99-108	99-110	99-108	99-108	99-108	99-110
L1	24-34	24-34	23-36	23-36	23-33	23-36	24-34	24-34	24-34	23-36
L2	50-56	50-56	52-58	52-58	49-55	52-58	50-56	50-56	50-56	52-58
L3	89-97	89-97	91-100	91-100	88-98	91-101	89-97	89-97	89-97	91-100

CDR	367D04	368D04	168B06	166G05	375G06	376B10	354A08	355B06	355E04	356A11
H1	31-35	31-35	31-35	31-35	31-35	31-35	30-34	31-35	31-35	31-35
H2	50-66	50-66	50-66	50-66	50-66	50-66	49-65	50-66	50-66	50-66
H3	99-110	99-110	99-108	99-108	99-108	99-108	98-109	99-110	99-110	99-110
L1	23-36	23-36	23-33	23-33	23-33	23-33	23-36	23-36	23-36	22-35
L2	52-58	52-58	49-55	49-55	49-55	49-55	52-58	52-58	52-58	51-58
L3	91-100	91-100	88-98	88-98	88-98	88-98	91-101	91-101	91-101	90-100

[0095]Anti-IL-22 antibodies of this invention may optionally comprise antibody constant regions or parts thereof. For example, a V_L domain may be attached at its C-terminal end to a light chain constant domain like C_κ or C_λ. Similarly, a V_H domain or portion thereof may be attached to all or part of a heavy chain like IgA, IgD, IgE, IgG, and IgM, and any isotype subclass. Constant regions are known in the art (see, for example, Kabat et al., Sequences of Proteins of Immunological Interest, No. 91-3242, National Institutes of Health Publications, Bethesda, MD (1991)). Therefore, antibodies within the scope of this invention include V_H and V_L domains, or a portion thereof, combined with constant regions known in the art.

[0096]Certain embodiments comprise a V_H domain, a V_L domain, or a combination thereof, of the F_v fragment from GIL01, GIL16, GIL45, GIL60, GIL68, GIL92, 097D09, 062A09, 062G05, 087B03, 367D04, 368D04, 166B06, 166G05, 375G06, 376B10, 354A08, 355B06, 355E04, or 356A11. Another embodiment comprises a V_H domain, a V_L domain, or a combination thereof, of the F_v fragment from an antibody chosen from 356A11, 354A08, 087B03, and 368D04. Further embodiments comprise one, two, three, four, five or six complementarity determining regions (CDRs) from the V_H and V_L domains. Antibodies whose CDR sequences are included within SEQ ID NO:5-13, 23-31, 41-49, 59-67, 77-85, 95-103, 113-121, 131-139, 149-157, 167-175, 185-193, 203-211, 221-229, 239-247, 257-265, 275-283, 293-301, 311-319, 329-337, 347-355, 365-373, 383-391, 401-409, 419-427, 437-445, 455-463, 473-481, 491-499, 509-517, 527-535, 545-553, 563-571, 581-589, 599-607, or 617-625 are encompassed within the scope of this invention. For example, in one embodiment, an antibody comprises a H3 fragment of the V_H domain of germlined or non-germlined GIL01, GIL16, GIL45, GIL60, GIL68, GIL92, 097D09, 062A09, 062G05, 087B03, 367D04, 368D04, 166B06, 166G05, 375G06, 376B10, 354A08, 355B06, 355E04, or 356A11 or from an antibody chosen from 356A11, 354A08, 087B03, and 368D04.

[0097]In certain embodiments, the V_H and/or V_L domains may be germlined, i.e., the framework regions (FR) of these domains are mutated using conventional molecular biology techniques to match those produced by the germline cells. In other embodiments, the FR sequences remain diverged from the consensus

germline sequences. In one embodiment of this invention, germlined antibodies are shown in Table 7.

[0098] In one embodiment, the invention provides amino acid and nucleic acid sequences for the germlined GIL01, GIL16, GIL45, GIL60, GIL68, GIL92, 097D09, 062A09, 062G05, 087B03, 367D04, 368D04, 166B06, 166G05, 375G06, 376B10, 354A08, 355B06, 355E04, or 356A11. Amino acid and nucleotide sequences for the V_H domain of the germlined GIL01, GIL16, GIL45, GIL60, GIL68, GIL92, 062A09, 087B03, 166B06, 166G05, 354A08, 355B06, 355E04, 356A11, and 368D04 are depicted in Table 7 and Figure 8. Amino acid and nucleotide sequences for the V_L domain of the germlined GIL01, GIL16, GIL45, GIL60, GIL68, GIL92, 062A09, 087B03, 166B06, 166G05, 354A08, 355B06, 355E04, 356A11, and 368D04 are also depicted in Table 7 and Figure 8.

[0099] In one embodiment, mutagenesis is used to make an antibody more similar to one or more germline sequences. This may be desirable when mutations are introduced into the framework region of an antibody through somatic mutagenesis or through error prone PCR. Germline sequences for the V_H and V_L domains can be identified by performing amino acid and nucleic acid sequence alignments against the VBASE database (MRC Center for Protein Engineering, UK). VBASE is a comprehensive directory of all human germline variable region sequences compiled from over a thousand published sequences, including those in the current releases of the Genbank and EMBL data libraries. In some embodiments, the FR regions of the scFvs are mutated in conformity with the closest matches in the VBASE database and the CDR portions are kept intact.

[00100] In certain embodiments, antibodies of this invention specifically react with an epitope that is the same as the epitope recognized by GIL01, GIL16, GIL45, GIL60, GIL68, GIL92, 097D09, 062A09, 062G05, 087B03, 367D04, 368D04, 166B06, 166G05, 375G06, 376B10, 354A08, 355B06, 355E04, or 356A11, such that they competitively inhibit the binding of GIL01, GIL16, GIL45, GIL60, GIL68, GIL92, 097D09, 062A09, 062G05, 087B03, 367D04, 368D04, 166B06, 166G05, 375G06, 376B10, 354A08, 355B06, 355E04, or 356A11 to human IL-22. Such antibodies can be determined in competitive binding assays. In one embodiment, the antibody, or antigen binding fragment thereof, binds to an IL-22 epitope that is recognized by 368D04, such that the antibody competitively

inhibits the binding of 368D04 to human IL-22. In another embodiment, the antibody, or antigen binding fragment thereof, binds to an IL-22 epitope that is recognized by 356A11, such that the antibody competitively inhibits the binding of 356A11 to human IL-22. In another embodiment, the antibody, or antigen binding fragment thereof, binds to an IL-22 epitope that is recognized by 354A08, such that the antibody competitively inhibits the binding of 354A08 to human IL-22. In another embodiment, the antibody, or antigen binding fragment thereof, binds to an IL-22 epitope that is recognized by 087B03, such that the antibody competitively inhibits the binding of 087B03 to human IL-22. In one embodiment, the association constant (K_A) of these antibodies for human IL-22 is at least 10^6 M^{-1} . In another embodiment, the association constant of these antibodies for human IL-22 is at least 10^9 M^{-1} . In other embodiments, the association constant of these antibodies for human IL-22 is at least 10^{10} M^{-1} , at least 10^{11} M^{-1} , or at least 10^{12} M^{-1} . The binding affinity may be determined using techniques known in the art, such as ELISA, biosensor technology, such as biospecific interaction analysis, or other techniques including those described in this application.

[00101] It is contemplated that antibodies of this invention may bind other proteins, such as, for example, recombinant proteins comprising all or a portion of IL-22.

[00102] One of ordinary skill in the art will recognize that the disclosed antibodies may be used to detect, measure, and/or inhibit proteins that differ somewhat from IL-22. For example, these proteins may be homologs of IL-22. Anti-IL-22 antibodies are expected to bind proteins that comprise a sequence which is at least about 60%, 70%, 80%, 90%, 95%, or more identical to any sequence of at least 100, 80, 60, 40, or 20 contiguous amino acids in the sequence set forth SEQ ID NO:1.

[00103] In addition to sequence homology analyses, epitope mapping (see, e.g., Epitope Mapping Protocols, ed. Morris, Humana Press, 1996), and secondary and tertiary structure analyses can be carried out to identify specific 3D structures assumed by the presently disclosed antibodies and their complexes with antigens. Such methods include, but are not limited to, X-ray crystallography (Engstrom (1974) Biochem. Exp. Biol., 11:7-13) and computer modeling of virtual representations of the present antibodies (Fletterick et al. (1986) Computer

Graphics and Molecular Modeling, in Current Communications in Molecular Biology, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY).

[00104] The disclosure provides a method for obtaining anti-IL-22 antibodies that comprises creating antibodies with altered Table 1 V_H and/or V_L sequence(s). Such antibodies may be derived by a skilled artisan using techniques known in the art. For example, amino acid substitutions, deletions, or additions can be introduced in FR and/or CDR regions. FR changes are usually designed to improve the stability and immunogenicity of the antibody, while CDR changes are typically designed to increase antibody affinity for its antigen. The changes that increase affinity may be tested by altering CDR sequence and measuring antibody affinity for its target (see Antibody Engineering, 2nd ed., Oxford University Press, ed. Borrebaeck, 1995).

[00105] Antibodies whose CDR sequences differ insubstantially from those included in or included within the sequences in SEQ ID NO: 5-13, 23-31, 41-49, 59-67, 77-85, 95-103, 113-121, 131-139, 149-157, 167-175, 185-193, 203-211, 221-229, 239-247, 257-265, 275-283, 293-301, 311-319, 329-337, 347-355, 365-373, 383-391, 401-409, 419-427, 437-445, 455-463, 473-481, 491-499, 509-517, 527-535, 545-553, 563-571, 581-589, 599-607, or 617-625, are encompassed within the scope of this invention. Typically, this involves substitution of an amino acid with an amino acid having similar charge, hydrophobic, or stereochemical characteristics. More drastic substitutions in FR regions, in contrast to CDR regions, may also be made as long as they do not adversely affect (e.g., reduce affinity by more than 50% as compared to unsubstituted antibody) the binding properties of the antibody. Substitutions may also be made to germline the antibody or stabilize the antigen binding site.

[00106] Conservative modifications will produce molecules having functional and chemical characteristics similar to those of the molecule from which such modifications are made. In contrast, substantial modifications in the functional and/or chemical characteristics of the molecules may be accomplished by selecting substitutions in the amino acid sequence that differ significantly in their effect on maintaining (1) the structure of the molecular backbone in the area of the substitution, for example, as a sheet or helical conformation, (2) the charge or hydrophobicity of the molecule at the target site, or (3) the size of the molecule.

[00107] For example, a "conservative amino acid substitution" may involve a substitution of a native amino acid residue with a nonnative residue such that there is little or no effect on the polarity or charge of the amino acid residue at that position. (See, for example, MacLennan et al., 1998, *Acta Physiol. Scand. Suppl.* 643:55-67; Sasaki et al., 1998, *Adv. Biophys.* 35:1-24).

[00108] Desired amino acid substitutions (whether conservative or non-conservative) can be determined by those skilled in the art at the time such substitutions are desired. For example, amino acid substitutions can be used to identify important residues of the molecule sequence, or to increase or decrease the affinity of the molecules described herein. Exemplary amino acid substitutions include, but are not limited to, those set forth in Table 3.

Table 3: Amino Acid Substitutions

Original Residues	Exemplary Substitutions	More Conservative Substitutions
Ala (A)	Val, Leu, Ile	Val
Arg (R)	Lys, Gln, Asn	Lys
Asn (N)	Gln	Gln
Asp (D)	Glu	Glu
Cys (C)	Ser, Ala	Ser
Gln (Q)	Asn	Asn
Gly (G)	Pro, Ala	Ala
His (H)	Asn, Gln, Lys, Arg	Arg
Ile (I)	Leu, Val, Met, Ala, Phe, Norleucine	Leu
Leu (L)	Norleucine, Ile, Val, Met, Ala, Phe	Ile
Lys (K)	Arg, 1, 4 Diamino-butyric Acid, Gln, Asn	Arg
Met (M)	Leu, Phe, Ile	Leu
Phe (F)	Leu, Val, Ile, Ala, Tyr	Leu
Pro (P)	Ala	Gly
Ser (S)	Thr, Ala, Cys	Thr
Thr (T)	Ser	Ser
Trp (W)	Tyr, Phe	Tyr
Tyr (Y)	Trp, Phe, Thr, Ser	Phe
Val (V)	Ile, Met, Leu, Phe, Ala, Norleucine	Leu

[00109] In certain embodiments, conservative amino acid substitutions also encompass non-naturally occurring amino acid residues which are typically incorporated by chemical peptide synthesis rather than by synthesis in biological systems.

[00110] In one embodiment, the method for making a variant V_H domain comprises adding, deleting, or substituting at least one amino acid in the disclosed

V_H domains, or combining the disclosed V_H domains with at least one V_L domain, and testing the variant V_H domain for IL-22 binding or modulation of IL-22 activity.

[00111] An analogous method for making a variant V_L domain comprises adding, deleting, or substituting at least one amino acid in the disclosed V_L domains, or combining the disclosed V_L domains with at least one V_H domain, and testing the variant V_L domain for IL-22 binding or modulation of IL-22 activity.

[00112] A further aspect of the disclosure provides a method for preparing antibodies or antigen-binding fragments that specifically bind IL-22. The method comprises:

- (a) providing a starting repertoire of nucleic acids encoding a V_H domain which lacks at least one CDR or contains at least one CDR to be replaced;
- (b) inserting into or replacing the CDR region of the starting repertoire with at least one donor nucleic acid encoding an amino acid sequence as substantially set out herein for a V_H CDR, yielding a product repertoire;
- (c) expressing the nucleic acids of the product repertoire;
- (d) selecting a specific antigen-binding fragment that binds to IL-22; and
- (e) recovering the specific antigen-binding fragment or nucleic acid encoding it.

[00113] In an analogous method at least one V_L CDR of the invention is combined with a repertoire of nucleic acids encoding a V_L domain which lacks at least one CDR or contains at least one CDR to be replaced. The at least one V_H or V_L CDR may be a CDR1, a CDR2, a CDR3, or a combination thereof, including combinations of V_H and V_L CDRs, such as those set forth in Tables 1 or 7, including those set out in SEQ ID NO:8, 9, 10, 11, 12, 13, 26, 27, 28, 29, 30, 31, 44, 45, 46, 47, 48, 49, 62, 63, 64, 65, 66, 67, 80, 81, 82, 83, 84, 85, 98, 99, 100, 101, 102, 103, 116, 117, 118, 119, 120, 121, 134, 135, 136, 137, 138, 139, 152, 153, 154, 155, 156, 157, 170, 171, 172, 173, 174, 175, 188, 189, 190, 191, 192, 193, 206, 207, 208, 209, 210, 211, 224, 225, 226, 227, 228, 229, 242, 243, 244, 245, 246, 247, 260, 261, 262, 263, 264, 265, 278, 279, 280, 281, 282, 283, 296, 297, 298, 299, 300, 301, 314, 315, 316, 317, 318, 319, 332, 333, 334, 335, 336, 337, 350, 351, 352, 353, 354, 355, 368, 369, 370, 371, 372, 373, 386, 387, 388, 389, 390, 391, 404, 405, 406, 407, 408, 409, 422, 423, 424, 425, 426, 427, 440, 441, 442, 443, 444, 445, 458, 459, 460, 461, 462, 463, 476, 477, 478, 479, 480, 481, 494,

495, 496, 497, 498, 499, 512, 513, 514, 515, 516, 517, 530, 531, 532, 533, 534, 535, 548, 549, 550, 551, 552, 553, 566, 567, 568, 569, 570, 571, 584, 585, 586, 587, 588, 589, 602, 603, 604, 605, 606, 607, 620, 621, 622, 623, 624, or 625.

[00114] In one embodiment, the variable domain includes a CDR3 to be replaced or lacks a CDR3 encoding region and the at least one donor nucleic acid encodes an amino acid substantially as set out in SEQ ID NO:10, 13, 28, 31, 46, 49, 64, 67, 82, 85, 100, 103, 118, 121, 136, 139, 154, 157, 172, 175, 190, 193, 208, 211, 226, 229, 244, 247, 262, 265, 280, 283, 298, 301, 316, 319, 334, 337, 352, 355, 370, 373, 388, 391, 406, 409, 424, 427, 442, 445, 460, 463, 478, 481, 496, 499, 514, 517, 532, 535, 550, 553, 568, 571, 586, 589, 604, 607, 622, or 625.

[00115] In another embodiment, the variable domain includes a CDR1 to be replaced or lacks a CDR1 encoding region and the at least one donor nucleic acid encodes an amino acid sequence substantially as set out in SEQ ID NO:8, 11, 26, 29, 44, 47, 62, 65, 80, 83, 98, 101, 116, 119, 134, 137, 152, 155, 170, 173, 188, 191, 206, 209, 224, 227, 242, 245, 260, 263, 278, 281, 296, 299, 314, 317, 332, 335, 350, 353, 368, 371, 386, 389, 404, 407, 422, 425, 440, 443, 458, 461, 476, 479, 494, 497, 512, 515, 530, 533, 548, 551, 566, 569, 584, 587, 602, 605, 620, or 623.

[00116] In another embodiment, the variable domain includes a CDR2 to be replaced or lacks a CDR2 encoding region and the at least one donor nucleic acid encodes an amino acid sequence substantially as set out in SEQ ID NO:9, 12, 27, 30, 45, 48, 63, 66, 81, 84, 99, 102, 117, 120, 135, 138, 153, 156, 171, 174, 189, 192, 207, 210, 225, 228, 243, 246, 261, 264, 279, 282, 297, 300, 315, 318, 333, 336, 351, 354, 369, 372, 387, 390, 405, 408, 423, 426, 441, 444, 459, 462, 477, 480, 495, 498, 513, 516, 531, 534, 549, 552, 567, 570, 585, 588, 603, 606, 621, or 624.

[00117] In another embodiment, the variable domain includes a CDR3 to be replaced or lacks a CDR3 encoding region and further comprises a CDR1 to be replaced or lacks a CDR1 encoding region, where the at least one donor nucleic acid encodes an amino acid sequence substantially as set out in Tables 1 or 7.

[00118] In another embodiment, the variable domain includes a CDR3 to be replaced or lacks a CDR3 encoding region and further comprises a CDR2 to be

replaced or lacks a CDR2 encoding region, where the at least one donor nucleic acid encodes an amino acid sequence substantially as set out in Tables 1 or 7.

[00119] In another embodiment, the variable domain includes a CDR3 to be replaced or lacks a CDR3 encoding region and further comprises a CDR1 and a CDR2 to be replaced or lacks a CDR1 and a CDR2 encoding region, where the at least one donor nucleic acid encodes an amino acid sequence substantially as set out in Tables 1 or 7.

[00120] Using recombinant DNA methodology, a disclosed CDR sequence may be introduced into a repertoire of V_H or V_L domains lacking the respective CDR (Marks et al. (BioTechnology (1992) 10: 779-783). For example, a primer adjacent to the 5' end of the variable domain and a primer to the third FR can be used to generate a repertoire of variable domain sequences lacking CDR3. This repertoire can be combined with a CDR3 of a disclosed antibody. Using analogous techniques, portions of a disclosed CDR sequence may be shuffled with portions of CDR sequences from other antibodies to provide a repertoire of antigen-binding fragments that bind IL-22. Either repertoire can be expressed in a host system such as phage display (described in WO 92/01047 and its corresponding U.S. Patent No. 5,969,108) so suitable antigen-binding fragments that bind to IL-22 can be selected.

[00121] A further alternative uses random mutagenesis of the disclosed V_H or V_L sequences to generate variant V_H or V_L domains still capable of binding IL-22. A technique using error-prone PCR is described by Gram et al. (Proc. Nat. Acad. Sci. U.S.A. (1992) 89: 3576-3580).

[00122] Another method uses direct mutagenesis of the disclosed V_H or V_L sequences. Such techniques are disclosed by Barbas et al. (Proc. Nat. Acad. Sci. U.S.A. (1994) 91: 3809-3813) and Schier et al. (J. Mol. Biol. (1996) 263: 551-567).

[00123] A portion of a variable domain will comprise at least one CDR region substantially as set out herein and, optionally, intervening framework regions from the V_H or V_L domains as set out herein. The portion may include the C-terminal half of FR1 and/or the N-terminal half of FR4. Additional residues at the N-terminal or C-terminal end of the variable domain may not be the same residues found in naturally occurring antibodies. For example, construction of antibodies by

recombinant DNA techniques often introduces N- or C-terminal residues from its use of linkers. Some linkers may be used to join variable domains to other variable domains (e.g., diabodies), constant domains, or proteinaceous labels.

[00124] Although the embodiments illustrated in the Examples comprise a "matching" pair of V_H and V_L domains, a skilled artisan will recognize that alternative embodiments may comprise antigen-binding fragments containing only a single CDR from either V_L or V_H domain. Either one of the single chain specific antigen-binding domains can be used to screen for complementary domains capable of forming a two-domain specific antigen-binding fragment capable of, for example, binding to IL-22. The screening may be accomplished by phage display screening methods using the so-called hierarchical dual combinatorial approach disclosed in WO 92/01047. In this approach, an individual colony containing either a H or L chain clone is used to infect a complete library of clones encoding the other chain (L or H), and the resulting two-chain specific antigen-binding domain is selected in accordance with phage display techniques as described.

[00125] In some alternative embodiments, the anti-IL-22 antibodies can be linked to a protein (e.g., albumin) by chemical cross-linking or recombinant methods. The disclosed antibodies may also be linked to a variety of nonproteinaceous polymers (e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes) in manners set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192; or 4,179,337. The antibodies can be chemically modified by covalent conjugation to a polymer, for example, to increase their half-life in blood circulation. Exemplary polymers and attachment methods are shown in U.S. Pat. Nos. 4,766,106; 4,179,337; 4,495,285; and 4,609,546.

[00126] The disclosed antibodies can be modified to alter their glycosylation; that is, at least one carbohydrate moiety can be deleted or added to the antibody. Deletion or addition of glycosylation sites can be accomplished by changing amino acid sequence to delete or create glycosylation consensus sites, which are well known in the art. Another means of adding carbohydrate moieties is the chemical or enzymatic coupling of glycosides to amino acid residues of the antibody (see WO 87/05330 and Aplin et al. (1981) *CRC Crit. Rev. Biochem.*, 22: 259-306). Removal of carbohydrate moieties can also be accomplished chemically or enzymatically (see Hakimuddin et al. (1987) *Arch. Biochem. Biophys.*, 259: 52;

Edge et al. (1981) *Anal. Biochem.*, 118: 131; Thotakura et al. (1987) *Meth. Enzymol.*, 138: 350).

[00127] Methods for altering an antibody constant region are known in the art. Antibodies with altered function (e.g., altered affinity for an effector ligand such as FcR on a cell or the C1 component of complement) can be produced by replacing at least one amino acid residue in the constant portion of the antibody with a different residue (see e.g., EP 388,151 A1, US 5,624,821 and US 5,648,260). Similar types of alterations could be described which if applied to a murine or other species antibody would reduce or eliminate similar functions.

[00128] For example, it is possible to alter the affinity of an Fc region of an antibody (e.g., an IgG, such as a human IgG) for FcR (e.g., Fc gamma R1) or C1q. The affinity may be altered by replacing at least one specified residue with at least one residue having an appropriate functionality on its side chain, or by introducing a charged functional group, such as glutamate or aspartate, or perhaps an aromatic non-polar residue such as phenylalanine, tyrosine, tryptophan or alanine (see e.g., US 5,624,821).

[00129] For example, replacing residue 297 (asparagine) with alanine in the IgG constant region significantly inhibits recruitment of effector cells, while only slightly reducing (about three fold weaker) affinity for C1q (see e.g., US 5,624,821). The numbering of the residues in the heavy chain is that of the EU index (see Kabat et al., 1991 *supra*). This alteration destroys the glycosylation site and it is believed that the presence of carbohydrate is required for Fc receptor binding. Any other substitution at this site that destroys the glycosylation site is believed to cause a similar decrease in lytic activity. Other amino acid substitutions, e.g., changing any one of residues 318 (Glu), 320 (Lys) and 322 (Lys), to Ala, are also known to abolish C1q binding to the Fc region of IgG antibodies (see e.g., US 5,624,821).

[00130] Modified antibodies can be produced which have a reduced interaction with an Fc receptor. For example, it has been shown that in human IgG₃, which binds to the human Fc gamma R1 receptor, changing Leu 235 to Glu destroys its interaction with the receptor. Mutations on adjacent or close sites in the hinge link region of an antibody (e.g., replacing residues 234, 236 or 237 with Ala) can also be used to affect antibody affinity for the Fc gamma R1 receptor. The

numbering of the residues in the heavy chain is based in the EU index (see Kabat et al., 1991 *supra*).

[00131] Additional methods for altering the lytic activity of an antibody, for example, by altering at least one amino acid in the N-terminal region of the CH2 domain, are described in WO 94/29351 by Morgan et al. and US 5,624,821.

[00132] The antibodies of this invention may be tagged with a detectable or functional label. These labels include radiolabels (e.g., ^{131}I or ^{99}Tc), enzymatic labels (e.g., horseradish peroxidase or alkaline phosphatase), and other chemical moieties (e.g., biotin).

[00133] The invention may also feature an isolated antibody that binds to IL-22, in particular, human IL-22. In certain embodiments, the anti-IL-22 antibody may have at least one of the following characteristics: (1) it is a monoclonal or single specificity antibody; (2) it is a human antibody; (3) it is an *in vitro* generated antibody; (4) it is an *in vivo* generated antibody (e.g., transgenic mouse system); (5) it binds to IL-22 with an association constant of at least 10^{12} M^{-1} ; (6) it binds to IL-22 with an association constant of at least 10^{11} M^{-1} ; (7) it binds to IL-22 with an association constant of at least 10^{10} M^{-1} ; (8) it binds to IL-22 with an association constant of at least 10^9 M^{-1} ; (9) it binds to IL-22 with an association constant of at least 10^6 M^{-1} ; (10) it binds to IL-22 with a dissociation constant of 500 nM or less; (11) it binds to IL-22 with a dissociation constant of 10 nM or less; (12) it binds to IL-22 with a dissociation constant of 150 pM or less; (13) it binds to IL-22 with a dissociation constant of 60 pM or less; (14) it inhibits binding of IL-22 to IL-22R or a receptor complex of IL-22R and IL-10R2 with an IC_{50} of 10 nM or less; (15) it blocks IL-22 mediated proliferation of IL-22 receptor engineered BaF3 cells with an IC_{50} of 1 nM or less in one embodiment, with an IC_{50} of 150 pM or less in another embodiment, with an IC_{50} of 100 pM or less in another embodiment, and with an IC_{50} of 10 pM or less in another embodiment; and (16) it blocks IL-22 mediated GRO α secretion from HT29 with an IC_{50} of 1 nM or less in one embodiment, with an IC_{50} of 150 pM or less in another embodiment, and with an IC_{50} of 10 pM or less in another embodiment.

[00134] One of skill in the art will appreciate that the modifications described above are not all-exhaustive, and that many other modifications are obvious to a skilled artisan in light of the teachings of the present disclosure.

III. Nucleic Acids, Cloning and Expression Systems

[00135] The disclosure provides isolated nucleic acids encoding the disclosed antibodies. The nucleic acids may comprise DNA or RNA, and they may be synthetic (completely or partially) or recombinant (completely or partially). Reference to a nucleotide sequence as set out herein encompasses a DNA molecule with the specified sequence, and encompasses a RNA molecule with the specified sequence in which U is substituted for T.

[00136] Also provided are nucleic acids that comprise a coding sequence for one, two, or three CDR's, a V_H domain, a V_L domain, or combinations thereof, as disclosed herein, or a sequence substantially identical thereto (e.g., a sequence at least 85%, 90%, 95%, 96%, 97%, 98%, 99% or higher identical thereto, or which is capable of hybridizing under stringent conditions to the sequences disclosed).

[00137] In one embodiment, the isolated nucleic acids have nucleotide sequences encoding heavy chain and light chain variable regions of an anti-IL-22 antibody having at least one CDR chosen from the amino acid sequences of SEQ ID NO: 8-13, 26-31, 44-49, 62-67, 80-85, 98-103, 116-121, 134-139, 152-157, 170-175, 188-193, 206-211, 224-229, 242-247, 260-265, 278-283, 296-301, 314-319, 332-337, 350-355, 368-373, 386-391, 404-409, 422-427, 440-445, 458-463, 476-481, 494-499, 512-517, 530-535, 548-553, 566-571, 584-589, 602-607, or 620-625; or sequence encoding a CDR which differs by one or two amino acids from the sequences described herein.

[00138] The nucleic acid can encode only the light chain or the heavy chain variable region, or can also encode an antibody light or heavy chain constant region, operatively linked to the corresponding variable region. In one embodiment, the light chain variable region is linked to a constant region chosen from a kappa or a lambda constant region. The light chain constant region may also be a human kappa or lambda type. In another embodiment, the heavy chain variable region is linked to a heavy chain constant region of an antibody isotype chosen from IgG (e.g., IgG₁, IgG₂, IgG₃, IgG₄), IgM, IgA₁, IgA₂, IgD, and IgE. The heavy chain constant region may be an IgG (e.g., an IgG₁) isotype.

[00139] The nucleic acid compositions of the present invention, while often in the native sequence (of cDNA or genomic DNA or mixtures thereof) except

for modified restriction sites and the like, may be mutated in accordance with standard techniques to provide gene sequences. For coding sequences, these mutations, may affect amino acid sequence as desired. In particular, nucleotide sequences substantially identical to or derived from native V, D, J, constant, switches and other such sequences described herein are contemplated (where "derived" indicates that a sequence is identical or modified from another sequence).

[00140] In one embodiment, the nucleic acid differs (e.g., differs by substitution, insertion, or deletion) from that of the sequences provided (e.g., as follows: by at least one but less than 10, 20, 30, or 40 nucleotides; at least one but less than 1%, 5%, 10% or 20% of the nucleotides in the subject nucleic acid). If necessary for this analysis the sequences should be aligned for maximum homology. "Looped" out sequences from deletions or insertions, or mismatches, are considered differences. The difference may be at a nucleotide(s) encoding a non-essential residue(s), or the difference may be a conservative substitution(s).

[00141] The disclosure also provides nucleic acid constructs in the form of plasmids, vectors, transcription or expression cassettes, which comprise at least one nucleic acid as described herein.

[00142] The disclosure further provides a host cell that comprises at least one nucleic acid construct described herein.

[00143] Also provided are the methods of making the encoded protein(s) from the nucleic acid(s) comprising sequence described herein. The method comprises culturing host cells under appropriate conditions so they express the protein from the nucleic acid. Following expression and production, the V_H or V_L domain, or specific binding member may be isolated and/or purified using any suitable technique, then used as appropriate. The method can also include the steps of fusing a nucleic acid encoding a scFv with nucleic acids encoding a Fc portion of an antibody and expressing the fused nucleic acid in a cell. The method can also include a step of germlining.

[00144] Antigen-binding fragments, V_H and/or V_L domains, and encoding nucleic acid molecules and vectors may be isolated and/or purified from their natural environment, in substantially pure or homogenous form, or, in the case of

nucleic acid, free or substantially free of nucleic acid or genes of origin other than the sequence encoding a polypeptide with the require function.

[00145] Systems for cloning and expressing polypeptides in a variety of host cells are known in the art. Cells suitable for producing antibodies are described in, for example, Fernandez et al. (1999) *Gene Expression Systems*, Academic Press, eds. In brief, suitable host cells include mammalian cells, insect cells, plant cells, yeast cells, or prokaryotic cells, e.g., *E. coli*. Mammalian cells available in the art for heterologous polypeptide expression include lymphocytic cell lines (e.g., NSO), HEK293 cells, Chinese hamster ovary (CHO) cells, COS cells, HeLa cells, baby hamster kidney cells, oocyte cells, and cells from a transgenic animal, e.g., mammary epithelial cell. In one embodiment, the GIL01, GIL16, GIL45, GIL60, GIL68, GIL92, 097D09, 062A09, 062G05, 087B03, 367D04, 368D04, 166B06, 166G05, 375G06, 376B10, 354A08, 355B06, 355E04, and 356A11 antibodies are expressed in HEK293 or CHO cells. In another embodiment, a selection of antibodies chosen from 365A11, 354A08, 087B03, and 368D04 are expressed in HEK293 or CHO cells. In other embodiments, the nucleic acids encoding the antibodies of the invention are placed under the control of a tissue-specific promoter (e.g., a mammary specific promoter) and the antibodies are produced in transgenic animals. For example, the antibodies are secreted into the milk of the transgenic animal, such as a transgenic cow, pig, horse, sheep, goat or rodent.

[00146] Suitable vectors may be chosen or constructed to contain appropriate regulatory sequences, including promoter sequences, terminator sequences, polyadenylation sequences, enhancer sequences, marker genes, and other sequences. The vectors may also contain a plasmid or viral backbone. For details, see Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor Laboratory Press (1989). Many established techniques used with vectors, including the manipulation, preparation, mutagenesis, sequencing, and transfection of DNA, are described in *Current Protocols in Molecular Biology*, Second Edition, Ausubel et al. eds., John Wiley & Sons (1992).

[00147] A further aspect of the disclosure provides a method of introducing the nucleic acid into a host cell. For eukaryotic cells, suitable transfection techniques may include calcium phosphate, DEAE-Dextran,

electroporation, liposome-mediated transfection, and transduction using retrovirus or other viruses, e.g., vaccinia or baculovirus. For bacterial cells, suitable techniques may include calcium chloride transformation, electroporation, and transfection using bacteriophage. DNA introduction may be followed by a selection method (e.g., drug resistance) to select cells that contain the nucleic acid.

IV. Uses of Anti-IL-22 Antibodies

[00148] Anti-IL-22 antibodies that act as antagonists to IL-22 can be used to regulate at least one IL-22-mediated immune response, such as acting on epithelial cells in solid tissue and indirectly modulating downstream immune responses, such as blocking expansion of T cell subsets, including, for example, T_H17 T cells.. In one embodiment, antibodies of the invention are used in a method for regulating an immune response, the method comprising contacting IL-22 with an antibody of the invention thereby regulating the immune response. In one embodiment, the immune response comprises cell proliferation, cytolytic activity, cytokine secretion, or chemokine secretion.

[00149] Accordingly, the antibodies of the invention can be used to directly or indirectly inhibit the activity (e.g., proliferation, differentiation, and/or survival) of an immune or hematopoietic cell (e.g., a cell of myeloid, lymphoid, or erythroid lineage, or precursor cells thereof), and, thus, can be used to treat a variety of immune disorders and hyperproliferative disorders. Non-limiting examples of immune disorders that can be treated include, but are not limited to, autoimmune disorders, e.g., arthritis (including rheumatoid arthritis, juvenile rheumatoid arthritis, osteoarthritis, psoriatic arthritis, lupus-associated arthritis or ankylosing spondylitis), scleroderma, systemic lupus erythematosus, HIV, Sjogren's syndrome, vasculitis, multiple sclerosis, autoimmune thyroiditis, dermatitis (including atopic dermatitis and eczematous dermatitis), myasthenia gravis, inflammatory bowel disease (IBD), Crohn's disease, colitis, diabetes mellitus (type I); inflammatory conditions of, e.g., the skin (e.g., psoriasis), cardiovascular system (e.g., atherosclerosis), nervous system (e.g., Alzheimer's disease), liver (e.g., hepatitis), kidney (e.g., nephritis) and pancreas (e.g., pancreatitis); cardiovascular disorders, e.g., cholesterol metabolic disorders, oxygen free radical injury, ischemia; disorders associated with wound healing; respiratory disorders, e.g., asthma and COPD (e.g., cystic fibrosis); acute inflammatory conditions (e.g.,

endotoxemia, sepsis and septicaemia, toxic shock syndrome and infectious disease); transplant rejection and allergy. In one embodiment, the IL-22-associated disorder is, an arthritic disorder, e.g., a disorder chosen from one or more of rheumatoid arthritis, juvenile rheumatoid arthritis, osteoarthritis, psoriatic arthritis, or ankylosing spondylitis; a respiratory disorder (e.g., asthma, chronic obstructive pulmonary disease (COPD); or an inflammatory condition of, e.g., the skin (e.g., psoriasis), cardiovascular system (e.g., atherosclerosis), nervous system (e.g., Alzheimer's disease), liver (e.g., hepatitis), kidney (e.g., nephritis), pancreas (e.g., pancreatitis), and gastrointestinal organs, e.g., colitis, Crohn's disease and IBD; acute inflammatory conditions, e.g., endotoxemia, sepsis and septicaemia, toxic shock syndrome and infectious disease; multiple organ failure; respiratory disease (ARD); amyloidosis; nephropathies such as glomerulosclerosis, membranous neuropathy, renal arteriosclerosis, glomerulonephritis, fibroproliferative diseases of the kidney, as well as other kidney disfunctions and renal tumors. Because of IL-22's effects on epithelia, anti-IL-22 antibodies can be used to treat epithelial cancers, e.g., carcinoma, melanoma and others. For a description of a rationale for IL-22 inhibition in these and other disease states see WO 03/083062 (pages 58-75).

[00150] Multiple sclerosis is a central nervous system disease that is characterized by inflammation and loss of myelin sheaths—the fatty material that insulates nerves and is needed for proper nerve function. Inflammation that results from an immune response that is dependent on IL-22 can be treated with the antibodies and compositions of this invention. In the experimental autoimmune encephalitis (EAE) mouse model for multiple sclerosis (Tuohy et al. (J. Immunol. (1988) 141: 1126-1130), Sobel et al. (J. Immunol. (1984) 132: 2393-2401), and Traugott (Cell Immunol. (1989) 119: 114-129), treatment of mice with GIL01, GIL16, GIL45, GIL60, GIL68, GIL92, 097D09, 062A09, 062G05, 087B03, 367D04, 368D04, 166B06, 166G05, 375G06, 376B10, 354A08, 355B06, 355E04, or 356A11 injections prior (and continuously) to EAE induction may profoundly delay the onset of the disease. This can serve as a model for confirming use of the antibody of the invention. The antibodies of this invention may similarly be used to treat multiple sclerosis in humans.

[00151] Arthritis is a disease characterized by inflammation in the joints. Rheumatoid Arthritis (RA) is the most frequent form of arthritis, involving inflammation of connective tissue and the synovial membrane, a membrane that lines the joint. The inflamed synovial membrane often infiltrates the joint and damages joint cartilage and bone. IL-22 and IL-22R protein and/or transcript is associated with both human diseases. In RA synovial biopsies, IL-22 protein is detected in vimentin⁺ synovial fibroblasts and some CD68⁺ macrophages while IL-22R is detected in synovial fibroblasts. Treatment of synovial fibroblasts with IL-22 induces the production of monocyte chemoattractant protein-1, MCP-1, as well as general metabolic activity (Ikeuchi, H., et al. (2005) *Arthritis Rheum.* 52:1037-46). Inhibitors of IL-22 ameliorate symptoms of rheumatoid arthritis (WO 2005/000897 A2; U.S. Patent No. 6,939,545). Increased secretion of inflammatory cytokines and chemokines, and more importantly, increased disease resulting from immune responses that are dependent on IL-22 may be treated with the antibodies of this invention. Similarly, the antibodies and compositions of this invention may be used to treat RA or other arthritic diseases in humans.

[00152] Transplant rejection is the immunological phenomenon where tissues from a donor are specifically "attacked" by immune cells of the host. The principle "attacking" cells are T cells, whose T cell receptors recognize the donor's MHC molecules as "foreign." This recognition activates the T cells, which proliferate and secrete a variety of cytokines and cytolytic proteins that ultimately destroy the transplant. MLR and transplantation models have been described by *Current Protocols in Immunology*, Second Edition, Coligan et al. eds., John Wiley & Sons, 1994; Kasaian et al. (*Immunity* (2002) 16: 559-569); Fulmer et al. (*Am. J. Anat.* (1963) 113: 273-285), and Lenschow et al. (*Science* (1992) 257: 789-792). The antibodies and compositions of this invention may be used to reduce the MLR and treat transplant rejection and related diseases (e.g., graft versus host disease) in humans that are dependent on IL-22.

[00153] The antibodies of this invention can also be used to treat hyperproliferative disorders associated with aberrant activity of IL-22-responsive cells and IL-22R/IL-10R2-responsive cells by administering the antibodies in an amount sufficient to inhibit or reduce hyperproliferation of IL-22 and/or IL-22R and/or IL-10R2-responsive cells in a subject and allowing the antibodies to treat or

prevent the disorder. IL-22 and IL-22R expression is constitutive on epithelial cells in a number of tissues including, but not limited to, pancreas, lung, skin, gut, liver, kidney (Kotenko, S.V. et al. (2001) *J. Biol. Chem.* 276:2725-32; Xie, M.H. et al. (2000) *J. Biol. Chem.* 275:31335-9; Wolk, K. et al. (2004) *Immunity* 21:241-54). In addition, IL-22 receptor complex is also expressed on the surface of fibroblasts from the diseased joint and normal gut (Ikeuchi, H. et al. (2005) *Arthritis Rheum.* 52:1037-46; Andoh, A. et al. (2005) *Gastroenterology* 129:969-84). Neoplastic derivatives of these cell types may be hyper responsive to IL-22, modulating these cells ability to survive in the organism. Hence antibodies to IL-22 may be used to inhibit the progression of such neoplasms, e.g. squamous cell carcinomas, basal cell carcinomas, transitional cell papillomas and carcinomas, adenomas, adenocarcinoma, linitis plastica, insulinoma, glucagonoma, gastrinoma, vipoma, cholangiocarcinoma, hepatocellular carcinoma, adenoid cystic carcinoma, carcinoid tumor of appendix, prolactinoma, oncocytoma, hurthle cell adenoma, renal cell carcinoma, Grawitz tumor, multiple endocrine adenomas, endometroid adenoma, adnexal and skin appendage neoplasms, mucoepidermoid neoplasms, cystic, mucinous and serous neoplasms, cystadenoma, pseudomyxoma peritonei, ductal, lobular and medullary neoplasms, acinar cell neoplasms, complex epithelial neoplasms, Warthin's tumor, thymoma, specialized gonadal neoplasms, sex cord-stromal tumor, thecoma, granulosa cell tumor, arrhenoblastoma, sertoli-leydig cell tumor, paraganglioma, pheochromocytoma, glomus tumor, melanocytic nevus, malignant melanoma, melanoma, nodular melanoma, dysplastic nevus, lentigo maligna, superficial spreading melanoma, or acral lentiginous melanoma. While the IL-22 receptor is not detected on *ex vivo* naïve or activated immune cells, dysregulation of the receptor might make such derivative neoplastic cells responsive to IL-22 and thus inhibition by an antibody to IL-22.

[00154] In another aspect, the invention features a method of decreasing, inhibiting or reducing an acute phase response in a subject. The method includes administering to the subject an anti-IL-22 antibody or fragment thereof as described herein, in an amount sufficient to decrease, inhibit or reduce the acute phase response in the subject. In one embodiment, the subject is a mammal, e.g., a human suffering from an IL-22-associated disorder as described herein, including, e.g., respiratory disorders, inflammatory disorders and

autoimmune disorders. In one embodiment, the IL-22 binding agent is administered locally, e.g., topically, subcutaneously, or other administrations that are not in the general circulation.

[00155] IL-22 is believed to exert its inflammatory effects locally, e.g. by acting (e.g., directly acting) as a modular or a regulator of tissue inflammation as opposed to direct systemic effects. Accordingly, inhibition of IL-22 activity using, e.g. an anti-IL-22 antibody of the present invention may provide a more effective (e.g., less toxic) tissue-specific, anti-inflammatory agent than systemic anti-inflammatory modalities. Furthermore, inhibition of local IL-22 using, e.g., an anti-IL-22 antibody or fragment thereof described herein, may provide a useful candidate for combination with systemic anti-inflammatory modalities.

V. Combination Therapy

[00156] In one embodiment, a pharmaceutical composition comprising at least one anti-IL-22 antibody and at least one therapeutic agent is administered in combination therapy. The therapy is useful for treating pathological conditions or disorders, such as immune and inflammatory disorders. The term "in combination" in this context means that the antibody composition and the therapeutic agent are given substantially contemporaneously, either simultaneously or sequentially. In one embodiment, if given sequentially, at the onset of administration of the second compound, the first of the two compounds is still detectable at effective concentrations at the site of treatment. In another embodiment, if given sequentially, at the onset of administration of the second compound, the first of the two compounds is not detectable at effective concentrations at the site of treatment.

[00157] For example, the combination therapy can include at least one anti-IL-22 antibody co-formulated with, and/or co-administered with, at least one additional therapeutic agent. The additional agents may include at least one cytokine inhibitor, growth factor inhibitor, immunosuppressant, anti-inflammatory agent, metabolic inhibitor, enzyme inhibitor, cytotoxic agent, and cytostatic agent, as described in more detail below. In one embodiment, the additional agent is a standard treatment for arthritis, including, but not limited to, non-steroidal anti-inflammatory agents (NSAIDs); corticosteroids, including prednisolone, prednisone, cortisone, and triamcinolone; and disease modifying anti-rheumatic drugs

(DMARDs), such as methotrexate, hydroxychloroquine (Plaquenil) and sulfasalazine, leflunomide (Arava), tumor necrosis factor inhibitors, including etanercept (Enbrel), infliximab (Remicade) (with or without methotrexate), and adalimumab (Humira), anti-CD20 antibody (e.g., Rituxan), soluble interleukin-1 receptor, such as anakinra (Kineret), gold, minocycline (Minocin), penicillamine, and cytotoxic agents, including azathioprine, cyclophosphamide, and cyclosporine. Such combination therapies may advantageously utilize lower dosages of the administered therapeutic agents, thus avoiding possible toxicities or complications associated with the various monotherapies. Moreover, the additional therapeutic agents disclosed herein act on pathways in addition to or that differ from the IL-22/IL-22R/IL-10R2 pathway, and thus are expected to enhance and/or synergize with the effects of the anti-IL-22 antibodies.

[00158] Therapeutic agents used in combination with anti-IL-22 antibodies may be those agents that interfere at different stages in the autoimmune and subsequent inflammatory response. In one embodiment, at least one anti-IL-22 antibody described herein may be co-formulated with, and/or co-administered with, at least one cytokine and/or growth factor antagonist. The antagonists may include soluble receptors, peptide inhibitors, small molecules, ligand fusions, antibodies and binding fragments thereof (that bind cytokines or growth factors or their receptors or other cell surface molecules), and "anti-inflammatory cytokines" and agonists thereof.

[00159] Non-limiting examples of the agents that can be used in combination with the anti-IL-22 antibodies described herein, include, but are not limited to, antagonists of at least one interleukin (e.g., IL-1, IL-2, IL-6, IL-7, IL-8, IL-12 (or one of its subunits p35 or p40), IL-13, IL-15, IL-16, IL-17A-F (including heterodimers thereof, for example, IL-17A/IL-17F heterodimer), IL-18, IL-19, IL-20, IL-21, and IL-23 (or one of its subunits p19 or p40)); cytokine (e.g., TNF α , LT, EMAP-II, and GM-CSF); and growth factor (e.g., FGF and PDGF). The agents may also include, but not limited to, antagonists of at least one receptor for an interleukin, cytokine, and growth factor. Anti-IL-22 antibodies can also be combined with inhibitors (e.g., antibodies or binding fragments thereof) to cell surface molecules such as CD2, CD3, CD4, CD8, CD20 (e.g. Rituxan), CD25, CD28, CD30, CD40, CD45, CD69, CD80 (B7.1), CD86 (B7.2), CD90, or their

ligands (e.g., CD154 (gp39, CD40L)), or LFA-1/ICAM-1 and VLA-4/VCAM-1 (Yusuf-Makagiansar et al. (2002) *Med Res Rev* 22(2):146-67)). In certain embodiments, antagonists that can be used in combination with anti-IL-22 antibodies described herein may include antagonists of IL-1, IL-12 (or one of its subunits p35 or p40), TNF α , IL-15, IL-17A-F (including heterodimers thereof, for example, IL-17A/IL-17F heterodimer), IL-18, IL-19, IL-20, IL-21, and IL-23 (or one of its subunits p19 or p40), and their receptors.

[00160] Examples of those agents include IL-12 antagonists (such as antibodies that bind IL-12 (see e.g., WO 00/56772) or one of its subunits p35 or p40); IL-12 receptor inhibitors (such as antibodies to the IL-12 receptor); and soluble IL-12 receptor and fragments thereof. Examples of IL-15 antagonists include antibodies against IL-15 or its receptor, soluble fragments of the IL-15 receptor, and IL-15-binding proteins. Examples of IL-18 antagonists include antibodies to IL-18, soluble fragments of the IL-18 receptor, and IL-18 binding proteins (IL-18BP, Mallet et al. (2001) *Circ. Res.* 28). Examples of IL-1 antagonists include Interleukin-1-Converting Enzyme (ICE) inhibitors (such as Vx740), IL-1 antagonists (e.g., IL-1RA (ANIKINRA, AMGEN)), sIL-1RII (Immunex), and anti-IL-1 receptor antibodies.

[00161] In one embodiment, the combination therapy includes at least one anti-IL-22 antibody co-formulated with, and/or co-administered with an antagonist, such as an antibody or antigen binding fragment thereof or a soluble receptor, of at least one of IL-17A, IL-17F, IL-17A/IL-17F heterodimer, or IL-23 (or one of its subunits p19 or p40).

[00162] Examples of TNF antagonists include antibodies to TNF (e.g., human TNF α), such as D2E7 (human anti-TNF α antibody, U.S. 6,258,562, HumiraTM, BASF); CDP-571/CDP-870/BAY-10-3356 (humanized anti-TNF α antibodies, Celltech/Pharmacia); cA2 (chimeric anti-TNF α antibody, RemicadeTM, Centocor); and anti-TNF antibody fragments (e.g., CPD870). Other examples include soluble TNF receptor (e.g., human p55 or p75) fragments and derivatives, such as p55 kdTNFR-IgG (55 kd TNF receptor-IgG fusion protein, LenerceptTM) and 75 kdTNFR-IgG (75 kd TNF receptor-IgG fusion protein, EnbrelTM, Immunex, see, e.g., *Arthritis & Rheumatism* (1994) Vol. 37, S295; *J. Invest. Med.* (1996) Vol. 44, 235A). Further examples include enzyme antagonists (e.g., TNF α converting

enzyme inhibitors (TACE) such as alpha-sulfonyl hydroxamic acid derivative (WO 01/55112) or N-hydroxyformamide inhibitor (GW 3333, -005, or -022)) and TNF-bp/s-TNFR (soluble TNF binding protein, see e.g., *Arthritis & Rheumatism* (1996) Vol. 39, No. 9 (supplement), S284; and *Am. J. Physiol. Heart Circ. Physiol.* (1995) Vol. 268, pp. 37-42). TNF antagonists may be soluble TNF receptor (e.g., human p55 or p75) fragments and derivatives, such as 75 kDTNFR-IgG; and TNF α converting enzyme (TACE) inhibitors.

[00163] In other embodiments, the anti-IL-22 antibodies described herein can be administered in combination with at least one of the following: IL-13 antagonists, such as soluble IL-13 receptors and/or anti-IL-13 antibodies; and IL-2 antagonists, such as IL-2 fusion proteins (e.g., DAB 486-IL-2 and/or DAB 389-IL-2, Seragen, see e.g., *Arthritis & Rheumatism* (1993) Vol. 36, 1223) and anti-IL-2R antibodies (e.g., anti-Tac (humanized antibody, Protein Design Labs, see *Cancer Res.* 1990 Mar 1;50(5):1495-502)). Another combination includes anti-IL-22 antibodies in combination with non-depleting anti-CD4 inhibitors such as IDEC-CE9.1/SB 210396 (anti-CD4 antibody, IDEC/SmithKline). Yet other combinations include anti-IL-22 antibodies with antagonists (such as antibodies, soluble receptors, or antagonistic ligands) of costimulatory molecules, such as CD80 (B7.1) and CD86 (B7.2); ICOSL, ICOS, CD28, and CTLA4 (e.g., CTLA4-Ig); P-selectin glycoprotein ligand (PSGL); and anti-inflammatory cytokines and agonists thereof (e.g., antibodies). The anti-inflammatory cytokines may include IL-4 (DNAX/Schering); IL-10 (SCH 52000, recombinant IL-10, DNAX/Schering); IL-13; and TGF.

[00164] In other embodiments, at least one anti-IL-22 antibody can be co-formulated with, and/or co-administered with, at least one anti-inflammatory drug, immunosuppressant, metabolic inhibitor, and enzymatic inhibitor. Non-limiting examples of the drugs or inhibitors that can be used in combination with the IL-22 antagonists described herein, include, but are not limited to, at least one of: non-steroidal anti-inflammatory drug (NSAID) (such as ibuprofen, Tenidap (see e.g., *Arthritis & Rheumatism* (1996) Vol. 39, No. 9 (supplement), S280)), Naproxen (see e.g., *Neuro Report* (1996) Vol. 7, pp. 1209-1213), Meloxicam, Piroxicam, Diclofenac, and Indomethacin); Sulfasalazine (see e.g., *Arthritis & Rheumatism* (1996) Vol. 39, No. 9 (supplement), S281); corticosteroid (such as prednisolone);

cytokine suppressive anti-inflammatory drug (CSAID); and an inhibitor of nucleotide biosynthesis (such as an inhibitor of purine biosynthesis (e.g., folate antagonist such as methotrexate) and an inhibitor of pyrimidine biosynthesis (e.g., a dihydroorotate dehydrogenase (DHODH) inhibitor such as leflunomide (see e.g., *Arthritis & Rheumatism* (1996) Vol. 39, No. 9 (supplement), S131; *Inflammation Research* (1996) Vol. 45, pp. 103-107)). Therapeutic agents for use in combination with IL-22/IL-22R or IL-22/IL-10R2 antagonists may include NSAIDs, CSAIDs, DHODH inhibitors (such as leflunomide), and folate antagonists (such as methotrexate).

[00165] Examples of additional inhibitors include at least one of: corticosteroid (oral, inhaled and local injection); immunosuppressant (such as cyclosporin and tacrolimus (FK-506)); a mTOR inhibitor (such as sirolimus (rapamycin) or a rapamycin derivative (e.g., ester rapamycin derivative such as CCI-779 (Elit. L. (2002) *Current Opinion Investig. Drugs* 3(8):1249-53; Huang, S. et al. (2002) *Current Opinion Investig. Drugs* 3(2):295-304))); an agent which interferes with the signaling of proinflammatory cytokines such as TNF α and IL-1 (e.g., IRAK, NIK, IKK, p38 or a MAP kinase inhibitor); a COX2 inhibitor (e.g., celecoxib and variants thereof (MK-966), see e.g., *Arthritis & Rheumatism* (1996) Vol. 39, No. 9 (supplement), S81); a phosphodiesterase inhibitor (such as R973401, see e.g., *Arthritis & Rheumatism* (1996) Vol. 39, No. 9 (supplement), S282)); a phospholipase inhibitor (e.g., an inhibitor of cytosolic phospholipase 2 (cPLA2) such as trifluoromethyl ketone analogs (U.S. 6,350,892)); an inhibitor of vascular endothelial cell growth factor (VEGF); an inhibitor of the VEGF receptor; and an inhibitor of angiogenesis. Therapeutic agents for use in combination with anti-IL-22 antibodies may include immunosuppressants (such as cyclosporine and tacrolimus (FK-506)); and mTOR inhibitors (such as sirolimus (rapamycin) or rapamycin derivatives (e.g., ester rapamycin derivatives such as CCI-779)); COX2 inhibitors (such as celecoxib and variants thereof); and phospholipase inhibitors (such as inhibitors of cytosolic phospholipase 2 (cPLA2) (e.g., trifluoromethyl ketone analogs)).

[00166] Examples of therapeutic agents that can be co-administered and/or co-formulated with at least one anti-IL-22 antibody, include, but are not limited to, at least one of: TNF antagonists (such as anti-TNF antibodies); soluble

fragments of TNF receptors (e.g., human p55 and p75) and derivatives thereof (such as p55 kDTNFR-IgG (55 kD TNF receptor-IgG fusion protein, Lenercept™) and 75 kDTNFR-IgG (75 kD TNF receptor-IgG fusion protein, Enbrel™)); TNF enzyme antagonists (such as TACE inhibitors); antagonists of IL-12 (or one of its subunits p35 or p40), IL-15, IL-17A-F (including heterodimers thereof, for example, IL-17A/IL-17F heterodimer), IL-18, IL-19, IL-20, IL-21, IL-22, and IL-23 (or one of its subunits p19 or p40); T cell and B cell depleting agents (such as anti-CD4 or anti-CD22 antibodies); small molecule inhibitors (such as methotrexate and leflunomide); sirolimus (rapamycin) and analogs thereof (such as CCI-779); Cox-2 and cPLA2 inhibitors; p38, TPL-2, Mk-2 and NFκB inhibitors; RAGE and soluble RAGE; P-selectin and PSGL-1 inhibitors (such as antibodies to and small molecule inhibitors); and estrogen receptor beta (ERB) agonists, and ERB-NFκB antagonists. Therapeutic agents that can be co-administered and/or co-formulated with at least one anti-IL-22 antibody may include at least one of: a soluble fragment of a TNF receptor (e.g., human p55 or p75) such as 75 kDTNFR-IgG (75 kD TNF receptor-IgG fusion protein, Enbrel™); methotrexate; leflunomide; and sirolimus (rapamycin) and analogs thereof (such as CCI-779).

[00167] The anti-IL-22 antibodies disclosed herein can be used in combination with other therapeutic agents to treat specific immune disorders as discussed in further detail below.

[00168] Non-limiting examples of agents for treating arthritic disorders (e.g., rheumatoid arthritis, inflammatory arthritis, rheumatoid arthritis, juvenile rheumatoid arthritis, osteoarthritis and psoriatic arthritis), with which an anti-IL-22 antibody can be combined include at least one of the following: TNF antagonists (such as anti-TNF antibodies); soluble fragments of TNF receptors (e.g., human p55 and p75) and derivatives thereof (such as p55 kDTNFR-IgG (55 kD TNF receptor-IgG fusion protein, Lenercept™) and 75 kDTNFR-IgG (75 kD TNF receptor-IgG fusion protein, Enbrel™)); TNF enzyme antagonists (such as TACE inhibitors); antagonists of IL-12 (or one of its subunits p35 or p40), IL-15, IL-17A-F (including heterodimers thereof, for example, IL-17A/IL-17F heterodimer), IL-18, IL-19, IL-20, IL-21, IL-22, IL-23 (or one of its subunits p19 or p40), and IL-24; T cell and B cell depleting agents (such as anti-CD4, anti-CD20, or anti-CD22 antibodies); small molecule inhibitors (such as methotrexate and leflunomide);

sirolimus (rapamycin) and analogs thereof (e.g., CCI-779); Cox-2 and cPLA2 inhibitors; NSAIDs; p38, TPL-2, Mk-2, and NFκB inhibitors; RAGE or soluble RAGE; P-selectin or PSGL-1 inhibitors (such as small molecule inhibitors and antibodies to); estrogen receptor beta (ERB) agonists, and ERB-NFκB antagonists. Therapeutic agents that can be co-administered and/or co-formulated with at least one IL-22/IL-22R/IL-10R2 antagonist may include at least one of: a soluble fragment of a TNF receptor (e.g., human p55 or p75) such as 75 kDTNFR-IgG (75 kD TNF receptor-IgG fusion protein, Enbrel™); methotrexate; leflunomide; and sirolimus (rapamycin) or an analog thereof (e.g., CCI-779).

[00169] Non-limiting examples of agents for treating multiple sclerosis with which anti-IL-22 antibody can be combined include interferon-β for example, IFNβ-1a and IFNβ-1b), copaxone, corticosteroids, IL-1 inhibitors, TNF inhibitors, antibodies to CD40 ligand, antibodies to CD80, and IL-12 antagonists, including antibodies that bind IL-12 (or one of its subunits p35 or p40).

[00170] Non-limiting examples of agents for treating inflammatory bowel disease or Crohn's disease with which an anti-IL-22 antibody can be combined include budenoside; epidermal growth factor; corticosteroids; cyclosporine; sulfasalazine; aminosalicylates; 6-mercaptopurine; azathioprine; metronidazole; lipoxigenase inhibitors; mesalamine; olsalazine; balsalazide; antioxidants; thromboxane inhibitors; IL-1 receptor antagonists; anti-IL-1 monoclonal antibodies; anti-IL-6 monoclonal antibodies; growth factors; elastase inhibitors; pyridinyl-imidazole compounds; TNF antagonists as described herein; IL-4, IL-10, IL-13, and/or TGFβ or agonists thereof (e.g., agonist antibodies); IL-11; glucuronide- or dextran-conjugated prodrugs of prednisolone, dexamethasone or budesonide; ICAM-1 antisense phosphorothioate oligodeoxynucleotides (ISIS 2302; Isis Pharmaceuticals, Inc.); soluble complement receptor 1 (TP10; T Cell Sciences, Inc.); slow-release mesalazine; methotrexate; antagonists of Platelet Activating Factor (PAF); ciprofloxacin; and lignocaine.

[00171] In other embodiments, an anti-IL-22 antibody can be used in combination with at least one antibody directed at other targets involved in regulating immune responses, e.g., transplant rejection or graft versus host disease. Non-limiting examples of agents for treating immune responses with which an IL-22/IL-22R/IL10R2 antagonist of the invention can be combined include

the following: antibodies against cell surface molecules, including but not limited to CD25 (IL-2 receptor α), CD11a (LFA-1), CD54 (ICAM-1), CD4, CD45, CD28/CTLA4, CD80 (B7-1), CD86 (B7-2), or combinations thereof. In another embodiment, an anti-IL-22 antibody is used in combination with at least one general immunosuppressive agent, such as cyclosporin A or FK506.

[00172] Another aspect of the present invention accordingly relates to kits for carrying out the combined administration of the anti-IL-22 antibodies with other therapeutic agents. In one embodiment, the kit comprises at least one anti-IL-22 antibody formulated in a pharmaceutical carrier, and at least one therapeutic agent, formulated as appropriate in one or more separate pharmaceutical preparations.

VI. Diagnostic Uses

[00173] The antibodies may also be used to detect the presence of IL-22 in biological samples. By correlating the presence or level of these proteins with a medical condition, one of skill in the art can diagnose the associated medical condition. For example, IL-22 induces changes associated with those caused by inflammatory cytokines (such as IL-1 and TNF α), and inhibitors of IL-22 ameliorate symptoms of rheumatoid arthritis (WO 2005/000897 A2). Illustrative medical conditions that may be diagnosed by the antibodies of this invention include multiple sclerosis, rheumatoid arthritis, psoriasis, inflammatory bowel disease, pancreatitis, and transplant rejection.

[00174] Antibody-based detection methods are well known in the art, and include ELISA, radioimmunoassays, immunoblots, Western blots, flow cytometry, immunofluorescence, immunoprecipitation, and other related techniques. The antibodies may be provided in a diagnostic kit that incorporates at least one of these procedures to detect IL-22. The kit may contain other components, packaging, instructions, or other material to aid the detection of the protein and use of the kit.

[00175] Antibodies may be modified with detectable markers, including ligand groups (e.g., biotin), fluorophores and chromophores, radioisotopes, electron-dense reagents, or enzymes. Enzymes are detected by their activity. For example, horseradish peroxidase is detected by its ability to convert tetramethylbenzidine (TMB) to a blue pigment, quantifiable with a

spectrophotometer. Other suitable binding partners include biotin and avidin, IgG and protein A, and other receptor-ligand pairs known in the art.

[00176] Antibodies can also be functionally linked (e.g., by chemical coupling, genetic fusion, non-covalent association or otherwise) to at least one other molecular entity, such as another antibody (e.g., a bispecific or a multispecific antibody), toxins, radioisotopes, cytotoxic or cytostatic agents, among others. Other permutations and possibilities are apparent to those of ordinary skill in the art, and they are considered equivalents within the scope of this invention.

VII. Pharmaceutical Compositions and Methods of Administration

[00177] Certain embodiments of the invention include compositions comprising the disclosed antibodies. The compositions may be suitable for pharmaceutical use and administration to patients. The compositions comprise an antibody of the present invention and a pharmaceutical excipient. As used herein, "pharmaceutical excipient" includes solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, etc., that are compatible with pharmaceutical administration. Use of these agents for pharmaceutically active substances is well known in the art. The compositions may also contain other active compounds providing supplemental, additional, or enhanced therapeutic functions. The pharmaceutical compositions may also be included in a container, pack, or dispenser together with instructions for administration.

[00178] A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Methods to accomplish the administration are known to those of ordinary skill in the art. Pharmaceutical compositions may be topically or orally administered, or capable of transmission across mucous membranes. Examples of administration of a pharmaceutical composition include oral ingestion or inhalation. Administration may also be intravenous, intraperitoneal, intramuscular, intracavity, subcutaneous, cutaneous, or transdermal.

[00179] Solutions or suspensions used for intradermal or subcutaneous application typically include at least one of the following components: a sterile diluent such as water, saline solution, fixed oils, polyethylene glycol, glycerine, propylene glycol, or other synthetic solvent; antibacterial agents such as benzyl

alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid (EDTA); buffers such as acetate, citrate, or phosphate; and tonicity agents such as sodium chloride or dextrose. The pH can be adjusted with acids or bases. Such preparations may be enclosed in ampoules, disposable syringes, or multiple dose vials.

[00180] Solutions or suspensions used for intravenous administration include a carrier such as physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, NJ), ethanol, or polyol. In all cases, the composition must be sterile and fluid for easy syringability. Proper fluidity can often be obtained using lecithin or surfactants. The composition must also be stable under the conditions of manufacture and storage. Prevention of microorganisms can be achieved with antibacterial and antifungal agents, e.g., parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, etc. In many cases, isotonic agents (sugar), polyalcohols (mannitol and sorbitol), or sodium chloride may be included in the composition. Prolonged absorption of the composition can be accomplished by adding an agent which delays absorption, e.g., aluminum monostearate and gelatin.

[00181] Oral compositions include an inert diluent or edible carrier. The composition can be enclosed in gelatin or compressed into tablets. For the purpose of oral administration, the antibodies can be incorporated with excipients and placed in tablets, troches, or capsules. Pharmaceutically compatible binding agents or adjuvant materials can be included in the composition. The tablets, troches, and capsules, may contain (1) a binder such as microcrystalline cellulose, gum tragacanth or gelatin; (2) an excipient such as starch or lactose, (3) a disintegrating agent such as alginic acid, Primogel, or corn starch; (4) a lubricant such as magnesium stearate; (5) a glidant such as colloidal silicon dioxide; or (6) a sweetening agent or a flavoring agent.

[00182] The composition may also be administered by a transmucosal or transdermal route. For example, antibodies that comprise a Fc portion may be capable of crossing mucous membranes in the intestine, mouth, or lungs (via Fc receptors). Transmucosal administration can be accomplished through the use of lozenges, nasal sprays, inhalers, or suppositories. Transdermal administration can also be accomplished through the use of a composition containing ointments,

salves, gels, or creams known in the art. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used. For administration by inhalation, the antibodies are delivered in an aerosol spray from a pressured container or dispenser, which contains a propellant (e.g., liquid or gas) or a nebulizer.

[00183] In certain embodiments, the antibodies of this invention are prepared with carriers to protect the antibodies against rapid elimination from the body. Biodegradable polymers (e.g., ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, polylactic acid) are often used. Methods for the preparation of such formulations are known by those skilled in the art. Liposomal suspensions can be used as pharmaceutically acceptable carriers too. The liposomes can be prepared according to established methods known in the art (U.S. Patent No. 4,522,811).

[00184] The antibodies or antibody compositions of the invention are administered in therapeutically effective amounts as described. Therapeutically effective amounts may vary with the subject's age, condition, sex, and severity of medical condition. Appropriate dosage may be determined by a physician based on clinical indications. The antibodies or compositions may be given as a bolus dose to maximize the circulating levels of antibodies for the greatest length of time. Continuous infusion may also be used after the bolus dose.

[00185] As used herein, the term "subject" is intended to include human and non-human animals. Subjects may include a human patient having a disorder characterized by cells that express IL-22, e.g., a cancer cell or an immune cell. The term "non-human animals" of the invention includes all vertebrates, such as non-human primates, sheep, dogs, cows, chickens, amphibians, reptiles, etc.

[00186] Examples of dosage ranges that can be administered to a subject can be chosen from: 1 μ g/kg to 20 mg/kg, 1 μ g/kg to 10 mg/kg, 1 μ g/kg to 1 mg/kg, 10 μ g/kg to 1 mg/kg, 10 μ g/kg to 100 μ g/kg, 100 μ g/kg to 1 mg/kg, 250 μ g/kg to 2 mg/kg, 250 μ g/kg to 1 mg/kg, 500 μ g/kg to 2 mg/kg, 500 μ g/kg to 1 mg/kg, 1 mg/kg to 2 mg/kg, 1 mg/kg to 5 mg/kg, 5 mg/kg to 10 mg/kg, 10 mg/kg to 20 mg/kg, 15 mg/kg to 20 mg/kg, 10 mg/kg to 25 mg/kg, 15 mg/kg to 25 mg/kg, 20 mg/kg to 25 mg/kg, and 20 mg/kg to 30 mg/kg (or higher). These dosages may be administered daily, weekly, biweekly, monthly, or less frequently, for example,

biannually, depending on dosage, method of administration, disorder or symptom(s) to be treated, and individual subject characteristics. Dosages can also be administered via continuous infusion (such as through a pump). The administered dose may also depend on the route of administration. For example, subcutaneous administration may require a higher dosage than intravenous administration.

[00187] In certain circumstances it may be advantageous to formulate compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited for the patient. Each dosage unit contains a predetermined quantity of antibody calculated to produce a therapeutic effect in association with the carrier. The dosage unit depends on the characteristics of the antibodies and the particular therapeutic effect to be achieved.

[00188] Toxicity and therapeutic efficacy of the composition can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., determining the LD₅₀ (the dose lethal to 50% of the population) and the ED₅₀ (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD₅₀/ED₅₀. Antibodies that exhibit large therapeutic indices may be less toxic and/or more therapeutically effective.

[00189] The data obtained from the cell culture assays and animal studies can be used to formulate a dosage range in humans. The dosage of these compounds may lie within the range of circulating antibody concentrations in the blood, that includes an ED₅₀ with little or no toxicity. The dosage may vary within this range depending upon the dosage composition form employed and the route of administration. For any antibody used in the present invention, the therapeutically effective dose can be estimated initially using cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range that includes the IC₅₀ (i.e., the concentration of antibody which achieves a half-maximal inhibition of symptoms). The effects of any particular dosage can be monitored by a suitable bioassay. Examples of suitable bioassays include DNA replication assays, transcription-based assays, IL-22/IL-22R binding assays, IL-

22/IL-10R2 binding assays, IL-22/IL-22R/IL-10R2, and other immunological assays.

EXAMPLES

Example 1: Selection of Anti-IL-22 scFv's

Selection of Parents GIL01 and GIL68

[00190] GIL01 and GIL68 were isolated from scFv libraries by soluble selection on IL-22. Soluble selections were carried out using biotinylated IL-22 with an N-terminal His/FLAG tagged protein (bio.IL-22 H/F). Bio.IL-22 H/F was initially used at a concentration of 100 nM. An scFv phagemid library, which is an expanded version of the 1.38×10^{10} library described (Vaughan et al., 1996), was used to select antibodies specific for IL-22. Purified scFv phage (10^{12} transducing units (tu)) were blocked for 30 minutes in 100 μ l 3% MPBS (3% milk powder in PBS), then bio.IL-22 H/F was added and incubated at room temperature for 1 hour. Phage/antigen was added to 50 μ l of Dynal M280 Streptavidin magnetic beads, which had been blocked for 1 hour at 37°C in 1 ml of 3% MPBS, then incubated for a further 15 minutes at room temperature. Beads were captured using a magnetic rack and washed 4x in 1 ml of 3% MPBS/ 0.1% (v/v) Tween 20 followed by three washes in PBS. After the last wash, beads were resuspended in 100 μ l PBS and used to infect 5 ml exponentially growing *E. coli* TG-1 cells. Cells and phage on beads were incubated for 1 hour at 37°C (30 minutes stationary, 30 minutes shaking at 250 rpm), then spread on 2TYAG plates. Plates were incubated at 30°C overnight and colonies visualized the next day. Colonies were scraped off the plates into 10 ml 2TY broth and 15% glycerol added for storage at -70°C.

[00191] Glycerol stock cultures from the first round panning selection were superinfected with helper phage and rescued to give scFv antibody-expressing phage particles for the second round of selection. A second and third round of soluble selection was carried out as described above, dropping the concentration of bio.IL-22 H/F to 50 nM.

Isolation of parents GIL16, GIL45, GIL60 and GIL92

[00192] GIL16, GIL45, GIL60 and GIL92 were isolated from scFv libraries by a combination of panning on an IL-22 fusion protein and soluble selection on bio.IL-22 H/F. Wells of a microtiter plate were coated with 10 μ g/ml (Dulbecco's PBS, pH 7.4) human IL-22 fusion protein and incubated overnight at

4°C. Wells were washed in PBS and blocked for 2 hours at 37°C in 3% MPBS. Purified phage (10^{12} tu) in 100 µl of 3% MPBS were added to blocked wells and incubated at room temperature for 1 hour. Wells were washed 10 times with PBST (PBS containing 0.1% v/v Tween20), then 10 times with PBS. Bound phage particles were eluted with 100 µl trypsin solution (0.5 µg/ml trypsin in 50 mM Tris pH 8, 1 mM CaCl_2) for 30 minutes at 37°C. The eluted phage were used to infect 10 ml exponentially growing *E. coli* TG1. Infected cells were grown in 2TY broth for 1 hour at 37°C, as above, then streaked onto 2TYAG plates and incubated overnight at 30°C. Output colonies were scraped off the plates and phage rescued as described above. A second round of soluble selection was carried out as described above, using 100 nM bio.IL-22 H/F.

Example 2: ScFv Blocks Binding of IL-22 to IL-22R

[00193] Inhibition assays were performed on the parent antibodies GIL01, GIL16, GIL45, GIL60, GIL68, and GIL92 to identify antibodies that block or alter binding of IL-22 to IL-22R and/or IL-22 receptor complex. Crude scFv containing periplasmic extracts were screened for the ability to inhibit the binding of bio.IL-22 H/F to a human IL-22 receptor protein (hIL-22R). Output colonies from selections were picked into 96 well plates containing 100 µl 2TYAG. ScFv production was induced by addition of 1 mM IPTG to exponentially growing cultures and overnight incubation at 30°C. Periplasmic extracts were prepared (Griffiths et al., 1993) in 50 mM MOPS pH 7.4/ 0.5 mM EDTA / 0.5M Sorbitol.

[00194] Microtiter plates were coated with 1.25 µg/ml of an IL-22 receptor protein antibody (in PBS) for 1.5 hours at room temperature. Plates were then washed three times in PBS, and blocked for 1 hour at room temperature with PBS containing 2% milk powder (2% MPBS). After a further 3 washes, 50 µl of 25% cell conditioned medium containing an IL-22 receptor protein was added to each well, and incubated overnight at 4°C. The following day, 25 µl of sample and 25µl of bio.IL-22 H/F (54 ng/ml in PBS/0.05% BSA/0.05% Tween) were added to the washed plates, and incubated for 1.5 hours at room temperature. After 3 washes in PBST, binding of bio.IL-22 H/F was detected with Europium-Streptavidin and TRF detected with the DELFIA® reagent kit and Victor 2™ Plate Reader (Perkin Elmer).

[00195] Clones that showed inhibition of IL-22 binding were retested as purified scFv. Both the IL-22/IL-22R binding assay (described above) and the IL-22 / IL-22 receptor complex assay (described below) were used. ScFv concentrations were titrated in order to establish the clone potencies as measured by assay IC₅₀ values. These were determined using GraphPad Prism software and four-parameter logistic equation curve fitting. Sample results from the IL-22 receptor complex assay are shown in Figure 1.

Example 3: Verification of IL-22 binding by phage ELISA

[00196] To establish the specificity of the scFv's for IL-22, a phage ELISA was performed using IL-22 fusion protein, IL-22 H/F and an unrelated protein. Individual *E. coli* colonies containing phagemid were inoculated into 96 well plates containing 100 µl 2TYAG medium per well. M13K07 helper phage were added to a multiplicity of infection (moi) of 10 to the exponentially growing culture and the plates incubated an additional 1 hour at 37°C. Plates were centrifuged in a benchtop centrifuge at 2000 rpm for 10 minutes. The supernatant was removed and cell pellets were resuspended in 100 µl 2TYAK and incubated at 30°C overnight with shaking. The next day, plates were centrifuged at 2000 rpm for 10 minutes and 100 µl phage-containing supernatant from each well was transferred to a fresh 96 well plate. Phage samples were blocked in a final concentration of 3% MPBS for 1 hour at room temperature.

[00197] Microtiter plates were coated with 1 µg/ml IL-22 fusion protein, IL-22 H/F or an unrelated protein and incubated overnight at 4°C. After coating, the solutions were removed from the wells, and the plates blocked for 1 hour at room temperature in 3% MPBS. Plates were rinsed with PBS then 50 µl of pre-blocked phage was added to each well. The plates were incubated at room temperature for 1 hour, then washed with 3 changes of PBST followed by 3 changes of PBS. To each well, 50 µl of a 1:5000 dilution of anti-M13-HRP conjugate (Pharmacia) was added and the plates incubated at room temperature for 1 hour. Plates were washed 3 times with PBST then 3 times with PBS. Fifty µl of TMB substrate was added to each well and incubated until color development. The reaction was stopped by the addition of 25 µl of 0.5 M H₂SO₄, and the absorbance at 450 nm measured. These experiments confirmed the specific binding of scFv clones to IL-22.

Example 4: Conversion of scF_v to IgG

[00198] Heavy and light chain V regions from scFv clones were amplified with clone-specific primers. PCR products were digested with appropriate restriction enzymes and subcloned into vectors containing human IgG4 heavy chain constant domain (for V_H domains) or vectors containing human lambda or kappa light chain constant domains as appropriate (V_L domains). The closest human germlines of the V_H and V_L segments were determined and this information was used to indicate whether kappa or lambda light chain constant domains were used (Table 4). Correct insertion of V region domains into plasmids was verified by sequencing of plasmid DNA from individual *E. coli* colonies. Plasmids were prepared from *E. coli* cultures by standard techniques and heavy and light chain constructs co-transfected into HEK 293 EBNA cells using standard techniques. Secreted IgG was purified using protein A sepharose (Pharmacia) and buffer exchanged into PBS.

Table 4: V_H and V_L germlines of IL-22 neutralizing clones

Clone	V _H germline	V _L germline
GIL01	3-11 (DP35)	Vk1:L12
GIL16	1-18 (DP14)	Vk1:L12
GIL45	3-33 (DP50)	VL2:2a2 (DPL11)
GIL60	3-20 (DP32)	VL2:2a2 (DPL11)
GIL68	1-2 (DP8)	VL3:3h
GIL92	1-2 (DP8)	VL1:1e (DPL8)

[00199] Potency of purified IgG was verified in the biochemical IL-22 receptor complex inhibition assay as described below. IgG concentrations were

titrated in order to obtain potency values. Sample potency data is shown in Table 5.

Table 5: Potency of IL-22 scFv and IgG in the IL-22 receptor complex inhibition assay

Clone	ScFv potency (nM)	IgG potency (nM)
GIL01	104	13
GIL16	49	10
GIL60	43	15
GIL68	7	2
GIL92	16	unobtainable
GIL45	358	180

Example 5: IL-22 Antibody Optimization

[00200] Large ribosome display libraries were created and screened for scFv's that specifically recognized recombinant human IL-22, essentially as described in Hanes *et al.* (2000). Initially the five parent clones (GIL01, GIL16, GIL60, GIL68 and GIL92) were converted to ribosome display format, and this template was subsequently used for library creation. On the DNA level, a T7 promoter was added at the 5'-end for efficient transcription to mRNA. On the mRNA level, the construct contained a prokaryotic ribosome-binding site (Shine-Dalgarno sequence) and 5' & 3' stem loops for mRNA stability. At the 3' end of the single chain, the stop codon was removed and a portion of gIII was added to act as a spacer, allowing folding of the scFv away from the ribosomal tunnel (Hanes *et al.* 2000).

[00201] Ribosome display libraries derived from the lead clones were created by mutagenesis of the single chain complementarity determining regions (CDRs) using PCR with non-proofreading *Taq* DNA polymerase. Affinity based selections were performed where the library was incubated with bio.IL-22H/F, followed by streptavidin coated paramagnetic beads (Dynal M280). Tertiary complexes (mRNA-ribosome-scFv) were recovered by magnetic separation, while unbound complexes were washed away. The mRNAs encoding the bound scFvs

were then rescued by RT-PCR as described (Hanes *et al.*, 2000) and the selection process repeated with decreasing concentrations (100 nM - 10 pM over 5 rounds) of bio.IL-22H/F.

[00202] Error prone PCR was introduced to further increase library size. The error rate that was employed created, on average, 7.2 mutations per 1,000 bp after a standard PCR reaction based on the method of Cadwell and Joyce (1992). Initial error prone PCR reactions took place between the first and second rounds of selection.

[00203] V_H/V_L recombination libraries for each parent clone were prepared from the V_H and V_L CDR ribosome display outputs after either the second or fourth round of selections. The V_H portion of the V_H CDR selection output for a particular lineage was specifically PCR amplified, using clone specific primers. The V_L portion of the V_L CDR selection output for the same lineage was amplified separately. These two PCR products were recombined via an overlapping PCR reaction. This created a complete library of scFv products containing all components required for further rounds of ribosome display selection.

[00204] For some clones, phage display libraries were also utilized. Phage libraries were created by mutagenesis of single chain CDRs using PCR reactions with appropriate primers, and selected as described above. These outputs were also combined with ribosome display selection outputs to create V_H/V_L recombination libraries. The V_H selection outputs from the fourth round of ribosome display, together with the outputs from the third round of phage display, were recombined with the V_L outputs from the same lineage. This was achieved using clone specific primers and over-lapping PCR to produce V_H/V_L recombination libraries. Selections with soluble bio.IL-22 H/F continued in ribosome display format, as described above. The scFv regions of selection outputs were directionally cloned into pCANTAB6 for production of scFv for biochemical high throughput screening.

Example 6: Identification of optimized clones

[00205] Two assays were used for high throughput screening of selection outputs. Outputs derived from clones GIL01, GIL16 and GIL68 were screened in a homogeneous time resolved fluorescence assay (HTRF®, Cis

Biointernational), while GIL60 and GIL92 outputs were screened in a DELFIA® (Perkin Elmer) assay.

HTRF® epitope competition assay

[00206] Crude scFv containing culture supernatants from GIL01, GIL16 and GIL68 output clones were prepared as described above and screened for inhibition of bio.IL-22H/F binding GIL68 in an HTRF assay.

[00207] Cryptate labeled GIL68 IgG (labeling kit from Cis Biointernational) was diluted 400 fold in assay buffer (PBS/0.4M KF/ 0.05% BSA/0.05% Tween), followed by the addition of 7.5 nM Streptavidin XL665 (Xlent, Cis Biointernational). This solution was mixed with crude scFv sample (diluted 125x), and bio.IL-22H/F in a Packard black 384 well Optiplate (Perkin Elmer). Plates were incubated for 1 hour at room temperature then read using a Victor 2™ Plate Reader (Perkin Elmer). The 665 nM/620 nM emission ratio was used to calculate the percentage of specific binding in each well.

DELFLA® Time Resolved Fluorescence assay

[00208] GIL60 and GIL92 output clones were screened for inhibition of bio.IL-22H/F binding to an IL-22 receptor complex.

[00209] Microtiter plates were coated with an IL-22 receptor complex antibody (1 µg/ml in PBS), and incubated for 1.5 hours at room temperature. Plates were washed three times in PBST, and blocked for 1 hour at room temperature with 2% MPBS. After a further 3 washes, diluted cell conditioned medium containing an IL-22 receptor complex was added and incubated overnight at 4°C. Crude scFv supernatants were prepared as described above. The following day, 25 µl of diluted scFv sample and 25 µl of bio.IL-22 H/F (6 ng/ml) were added to the washed plates, and incubated for 1.5 hours at room temperature. Plates were washed 3 times in PBST, then binding of bio.IL-22H/F to the IL-22 receptor complex was detected with Europium-Streptavidin and the DELFLA® reagent kit (PerkinElmer). Time Resolved Fluorescence was measured using a Victor 2™ Plate Reader (Perkin Elmer).

[00210] Purified scFv from positive clones identified from the screening were tested in the DELFLA® IL-22 receptor complex competition assay as described above. A titration of scFv concentrations was used in order to establish the clone potency as measured by IC₅₀ values in the assay. Sample results are

shown in Figure 2. Fourteen optimized clones were designated 097D09, 062A09, 062G05, 087B03, 367D04, 368D04, 166B06, 166G05, 375G06, 376B10, 354A08, 355B06, 355E04, and 356A11.

Example 7: Ranking of Optimized Clones in the BAF3-IL-22 Proliferation Assay

[00211] Proliferation assays were performed to assess the antibody's ability to block the IL-22 mediated BaF3 cell proliferation. BaF3 cells expressing hIL22R/hIL10R2 were generated by co-transfection of BaF3 cells with hIL22R-GFP and hIL10R2-YFP. BaF3 cells expressing both hIL22R and hIL10R2 (BaF3-IL-22 receptor cells) were sorted and collected by FACS.

[00212] BaF3-IL-22 receptor cells were routinely maintained in RPMI1640 with 10% FBS and 1 ng/mL murine IL-3. Immediately before assay setup, cells were washed 4 times in assay medium (RPMI1640 with 10% FBS, 100U/ml Penicillin and 100µg/ml Streptomycin), resuspended in assay medium and incubated at 37°C, 5% CO₂ for 6-8 hours. To prepare assay plates, 100 µl of cells (1x10⁵/ml in assay medium) were added to the central 60 wells of a 96 well flat-bottomed tissue culture plate (Costar). Test scFv or IgG samples were prepared by diluting the stock sample in assay medium followed by filtration through a 0.22 µm filter. Serial 5-fold dilutions of samples were prepared in a separate dilution plate. Cell containing wells were treated with 50 µl of sample followed by 50 µl of human IL-22, (40 ng/ml in assay medium), and were then incubated for 40 hours at 37°C in 5% CO₂. Control wells included media alone and cells either alone or in the presence of 10 ng/mL human IL-22.

[00213] Cell proliferation was detected by the addition of 20 µl of Alamar Blue (Serotec) to wells, followed by incubation for 5 hours ± 30 mins at 37°C in 5% CO₂. Plates were mixed by gentle tapping to ensure even signal throughout the wells before measurement of fluorescence (excitation=560 nM, emission=590 nM). EC₅₀ and IC₅₀ values were estimated using four-parameter logistic curve fitting (Graphpad Prism 2 Software) and were used to rank antibodies. Sample potency data for optimized scFvs and IgGs are shown in Table 6.

Table 6. IC₅₀ values of scFv and IgG clones in BaF3-IL-22 proliferation assay

Clone	Parent	IC ₅₀ of scFv (pM)	IC ₅₀ of IgG (pM)
097D09	GIL01	298±246	197±42
062A09	GIL16	267	83±37
062G05	GIL16	182	112±30
087B03	GIL60	212	105±17
367D04	GIL60	160±49	126±6
368D04	GIL60	186±66	127±10
166B06	GIL68	460	71±23
166G05	GIL68	204	97±23
375G06	GIL68	118±98	100±1
376B10	GIL68	104±47	119±6
354A08	GIL92	219±83	79±15*
355B06	GIL92	183±3	92±14*
355E04	GIL92	192±47	100±14*
356A11	GIL92	124±21	53±5*

*GIL92-derived clones were tested as germlined IgGs.

Example 8: Germlining

[00214] Sequence data for the six parent clones was used to identify the nearest germline sequence for the heavy and light chain of each clone. Appropriate mutations were made using standard site directed mutagenesis techniques with the appropriate mutagenic primers. Mutation of sequences was confirmed by sequence analysis. The sequences for the germlined clones and their scFv and V_H and V_L domains are shown in Table 7. Purified scFv from the germlined parent clones were tested in the biotinylated IL-22 binding IL-22 receptor complex competition assay as described earlier, in order to establish the clone potency as measured by IC₅₀ values in the assay. Results are summarized in Table 8.

Table 7A: Amino Acid and Nucleotide Sequences of V_H and V_L Domains, F_V, and CDRs of Germlined Antibodies (GIL01, GIL16, GIL45, GIL60, GIL68, GIL92, 062A09, and 087B03)

Region	Type	GIL01 SEQ ID	GIL16 SEQ ID	GIL45 SEQ ID	GIL60 SEQ ID	GIL68 SEQ ID	GIL92 SEQ ID	062A09 SEQ ID	087B03 SEQ ID
V _H	AA	NO:365	NO:383	NO:401	NO:419	NO:437	NO:455	NO:473	NO:491
V _L	AA	NO:366	NO:384	NO:402	NO:420	NO:438	NO:456	NO:474	NO:492
scF _v	AA	NO:367	NO:385	NO:403	NO:421	NO:439	NO:457	NO:475	NO:493
H1	AA	NO:368	NO:386	NO:404	NO:422	NO:440	NO:458	NO:476	NO:494
H2	AA	NO:369	NO:387	NO:405	NO:423	NO:441	NO:459	NO:477	NO:495
H3	AA	NO:370	NO:388	NO:406	NO:424	NO:442	NO:460	NO:478	NO:496
L1	AA	NO:371	NO:389	NO:407	NO:425	NO:443	NO:461	NO:479	NO:497
L2	AA	NO:372	NO:390	NO:408	NO:426	NO:444	NO:462	NO:480	NO:498
L3	AA	NO:373	NO:391	NO:409	NO:427	NO:445	NO:463	NO:481	NO:499
V _H	DNA	NO:374	NO:392	NO:410	NO:428	NO:446	NO:464	NO:482	NO:500
V _L	DNA	NO:375	NO:393	NO:411	NO:429	NO:447	NO:465	NO:483	NO:501
scF _v	DNA	NO:376	NO:394	NO:412	NO:430	NO:448	NO:466	NO:484	NO:502
H1	DNA	NO:377	NO:395	NO:413	NO:431	NO:449	NO:467	NO:485	NO:503
H2	DNA	NO:378	NO:396	NO:414	NO:432	NO:450	NO:468	NO:486	NO:504
H3	DNA	NO:379	NO:397	NO:415	NO:433	NO:451	NO:469	NO:487	NO:505
L1		NO:380	NO:398	NO:416	NO:434	NO:452	NO:470	NO:488	NO:506
L2	DNA	NO:381	NO:399	NO:417	NO:435	NO:453	NO:471	NO:489	NO:507
L3	DNA	NO:382	NO:400	NO:418	NO:436	NO:454	NO:472	NO:490	NO:508

Table 7B: Amino Acid and Nucleotide Sequences of V_H and V_L Domains, F_v, and CDRs of Germlined Antibodies (166B06, 166G05, 354A08, 355B06, 355E04, 356A11, and 368D04)

Region	Type	166B06 SEQ ID	166G05 SEQ ID	354A08	355B06 SEQ ID	355E04 SEQ ID	356A11 SEQ ID	368D04 SEQ ID
V _H	AA	NO:509	NO:527	NO:545	NO:563	NO:581	NO:599	NO:617
V _L	AA	NO:510	NO:528	NO:546	NO:564	NO:582	NO:600	NO:618
scF _v	AA	NO:511	NO:529	NO:547	NO:565	NO:583	NO:601	NO:619
H1	AA	NO:512	NO:530	NO:548	NO:566	NO:584	NO:602	NO:620
H2	AA	NO:513	NO:531	NO:549	NO:567	NO:585	NO:603	NO:621
H3	AA	NO:514	NO:532	NO:550	NO:568	NO:586	NO:604	NO:622
L1	AA	NO:515	NO:533	NO:551	NO:569	NO:587	NO:605	NO:623
L2	AA	NO:516	NO:534	NO:552	NO:570	NO:588	NO:606	NO:624
L3	AA	NO:517	NO:535	NO:553	NO:571	NO:589	NO:607	NO:625
V _H	DNA	NO:518	NO:536	NO:554	NO:572	NO:590	NO:608	NO:626
V _L	DNA	NO:519	NO:537	NO:555	NO:573	NO:591	NO:609	NO:627
scF _v	DNA	NO:520	NO:538	NO:556	NO:574	NO:592	NO:610	NO:628
H1	DNA	NO:521	NO:539	NO:557	NO:575	NO:593	NO:611	NO:629
H2	DNA	NO:522	NO:540	NO:558	NO:576	NO:594	NO:612	NO:630
H3	DNA	NO:523	NO:541	NO:559	NO:577	NO:595	NO:613	NO:631
L1	DNA	NO:524	NO:542	NO:560	NO:578	NO:596	NO:614	NO:632
L2	DNA	NO:525	NO:543	NO:561	NO:579	NO:597	NO:615	NO:633
L3	DNA	NO:526	NO:544	NO:562	NO:580	NO:598	NO:616	NO:634

Table 8: ScFv potencies of ungermlined and germlined parent clones in the IL-22 receptor competition assay

Parent clone scFv	Average IC ₅₀ nM in IL-22 competition assay	
	Parent	Fully germlined
GIL01	124±50	143±45
GIL16	44±1	38±1
GIL60	51±16	82±3
GIL68	9±1	14±1
GIL92	18±2	40±11

[00215] Nine of the optimized antibodies were germlined as described above. Eight germlined IgGs were tested in the BaF3-IL-22 proliferation assay as described above. Antibody IC₅₀ values from a representative experiment are shown in Table 9.

[00216] Antibody sequences were then sent to GENEART North America (28 Kirk Bradden Rd. East, Toronto, ON, Canada M8Y2E6), where they were synthesized for optimized expression in CHO cells using GENEART's proprietary optimization algorithm.

Table 9: IgG potencies of germlined optimized clones in the BaF3-IL-22R proliferation assay

Clone	Parent	IC ₅₀ (pM) of non-germlined IgG	IC ₅₀ (pM) of germlined IgG
087B03	GIL60	72±6	118±19
166B06	GIL68	109±16	169±32
166G05	GIL68	366±226*	109±31
356A11	GIL92	ND	53±5
355B06	GIL92	ND	92±14
355E04	GIL92	ND	100±14
354A08	GIL92	ND	79±15
062A09	GIL16	108±23	unobtainable

*sample contained precipitate ND= not determined

Example 9: Antibody inhibits IL-22 induced GROa secretion from HT29 cells

[00217] GROa assays were performed to assess the antibody's ability to block the IL-22 induced GROa secretion from HT29 cells. HT29 cells were seeded in 96 well flat bottom tissue culture plate (Corning Inc. Cat. #3595) in DMEM medium (DMEM + 10% FBS + 100 unit/ml penicillin and streptomycin + 2 mM Glutamine) at 5×10^4 /well. 10 ng/ml IL-22 was mixed with serially diluted antibody in DMEM medium and incubated for 30 min at 37°C. 24 hours after seeding, medium was removed from HT29 cells and pre-mixed IL-22 and antibody were added to the cells in 96 well plate.

[00218] After 48 hours of incubation at 37°C with 5% CO₂, medium was collected and secreted GROa was tested using Human GROa Immunoassay kit (R&D Systems, Cat. DGR00), according to the manufacturer's directions. Results are presented in Figure 3.

Example 10: Antibody binds to and inhibits different species IL-22

[00219] Cross species reactivity of germlined and non-germlined optimized antibodies were determined as follows: ELISA plates (Costar, Cat. #3590) were coated overnight with 1 µg/ml of rat, mouse, or human IL-22 or human IL-26 in PBS buffer. Plates were washed with PBST buffer (0.05% Tween20 in

PBS) 3 times, then blocked with 1% BSA (Sigma A8918) / PBST for 1 hr at RT. Antibodies were added at 1 µg/ml, incubated 1 hr at 25°C. The plates were washed, then HRP-conjugated goat anti-human IgG antibody (Southern Biotech Association, Cat. #2040-05) was added. The plates were incubated for 1 hour at 25°C, then washed with PBST, and developed with TMB (KPL, Cat. #50-76-04). Reaction was stopped with 0.18 M H₂SO₄. Plates were read at OD 450 nm. Results are presented in Figure 4.

[00220] These antibodies were also evaluated in both the GROa cell assay and BaF3-IL-22 proliferation assay. As shown in Tables 10(a) and 10(b), the antibodies blocked the activity of human, monkey, rat, and mouse IL-22 signalling via a human IL-22 receptor. 356A11 and 368D04 also demonstrated cross-species reactivity against murine, rat, and monkey IL-22 using real-time biospecific interaction analysis (BIA), as discussed further in Example 11.

[00221] **Table 10(a).** IL-22 antibodies are highly potent for blocking other species of IL-22 as shown in the GROa cell based assay system. Values shown represent IC₅₀ values in pM.

Protein ID	human IL-22	murine IL-22	rat IL-22	monkey IL-22
356A11	123.64	143.76	210.91	89.57
368D04	154.07	156.25	281.12	184.10
control 1	353.18	468.34	1161.57	343.19
control 2	1955.80	3399.79	10697.17	1459.27

[00222] **Table 10(b).** IL-22 antibodies are highly potent for blocking other species of IL-22 as shown in the BaF3 cell based assay system. Values shown represent IC₅₀ values in pM.

Protein ID	human IL-22	murine IL-22	rat IL-22	monkey IL-22
356A11	3.57	2.53	10.69	2.58
368D04	3.63	1.47	12.07	3.87
control 1	6.40	5~6	27.37	7.18
control 2	204.98	1033.26	2500.00	134.27

Example 11: Comparison of Binding Kinetics Between Rat Anti-IL-22 Monoclonal Antibodies and Human Anti-IL-22 Monoclonal Antibodies

[00223] The binding kinetics of human, monoclonal anti-IL-22 antibodies (356A11 and 368D04) and rat, monoclonal anti-IL-22 antibodies (P3/3 (Ab-02) and P3/2 (Ab-04) from WO 2005/000897 and WO 02/068476) to human IL-22 were evaluated by real-time biospecific interaction analysis (BIA) using surface plasmon resonance technology.

[00224] To prepare the biosensor surface for the rat monoclonal antibodies, Protein A/G (Pierce #21186, Rockford, IL) was immobilized onto a research-grade carboxymethyl dextran chip (CM5) using amine coupling. The surface was activated with EDC/NHS. The protein A/G was injected at a concentration of 50 µg/ml in sodium acetate buffer (pH 4.0). The immobilization was done using the wizard tools with aim of 3000 (RUs) for the protein A/G. Remaining activated groups were blocked with 1.0 M ethanolamine (pH 8.0). The first flow cell was used as a reference surface to correct for bulk refractive index, matrix effects, and non-specific binding. The second, third, and fourth flow cells were coated with the capturing molecule. The rat monoclonal antibodies Ab-02 and Ab-04, which bind to protein A/G, were captured onto the protein A/G surface by injecting 30 µl of a 1 µg/ml solution. The net difference between the baseline and the point approximately 90 seconds after completing Ab-02 or Ab-04 injection was used to represent the amount of ligand bound.

[00225] To prepare the biosensor surface for the human monoclonal antibodies, either human monoclonal antibody (356A11 or 368D04) or control antibody PD-1 (#17) were immobilized onto a research-grade carboxymethyl dextran chip (CM5) using standard amine coupling. The surface was activated with EDC/NHS. The capturing antibodies were injected at a concentration of 1 µg/ml in sodium acetate buffer (pH 5.5). Remaining activated groups were blocked with 1.0 M ethanolamine (pH 8.0). The first flow cell was used as a reference surface to correct for bulk refractive index, matrix effects, and non-specific binding. The second, third, and fourth flow cells were coated with the capturing molecule.

[00226] For Ab-02 and Ab-04, solutions of human IL-22 at 300, 100, 50, 25, 12.5, 6.4, 3.2, 1.6 and 0 nM concentrations were injected in triplicates at a flow rate of 30 µl per minute for 3 minutes and the amount of bound material as a function of time was recorded as sensorgrams. The dissociation phase was monitored in HBS/EP buffer for 10 minutes at the same flow rate followed by a 5 µl injection of 0.1% TFA and a 5 µl injection of glycine pH 1.5 to regenerate a fully active capturing surface.

[00227] For 356A11 and 368D04, solutions of human IL-22 at 400, 200, 100, 50, 25, 12.5, 6.25 and 0 nM were injected in triplicates at a flow rate of 100 µl per minute (high flow to avoid non specific binding) for 3 minutes, and the amount of bound material as a function of time was recorded as sensorgrams. The dissociation phase was monitored in HBS/EP buffer for 60 minutes at the same flow rate followed by two 5 µl injections of glycine pH 1.5 to regenerate a fully active capturing surface.

[00228] All kinetic experiments were done at 22.5°C in HBS/EP buffer. Blank and buffer effects were subtracted for each sensorgram using double referencing. In control experiments the first injection contained buffer.

[00229] The kinetic data were analyzed using BIAevaluation software 3.0.2 applied to a 1:1 model. The apparent dissociation (K_d) and association (K_a) rate constants were calculated from the appropriate regions of the sensorgrams using a global analysis. The affinity constants of the interaction between antibody and analyte were calculated from the kinetic rate constants by the following formulae: $K_D = K_d / K_a$, where K_D is the dissociation constant and $K_A = K_a / K_d$, where K_A is the association constant. The binding data for Ab-02 and AB-04 are

summarized in Tables 11A and 11B. The binding data for 356A11 and 368D04 are summarized in Table 12.

Table 11A. Kinetic parameters for the interaction between human IL-22 and anti-IL-22 antibodies Ab-02 and Ab-04

	Ab-02 k_a ($M^{-1}s^{-1}$)	Ab-02 k_d (s^{-1})	Ab-04 k_a ($M^{-1}s^{-1}$)	Ab-04 k_d (s^{-1})
Protein A/G	2.78 E+05	1.45 E- 03	5.15 E+05	1.23 E- 03

Table 11B. Kinetic data of rat monoclonal antibodies for human IL-22

Antibody	K_a (1/Ms)	K_d (1 /s)	KA (1/M)	KD (M)	Chi2
Ab-02	2.78 E+05	1.45 E-03	1.92 E+08	5.22 E-08	0.49
Ab-04	5.15 E+05	1.23 E-03	4.22 E+08	2.38 E-09	0.53

Table 12. Kinetic data of human monoclonal antibodies for human IL-22

Antibody	K_a (1/Ms)	K_d (1 /s)	KA (1/M)	KD (M)	Chi2
356A11	7.91 E+04	4.27 E-06	1.85 E+10	5.40 E-11	0.223
368D04	1.89 E+05	2.50 E-05	7.56 E+09	1.32 E-10	0.298

[00230] These results show that the human monoclonal anti-IL-22 antibodies of this invention have a significantly higher affinity for human IL-22 than the rat monoclonal anti-IL-22 antibodies Ab-02 and Ab-04, described in WO 2005/000897 and WO 02/068476 as having the ability to neutralize human IL-22. Specifically, the dissociation constant of 356A11 ($K_D = 5.40 \times 10^{-11}$ M or 0.054 nM) for human IL-22 is approximately 1000-fold and more than 40-fold greater than the

dissociation constants of Ab-02 ($K_D = 5.22 \times 10^{-8}$ M or 52 nM) and Ab-04 ($K_D = 2.38 \times 10^{-9}$ M or 2.38 nM), respectively. Similarly, 368D04 ($K_D = 1.32 \times 10^{-10}$ M or 0.132 nM) has an approximately 400-fold and 18-fold stronger affinity for human IL-22 than Ab-02 and Ab-04, respectively. The binding profiles of 356A11 and 36804 for monkey, murine, and rat IL-22 were similar to that of human IL-22 (data not shown).

[00231] The binding specificities of 356A11 and 368D04 were also evaluated using BIA. Neither antibody showed cross reactivity with human IL-10, human IL-19, human IL-20, human IL-24, human IL-28A, human IL-29, human IFN- α 2c, or human IFN- ω (data not shown).

Example 12: Model for Treatment of Arthritis

[00232] Arthritis is a disease characterized by inflammation in the joints. Rheumatoid Arthritis (RA) is the most frequent form of arthritis, involving inflammation of connective tissue and the synovial membrane, a membrane that lines the joint. The inflamed synovial membrane often infiltrates the joint and damages joint cartilage and bone. Both IL-22 and IL-22R protein and/or transcript are associated with human disease. In RA synovial biopsies, IL-22 protein is detected in vimentin⁺ synovial fibroblasts and some CD68⁺ macrophages while IL-22R is detected in synovial fibroblasts. Treatment of synovial fibroblasts with IL-22 induces the production of monocyte chemoattractant protein-1, MCP-1, as well as general metabolic activity (Ikeuchi, H. et al. (2005) *Arthritis Rheum.* 52:1037-46).

[00233] IL-22 is used to study its effect on cells from the synovial membrane, the membrane that lines the joints. Human fibroblast-like synoviocytes (HFLS) (Cell Applications (San Diego, CA)) are isolated from synovial tissues of rheumatoid arthritis patients undergoing joint surgery. HFLS are cultured with human IL-22 for 48 hours, and the supernatants are removed and tested for chemokines and cytokines by ELISA. IL-22 will increase HFLS secretion of chemokines MCP-1, Eotaxin, and IP-10, and cytokines TNF α , IL-6, and IL-8. These chemokines and cytokines are known in the art to promote inflammation through a number of activities, and increased concentrations in the joints caused by IL-22 exacerbates inflammation and RA.

[00234] IL-22 is used to regulate the clinical progression of CIA (Collagen Induced Arthritis). CIA is the standard mouse and rat model for studying

rheumatoid arthritis, see e.g., Holmdahl et al., (2002) Ageing Res. Rev., 1:135. On day 0, mice are injected with 100 µg of Collagen Type II in complete Freund's adjuvant, and on day 21, the mice are boosted with 100 µg of Collagen Type II in incomplete Freund's adjuvant. On day 21, the mice are also injected daily with 1 µg of IL-22, and each day, the mice are examined for disease. The clinical signs are scored as follows: 0 = no swelling, 1 = 1 to 2 swollen digits or swollen ankle, 2 = more than 2 swollen digits or mild paw swelling, 3 = extensive paw swelling, and 4 = ankylosis of paw. Mice injected with PBS after the collagen injections progressively develop disease. Mice that are injected with IL-22 after the collagen injections progressively develop more severe disease. Because treatment with IL-22 specifically exacerbates CIA, treatment with anti-IL-22 antibodies, for example with germlined 087B03, 368D04, 354A08 or 356A11, is expected to suppress or delay CIA. Thus, since this model predicts treatment efficacy for RA, treatment with anti-IL-22 antibodies, including germlined or non-germlined 087B03, 368D04, 354A08 or 356A11, is expected to suppress or delay RA in humans.

Example 13: Treatment of Patients

[00235] Patients with an autoimmune disorder, respiratory disorder, inflammatory condition of the skin, cardiovascular system, nervous system, kidneys, liver and pancreas or transplant patients are among the types of patients that may be treated with the antibodies of the invention. Exemplary treatment regimens and expected outcomes of antibodies according to this invention, including 087B03, 368D04, 354A08, and 356A11, are provided below. Dosages and frequencies of administration other than those in Table 13 may also be used. The skilled artisan can adjust treatment regimens as necessary based on route of administration or other known variables, such as the age, weight, condition, sex, severity of medical condition, etc. of the patient to be treated.

Table 13: Treatment Regimens

Disorder	Treated with	Dosage Range	Frequency	Expected Outcome
Multiple Sclerosis	087B03, 368D04, 356A11, or 354A08	250 $\mu\text{g/kg}$ to 2 mg/kg	weekly, biweekly, or monthly	improvement or stabilization of condition
Rheumatoid Arthritis	087B03, 368D04, 356A11, or 354A08	250 $\mu\text{g/kg}$ to 2 mg/kg	weekly, biweekly, or monthly	improvement or stabilization of condition
Psoriasis	087B03, 368D04, 356A11, or 354A08	250 $\mu\text{g/kg}$ to 2 mg/kg	weekly, biweekly, or monthly	improvement or stabilization of condition
IBD	087B03, 368D04, 356A11, or 354A08	250 $\mu\text{g/kg}$ to 2 mg/kg	monthly, biweekly, or monthly	improvement or stabilization of condition
Alzheimer's Disease	087B03, 368D04, 356A11, or 354A08	250 $\mu\text{g/kg}$ to 2 mg/kg	monthly, biweekly, or monthly	improvement or stabilization of condition

[00236] The specification is most thoroughly understood in light of the teachings of the references cited within the specification. The embodiments within the specification provide an illustration of embodiments of the invention and should not be construed to limit the scope of the invention. The skilled artisan readily recognizes that many other embodiments are encompassed by the invention. All publications and patents cited in this disclosure are incorporated by reference in

their entirety. To the extent the material incorporated by reference contradicts or is inconsistent with this specification, the specification will supercede any such material. The citation of any references herein is not an admission that such references are prior art to the present invention.

[00237] Unless otherwise indicated, all numbers expressing quantities of ingredients, reaction conditions, and so forth used in the specification, including claims, are to be understood as being modified in all instances by the term "about." Accordingly, unless otherwise indicated to the contrary, the numerical parameters are approximations and may vary depending upon the desired properties sought to be obtained by the present invention. At the very least, and not as an attempt to limit the application of the doctrine of equivalents to the scope of the claims, each numerical parameter should be construed in light of the number of significant digits and ordinary rounding approaches.

[00238] Unless otherwise indicated, the term "at least" preceding a series of elements is to be understood to refer to every element in the series. Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

CLAIMS

We claim:

1. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to IL-22, wherein the antibody, or antigen-binding fragment thereof, comprises an amino acid sequence which is at least 95% identical to the amino acid sequence shown in SEQ ID NO:5, 6, 7, 23, 24, 25, 41, 42, 43, 59, 60, 61, 77, 78, 79, 95, 96, 97, 113, 114, 115, 131, 132, 133, 149, 150, 151, 167, 168, 169, 185, 186, 187, 203, 204, 205, 221, 222, 223, 239, 240, 241, 257, 258, 259, 275, 276, 277, 293, 294, 295, 311, 312, 313, 329, 330, 331, 347, 348, 349, 365, 366, 367, 383, 384, 385, 401, 402, 403, 419, 420, 421, 437, 438, 439, 455, 456, 457, 473, 474, 475, 491, 492, 493, 509, 510, 511, 527, 528, 529, 545, 546, 547, 563, 564, 565, 581, 582, 583, 599, 600, 601, 617, 618, or 619.

2. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to IL-22, wherein the antibody, or antigen-binding fragment thereof, comprises an amino acid sequence encoded by a nucleotide sequence which is at least 95% identical to the nucleotide sequence shown in SEQ ID NO:14, 15, 16, 32, 33, 34, 50, 51, 52, 68, 69, 70, 86, 87, 88, 104, 105, 106, 122, 123, 124, 140, 141, 142, 158, 159, 160, 176, 177, 178, 194, 195, 196, 212, 213, 214, 230, 231, 232, 248, 249, 250, 266, 267, 268, 284, 285, 286, 302, 303, 304, 320, 321, 322, 338, 339, 340, 356, 357, 358, 374, 375, 376, 392, 393, 394, 410, 411, 412, 428, 429, 430, 446, 447, 448, 464, 465, 466, 482, 483, 484, 500, 501, 502, 518, 519, 520, 536, 537, 538, 554, 555, 556, 572, 573, 574, 590, 591, 592, 608, 609, 610, 626, 627, or 628.

3. The antibody of claim 1, comprising the amino acid sequence as set out in SEQ ID NO:5, 6, 7, 23, 24, 25, 41, 42, 43, 59, 60, 61, 77, 78, 79, 95, 96, 97, 113, 114, 115, 131, 132, 133, 149, 150, 151, 167, 168, 169, 185, 186, 187, 203, 204, 205, 221, 222, 223, 239, 240, 241, 257, 258, 259, 275, 276, 277, 293, 294, 295, 311, 312, 313, 329, 330, 331, 347, 348, 349, 365, 366, 367, 383, 384, 385, 401, 402, 403, 419, 420, 421, 437, 438, 439, 455, 456, 457, 473, 474, 475, 491, 492, 493, 509, 510, 511, 527, 528, 529, 545, 546, 547, 563, 564, 565, 581, 582, 583, 599, 600, 601, 617, 618, or 619.

4. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to IL-22, wherein the antibody, or antigen-binding fragment thereof, comprises a V_L domain having a light chain variable region and a V_H domain having a heavy chain variable region, wherein the heavy chain variable region comprises one or more of SEQ ID NO:8, 9, 10, 26, 27, 28, 44, 45, 46, 62, 63, 64, 80, 81, 82, 98, 99, 100, 116, 117, 118, 134, 135, 136, 152, 153, 154, 170, 171, 172, 188, 189, 190, 206, 207, 208, 224, 225, 226, 242, 243, 244, 260, 261, 262, 278, 279, 280, 296, 297, 298, 314, 315, 316, 332, 333, 334, 350, 351, 352, 368, 369, 370, 386, 387, 388, 404, 405, 406, 422, 423, 424, 440, 441, 442, 458, 459, 460, 476, 477, 478, 494, 495, 496, 512, 513, 514, 530, 531, 532, 548, 549, 550, 566, 567, 568, 584, 585, 586, 602, 603, 604, 620, 621, or 622.

5. The antibody of claim 4, wherein the light chain variable region comprises one or more of SEQ ID NO:11, 12, 13, 29, 30, 31, 47, 48, 49, 65, 66, 67, 83, 84, 85, 101, 102, 103, 119, 120, 121, 137, 138, 139, 155, 156, 157, 173, 174, 175, 191, 192, 193, 209, 210, 211, 227, 228, 229, 245, 246, 247, 263, 264, 265, 281, 282, 283, 299, 300, 301, 317, 318, 319, 335, 336, 337, 353, 354, 355, 371, 372, 373, 389, 390, 391, 407, 408, 409, 425, 426, 427, 443, 444, 445, 461, 462, 463, 479, 480, 481, 497, 498, 499, 515, 516, 517, 533, 534, 535, 551, 552, 553, 569, 570, 571, 587, 588, 589, 605, 606, 607, 623, 624, and 625.

6. The antibody of claim 5, wherein the V_H domain comprises the amino acid sequence of any one of SEQ ID NO:5, 23, 41, 59, 77, 95, 113, 131, 149, 167, 185, 203, 221, 239, 257, 275, 293, 311, 329, 347, 365, 383, 401, 419, 437, 455, 473, 491, 509, 527, 545, 563, 581, 599, or 617 and the V_L domain comprises the amino acid sequence of any one of SEQ ID NO:6, 24, 42, 60, 78, 96, 114, 132, 150, 168, 186, 204, 222, 240, 258, 276, 294, 312, 330, 348, 366, 384, 402, 420, 438, 456, 474, 492, 510, 528, 546, 564, 582, 600, or 618.

7. The antibody of claim 6, wherein:

- a) the V_H domain comprises the amino acid sequence set out in SEQ ID NO:167 or 491; and

- b) the V_L domain comprises the amino acid sequence set out in SEQ ID NO:168 or 492.
8. The antibody of claim 6, wherein:
- a) the V_H domain comprises the amino acid sequence set out in SEQ ID NO:293 or 545; and
 - b) the V_L domain comprises the amino acid sequence set out in SEQ ID NO:294 or 546.
9. The antibody of claim 6, wherein:
- a) the V_H domain comprises the amino acid sequence set out in SEQ ID NO:203 or 617; and
 - b) the V_L domain comprises the amino acid sequence set out in SEQ ID NO:204 or 618.
10. The antibody of claim 6, wherein:
- a) the V_H domain comprises the amino acid sequence set out in SEQ ID NO:347 or 599; and
 - b) the V_L domain comprises the amino acid sequence set out in SEQ ID NO:348 or 600.
11. The antibody of claim 4, wherein the heavy chain variable region comprises:
- a) SEQ ID NO:170 or 494,
 - b) SEQ ID NO:171 or 495; and
 - c) SEQ ID NO:172 or 496.
12. The antibody of claim 4, wherein the heavy chain variable region comprises:
- a) SEQ ID NO:296 or 548,
 - b) SEQ ID NO:297 or 549; and
 - c) SEQ ID NO:298 or 550.

13. The antibody of claim 4, wherein the heavy chain variable region comprises:

- a) SEQ ID NO:206 or 620,
- b) SEQ ID NO:207 or 621; and
- c) SEQ ID NO:208 or 622.

14. The antibody of claim 4, wherein the heavy chain variable region comprises:

- a) SEQ ID NO:350 or 602,
- b) SEQ ID NO:351 or 603; and
- c) SEQ ID NO:352 or 604.

15. The antibody of claim 11, wherein the light chain variable region comprises:

- a) SEQ ID NO:173 or 497,
- b) SEQ ID NO:174 or 498; and
- c) SEQ ID NO:175 or 499.

16. The antibody of claim 12, wherein the light chain variable region comprises:

- a) SEQ ID NO:299 or 551,
- b) SEQ ID NO:300 or 552; and
- c) SEQ ID NO:301 or 553.

17. The antibody of claim 13, wherein the light chain variable region comprises:

- a) SEQ ID NO:209 or 623,
- b) SEQ ID NO:210 or 624; and
- c) SEQ ID NO:211 or 625.

18. The antibody of claim 14, wherein the light chain variable region comprises:

- a) SEQ ID NO:353 or 605,
- b) SEQ ID NO:354 or 606; and
- c) SEQ ID NO:355 or 607.

19. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to an IL-22 epitope that is recognized by GIL01, GIL16, GIL45, GIL60, GIL68, GIL92, 097D09, 062A09, 062G05, 087B03, 367D04, 368D04, 166B06, 166G05, 375G06, 376B10, 354A08, 355B06, 355E04, or 356A11, such that the antibody competitively inhibits the binding of GIL01, GIL16, GIL45, GIL60, GIL68, GIL92, 097D09, 062A09, 062G05, 087B03, 367D04, 368D04, 166B06, 166G05, 375G06, 376B10, 354A08, 355B06, 355E04, or 356A11 to human IL-22.

20. The antibody of claim 19, comprising a V_H domain, a V_L domain, or a F_v fragment as set out in SEQ ID NO:5, 6, 7, 23, 24, 25, 41, 42, 43, 59, 60, 61, 77, 78, 79, 95, 96, 97, 113, 114, 115, 131, 132, 133, 149, 150, 151, 167, 168, 169, 185, 186, 187, 203, 204, 205, 221, 222, 223, 239, 240, 241, 257, 258, 259, 275, 276, 277, 293, 294, 295, 311, 312, 313, 329, 330, 331, 347, 348, 349, 365, 366, 367, 383, 384, 385, 401, 402, 403, 419, 420, 421, 437, 438, 439, 455, 456, 457, 473, 474, 475, 491, 492, 493, 509, 510, 511, 527, 528, 529, 545, 546, 547, 563, 564, 565, 581, 582, 583, 599, 600, 601, 617, 618, or 619.

21. The antibody of claim 20, wherein the V_H domain comprises SEQ ID NO:167 or 491.

22. The antibody of claim 21, wherein the V_L domain comprises SEQ ID NO:168 or 492.

23. The antibody of claim 20, wherein the V_H domain comprises SEQ ID NO:293 or 545.

24. The antibody of claim 23, wherein the V_L domain comprises SEQ ID NO:294 or 546.

25. The antibody of claim 20, wherein the V_H domain comprises SEQ ID NO:203 or 617.

26. The antibody of claim 25, wherein the V_L domain comprises SEQ ID NO:204 or 618.

27. The antibody of claim 20, wherein the V_H domain comprises SEQ ID NO:347 or 599.

28. The antibody of claim 27, wherein the V_L domain comprises SEQ ID NO:348 or 600.

29. The antibody of claim 19 that specifically binds to an IL-22 epitope that is recognized by 087B03, such that the antibody competitively inhibits the binding of 087B03 to human IL-22.

30. The antibody of claim 19 that specifically binds to an IL-22 epitope that is recognized by 354A08, such that the antibody competitively inhibits the binding of 354A08 to human IL-22.

31. The antibody of claim 19 that specifically binds to an IL-22 epitope that is recognized by 368D04, such that the antibody competitively inhibits the binding of 368D04 to human IL-22.

32. The antibody of claim 19 that specifically binds to an IL-22 epitope that is recognized by 356A11, such that the antibody competitively inhibits the binding of 356A11 to human IL-22.

33. The antibody of claim 22, wherein the antibody is 087B03.

34. The antibody of claim 24, wherein the antibody is 354A08.

35. The antibody of claim 26, wherein the antibody is 368D04.

36. The antibody of claim 28, wherein the antibody is 356A11.
37. The antibody of claim 1 or 2, wherein the association constant of the antibody for human IL-22 is at least 10^{10} M^{-1} .
38. The antibody of claim 1 or 2, wherein the antibody blocks IL-22 mediated proliferation of BaF3 cells with an IC_{50} of 150 pM or less and wherein the BaF3 cells comprise a human IL-22 receptor.
39. The antibody of claim 1 or 2, wherein the antibody blocks IL-22 mediated GRO α secretion from HT29 cells with an IC_{50} of 150 pM or less.
40. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to IL-22, wherein the association constant of the antibody for human IL-22 is at least 10^{10} M^{-1} .
41. An isolated antibody, or antigen-binding fragment thereof, wherein the antibody blocks IL-22 mediated proliferation of BaF3 cells with an IC_{50} of 150 pM or less and wherein the BaF3 cells comprise a human IL-22 receptor.
42. The antibody of claim 1 or 2, wherein the antibody specifically binds to an amino acid sequence that is at least 95% identical to any sequence of at least 100 contiguous amino acids in the sequence set forth SEQ ID NO:1.
43. The antibody of claim 1 or 2, wherein the antibody inhibits the binding of IL-22 to IL-22R or a receptor complex comprising IL-22R and IL-10R2.
44. The antibody of claim 1 or 2, wherein the antibody is human.
45. The antibody of claim 1 or 2, wherein the antibody is IgG1 or IgG4.
46. A pharmaceutical composition comprising the antibody of claim 1 or 2.

47. An isolated nucleic acid encoding the antibody of claim 1 or 2.
48. An expression vector comprising the nucleic acid of claim 47.
49. A host cell transformed with the vector of claim 48.
50. The host cell of claim 49, wherein the host cell is a bacteria, mammalian cell, yeast cell, plant cell, or an insect cell.
51. A method of producing an antibody that binds to IL-22, comprising culturing the host cell of claim 50 under conditions that allow expression of the antibody, and isolating the antibody from the cell culture.
52. The nucleic acid of claim 47, wherein the nucleic acid encodes a protein comprising an amino acid sequence set out in one of SEQ ID NO:5-13, 23-31, 41-49, 59-67, 77-85, 95-103, 113-121, 131-139, 149-157, 167-175, 185-193, 203-211, 221-229, 239-247, 257-265, 275-283, 293-301, 311-319, 329-337, 347-355, 365-373, 383-391, 401-409, 419-427, 437-445, 455-463, 473-481, 491-499, 509-517, 527-535, 545-553, 563-571, 581-589, 599-607, or 617-625.
53. The nucleic acid of claim 52, wherein the nucleic acid comprises a nucleotide sequence of one of SEQ ID NO:14-22, 32-40, 50-58, 68-76, 86-94, 104-112, 122-130, 140-148, 158-166, 176-184, 194-202, 212-220, 230-238, 248-256, 266-274, 284-292, 302-310, 320-328, 338-346, 356-364, 374-382, 392-400, 410-418, 428-436, 446-454, 464-472, 482-490, 500-508, 518-526, 536-544, 554-562, 572-580, 590-598, 608-616, or 626-634.
54. The nucleic acid of claim 52, wherein the nucleic acid encodes a protein comprising an amino acid sequence set out in SEQ ID NO:167, 168, 169, 170, 171, 172, 173, 174, 175, 491, 492, 493, 494, 495, 496, 497, 498, or 499.

55. The nucleic acid of claim 52, wherein the nucleic acid encodes a protein comprising an amino acid sequence set out in SEQ ID NO:293, 294, 295, 296, 297, 298, 299, 300, 301, 545, 546, 547, 548, 549, 550, 551, 552, or 553.

56. The nucleic acid of claim 52, wherein the nucleic acid encodes a protein comprising an amino acid sequence set out in SEQ ID NO:203, 204, 205, 206, 207, 208, 209, 210, 211, 617, 618, 619, 620, 621, 622, 623, 624, or 625.

57. The nucleic acid of claim 52, wherein the nucleic acid encodes a protein comprising an amino acid sequence set out in SEQ ID NO:347, 348, 349, 350, 351, 352, 353, 354, 355, 599, 600, 601, 602, 603, 604, 605, 606, or 607.

58. The nucleic acid of claim 53, wherein the the nucleic acid comprises a nucleotide sequence of SEQ ID NO:176, 177, 178, 179, 180, 181, 182, 183, 184, 500, 501, 502, 503, 504, 505, 506, 507, or 508.

59. The nucleic acid of claim 53, wherein the the nucleic acid comprises a nucleotide sequence of SEQ ID NO:302, 303, 304, 305, 306, 307, 308, 309, 310, 554, 555, 556, 557, 558, 559, 560, 561, or 562.

60. The nucleic acid of claim 53, wherein the the nucleic acid comprises a nucleotide sequence of SEQ ID NO:212, 213, 214, 215, 216, 217, 218, 219, 220, 626, 627, 628, 629, 630, 631, 632, 633, or 634.

61. The nucleic acid of claim 53, wherein the the nucleic acid comprises a nucleotide sequence of SEQ ID NO:356, 357, 358, 359, 360, 361, 362, 363, 364, 608, 609, 610, 611, 612, 613, 614, 615, or 616.

62. A diagnostic kit comprising the antibody of claim 1 or 2.

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SEQUENCE LISTING

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<151> 2006-02-21

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Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
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<210> 38
<211> 33
<212> DNA
<213> Homo sapiens

<400> 38
cgggccagtg aggggtattta tcaactgggtg gcc

33

<210> 39
<211> 21
<212> DNA
<213> Homo sapiens

<400> 39
aaggcctcta gtttagccag t

21

<210> 40
<211> 27
<212> DNA
<213> Homo sapiens

<400> 40
caacaatata gtaattatcc gctcact

27

<210> 41
<211> 119
<212> PRT
<213> Homo sapiens

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<400> 41

Gln Met Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Gly Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala His Ile Trp Tyr Asp Gly Ser Asn Glu Lys Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Met Thr Val Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Thr Glu Gln His Trp Ile Thr Ala Phe Asp Ile Trp Gly Lys Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 42

<211> 111

<212> PRT

<213> Homo sapiens

<400> 42

Gln Ser Val Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
20 25 30

Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Met Ile Tyr Glu Gly Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

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Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Thr Thr Arg
85 90 95

Ser Thr Arg Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 43

<211> 249

<212> PRT

<213> Homo sapiens

<400> 43

Gln Met Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Gly Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala His Ile Trp Tyr Asp Gly Ser Asn Glu Lys Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Met Thr Val Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Thr Glu Gln His Trp Ile Thr Ala Phe Asp Ile Trp Gly Lys Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Ala Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Ala Ser Val
130 135 140

Ser Gly Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser
145 150 155 160

Ser Asp Val Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln Gln His Pro
165 170 175

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Gly Lys Ala Pro Lys Leu Met Ile Tyr Glu Gly Ser Lys Arg Pro Ser
180 185 190

Gly Val Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser
195 200 205

Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
210 215 220

Ser Ser Tyr Thr Thr Arg Ser Thr Arg Val Phe Gly Gly Gly Thr Lys
225 230 235 240

Leu Thr Val Leu Gly Ala Ala Ala His
245

<210> 44
<211> 5
<212> PRT
<213> Homo sapiens

<400> 44
Asn Tyr Gly Met Tyr
1 5

<210> 45
<211> 17
<212> PRT
<213> Homo sapiens

<400> 45
His Ile Trp Tyr Asp Gly Ser Asn Glu Lys Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 46
<211> 10
<212> PRT
<213> Homo sapiens

<400> 46
Glu Gln His Trp Ile Thr Ala Phe Asp Ile
1 5 10

<210> 47
 <211> 14
 <212> PRT
 <213> Homo sapiens

<400> 47
 Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr Asn Tyr Val Ser
 1 5 10

<210> 48
 <211> 7
 <212> PRT
 <213> Homo sapiens

<400> 48
 Glu Gly Ser Lys Arg Pro Ser
 1 5

<210> 49
 <211> 10
 <212> PRT
 <213> Homo sapiens

<400> 49
 Ser Ser Tyr Thr Thr Arg Ser Thr Arg Val
 1 5 10

<210> 50
 <211> 357
 <212> DNA
 <213> Homo sapiens

<400> 50
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 tctgtgtcag cctctggatt caccttcagt aactatggca tgtactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg ggtggcacat atttggtatg atggaagtaa tgaaaagtat 180
 gcagactccg tgaagggccg aatgaccgtc tccagagaca attccaggaa cacgttgtat 240
 ttgcaaataa acagcctgag agccgaggac acggctgtgt attactgtgc gacagagcaa 300
 cactggatta ctgcttttga tatctggggc aaaggcacc cttgtaccgt ctctctca 357

<210> 51
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 51
 cagtctgtgc tgactcagcc tgctctcgtg tctgggtctc ctggacagtc gatcaccatc 60
 tctgtcactg gaaccagcag tgacgttggg gggtataact atgtctcctg gtaccaacaa 120

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cacccaggca aagcccccaa actcatgatt tatgagggca gtaagcggcc ctcaggggtt	180
tctaatacgt tctctggctc caagtctggc aacacggcct cctgacaat ctctgggctc	240
caggctgagg acgaggctga ttattactgc agctcatata caaccaggag cactcgagtt	300
ttcggcggag ggaccaagct gaccgtccta ggt	333

<210> 52
<211> 744
<212> DNA
<213> Homo sapiens

<400> 52 cagatgcagc tgggtgcagtc tgggggagggc gtggtccagc ctgggaggtc cctgagactc	60
tctgtgcag cctctggatt caccttcagt aactatggca tgtactgggt ccgccaggct	120
ccaggcaagg ggctggagtg ggtggcacat atttggtatg atggaagtaa tgaaaagtat	180
gcagactcog tgaagggccg aatgaccgtc tccagagaca attccaggaa cacgttgtat	240
ttgcaaatac acagcctgag agccgaggac acggctgtgt attactgtgc gacagagcaa	300
cactggatta ctgcttttga tatctggggc aaaggcacc cggtcaccgt ctctcagggt	360
ggaggcgggt caggcgcagg tggcagcggc ggtggcggat cgcagtctgt gctgactcag	420
cctgcctcog tgtctgggtc tcttgacag tcgatcacca tctctgcac tggaaaccagc	480
agtgaagttg gtggttataa ctatgtctcc tggtaaccaac aacaccagg caaagccccc	540
aaactcatga tttatgaggg cagtaagcgg ccctcagggg tttctaatac cttctctggc	600
tccaagtctg gcaacacggc ctccctgaca atctctgggc tccaggctga ggacgaggct	660
gattattact gcagctcata tacaaccagg agcactcgag ttttcggcgg agggaccaag	720
ctgaccgtcc taggtgcggc cgca	744

<210> 53
<211> 15
<212> DNA
<213> Homo sapiens

<400> 53 aactatggca tgtac	15

<210> 54
<211> 51
<212> DNA
<213> Homo sapiens

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<400> 54
catatttggt atgatggaag taatgaaaag tatgcagact ccgtgaaggg c 51

<210> 55
<211> 30
<212> DNA
<213> Homo sapiens

<400> 55
gagcaacact ggattactgc ttttgatata 30

<210> 56
<211> 42
<212> DNA
<213> Homo sapiens

<400> 56
actggaacca gcagtgcagt tgggtggttat aactatgtct cc 42

<210> 57
<211> 21
<212> DNA
<213> Homo sapiens

<400> 57
gagggcagta agcggccctc a 21

<210> 58
<211> 30
<212> DNA
<213> Homo sapiens

<400> 58
agctcatata caaccaggag cactcgagtt 30

<210> 59
<211> 121
<212> PRT
<213> Homo sapiens

<400> 59
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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Ser Gly Val Asn Trp Asn Gly Gly Thr Arg Asp Tyr Ala Ala Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Arg Gly Trp Tyr Ser Gly Ser Phe Tyr Tyr Phe Gly Tyr Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 60
<211> 111
<212> PRT
<213> Homo sapiens

<400> 60
Gln Ala Val Leu Thr Gln Pro Ser Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

Ser Ile Thr Ile Ser Cys Thr Gly Ala Ser Gly Asp Val Gly Ala Tyr
20 25 30

Asn Phe Val Ser Trp Tyr Gln Gln His Pro Gly Lys Thr Pro Lys Leu
35 40 45

Ile Ile Tyr Asp Val Asn Lys Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ser Asp Tyr Tyr Cys Ser Ser Tyr Thr Ser Thr
85 90 95

Phe Ser Val Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly
100 105 110

<210> 61
<211> 250
<212> PRT
<213> Homo sapiens

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<400> 61

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Val Asn Gly Asn Gly Gly Thr Arg Asp Tyr Ala Ala Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Arg Gly Trp Tyr Ser Gly Ser Phe Tyr Tyr Phe Gly Tyr Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Ala Val Leu Thr Gln Pro
130 135 140

Ser Ser Val Ser Gly Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr
145 150 155 160

Gly Ala Ser Gly Asp Val Gly Ala Tyr Asn Phe Val Ser Trp Tyr Gln
165 170 175

Gln His Pro Gly Lys Thr Pro Lys Leu Ile Ile Tyr Asp Val Asn Lys
180 185 190

Arg Pro Ser Gly Val Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn
195 200 205

Thr Ala Ser Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ser Asp
210 215 220

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Tyr Tyr Cys Ser Ser Tyr Thr Ser Thr Phe Ser Val Val Phe Gly Gly
225 230 235 240

Gly Thr Lys Val Thr Val Leu Gly Ala Ala
245 250

<210> 62
<211> 5
<212> PRT
<213> Homo sapiens

<400> 62
Asp Tyr Gly Met Asn
1 5

<210> 63
<211> 17
<212> PRT
<213> Homo sapiens

<400> 63
Gly Val Asn Trp Asn Gly Gly Thr Arg Asp Tyr Ala Ala Ser Val Lys
1 5 10 15

Gly

<210> 64
<211> 12
<212> PRT
<213> Homo sapiens

<400> 64
Gly Trp Tyr Ser Gly Ser Phe Tyr Tyr Phe Gly Tyr
1 5 10

<210> 65
<211> 14
<212> PRT
<213> Homo sapiens

<400> 65
Thr Gly Ala Ser Gly Asp Val Gly Ala Tyr Asn Phe Val Ser
1 5 10

<210> 66
<211> 7
<212> PRT
<213> Homo sapiens

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<400> 66
Asp Val Asn Lys Arg Pro Ser
1 5

<210> 67
<211> 10
<212> PRT
<213> Homo sapiens

<400> 67
Ser Ser Tyr Thr Ser Thr Phe Ser Val Val
1 5 10

<210> 68
<211> 363
<212> DNA
<213> Homo sapiens

<400> 68
gaggtgcagc tgggtggagtc cgggggaggt gtggtacggc ctgggggggtc cctgagactc 60
tcttgtgcag cctctggatt cacctttgac gattatggca tgaactgggt ccgccaagct 120
ccagggaagg ggctggagtg ggtctctggt gttaattgga atggtgggtac cagagattat 180
gcagcctccg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaataa acagtctgag agccgaggac acggccttgt attactgtgc gagaggatgg 300
tatagtggga gcttctacta ctttggctac tggggccgag gaaccctggt caccgtctcc 360
tca 363

<210> 69
<211> 333
<212> DNA
<213> Homo sapiens

<400> 69
caggctgtgc tgactcagcc gtctctcgtg tctgggtctc ctggacagtc gatcaccatc 60
tcttgcactg gagccagcgg tgacgttggt gcttataact ttgtctcctg gtaccaacaa 120
caccagggca aaacccccaa actcataatt tatgatgtca ataagcggcc ctccaggggtt 180
tctaatoget tctctggctc caagtctggc aacaaggcct ccttgaccat ctctgggctc 240
caggccgagg acgagtctga ttattactgc agctcatata caagcacctt ctctgtggtg 300
tttggcggag ggaccaaggt caccgtccta ggt 333

<210> 70
 <211> 750
 <212> DNA
 <213> Homo sapiens

<400> 70
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 tcctgtgcag cctctggatt cacctttgac gatttatggca tgaactgggt ccgccaagct 120
 ccaggggaagg ggctggagtg ggtctctggt gttaatggga atggtggtac cagagattat 180
 gcagcctccg tgaaggggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
 ctgcaaataa acagtctgag agccgaggac acggccttgt attactgtgc gagaggatgg 300
 tatagtggga gcttctacta ctttggctac tggggccgag gaaccctggt caccgtctcg 360
 agtggaggcg gcggttcagg cggaggtggc tctggcggtg gcggaagtgc acaggctgtg 420
 ctgactcagc cgtcctccgt gtctgggtct cctggacagt cgatcaccat ctccctgcact 480
 ggagccagcg gtgacgttgg tgcttataac tttgtctcct ggtaccaaca acaccagggc 540
 aaaaccccc aactcataat ttatgatgtc aataagcggc cctcaggggt ttctaatacgc 600
 ttctctggct ccaagtctgg caacacggcc tccttgacca tctctgggct ccaggccgag 660
 gacgagtctg attattactg cagctcatat acaagcacct tctctgtggt atttggcgga 720
 gggaccaagg tcaccgtcct aggtgcggcc 750

<210> 71
 <211> 15
 <212> DNA
 <213> Homo sapiens

<400> 71
 gatttatggca tgaac 15

<210> 72
 <211> 51
 <212> DNA
 <213> Homo sapiens

<400> 72
 ggtgttaatt ggaatggtgg taccagagat tatgcagcct ccgtgaaggg c 51

<210> 73
 <211> 36
 <212> DNA
 <213> Homo sapiens

<400> 73
 ggatggtata gtgggagctt ctactacttt ggctac 36

<210> 74
 <211> 42
 <212> DNA
 <213> Homo sapiens

<400> 74
 actggagcca gcggtgacgt tgggtgcttat aactttgtct cc 42

<210> 75
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 75
 gatgtcaata agcggccctc a 21

<210> 76
 <211> 30
 <212> DNA
 <213> Homo sapiens

<400> 76
 agtcatata caagcacctt ctctgtgcta 30

<210> 77
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 77
 Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Thr Phe Ser Asp Tyr
 20 25 30

Tyr Ile His Trp Val Arg Gln Thr Pro Gly Gln Gly Phe Glu Trp Met
 35 40 45

Gly Trp Val Asn Pro Asp Thr Gly Gly Thr Arg Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Trp Val Thr Met Thr Arg Asp Met Ser Asn Thr Thr Ala Tyr
 65 70 75 80

Met Glu Leu Pro Arg Leu Arg Asp Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

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Ala Arg Asp Leu Thr Gly Phe Asp Pro Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 78
<211> 109
<212> PRT
<213> Homo sapiens

<400> 78
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Lys
1 5 10 15

Thr Ala Thr Ile Thr Cys Gly Gly Asn Asn Phe Arg Asn Lys Arg Val
20 25 30

His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

Tyr Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Arg Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80

Asp Glu Ala Asp Phe Tyr Cys Gln Val Trp Asp Ser Ser Thr Asp Arg
85 90 95

Pro Leu Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105

<210> 79
<211> 247
<212> PRT
<213> Homo sapiens

<400> 79
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Thr Phe Ser Asp Tyr
20 25 30

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Tyr Ile His Trp Val Arg Gln Thr Pro Gly Gln Gly Phe Glu Trp Met
35 40 45

Gly Trp Val Asn Pro Asp Thr Gly Gly Thr Arg Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Trp Val Thr Met Thr Arg Asp Met Ser Asn Thr Thr Ala Tyr
65 70 75 80

Met Glu Leu Pro Arg Leu Arg Asp Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Leu Thr Gly Phe Asp Pro Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Ala Gln Ser Val Leu Thr Gln Pro Pro Ser
130 135 140

Val Ser Val Ala Pro Gly Lys Thr Ala Thr Ile Thr Cys Gly Gly Asn
145 150 155 160

Asn Phe Arg Asn Lys Arg Val His Trp Tyr Gln Gln Arg Pro Gly Gln
165 170 175

Ala Pro Val Leu Val Ile Tyr Tyr Asp Ser Asp Arg Pro Ser Gly Ile
180 185 190

Pro Glu Arg Phe Ser Gly Ser Arg Ser Gly Asn Thr Ala Thr Leu Thr
195 200 205

Ile Ser Arg Val Glu Ala Gly Asp Glu Ala Asp Phe Tyr Cys Gln Val
210 215 220

Trp Asp Ser Ser Thr Asp Arg Pro Leu Phe Gly Gly Gly Thr Lys Leu
225 230 235 240

Thr Val Leu Gly Ala Ala Ala
245

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<210> 80
<211> 5
<212> PRT
<213> Homo sapiens

<400> 80
Asp Tyr Tyr Ile His
1 5

<210> 81
<211> 17
<212> PRT
<213> Homo sapiens

<400> 81
Trp Val Asn Pro Asp Thr Gly Gly Thr Arg Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 82
<211> 10
<212> PRT
<213> Homo sapiens

<400> 82
Asp Leu Thr Gly Phe Asp Pro Phe Asp Ile
1 5 10

<210> 83
<211> 11
<212> PRT
<213> Homo sapiens

<400> 83
Gly Gly Asn Asn Phe Arg Asn Lys Arg Val His
1 5 10

<210> 84
<211> 7
<212> PRT
<213> Homo sapiens

<400> 84
Tyr Asp Ser Asp Arg Pro Ser
1 5

<210> 85
<211> 11
<212> PRT
<213> Homo sapiens

<400> 85

Gln Val Trp Asp Ser Ser Thr Asp Arg Pro Leu

1 5 10

<210> 86

<211> 357

<212> DNA

<213> Homo sapiens

<400> 86

gagggtgcagc	tggtgcagtc	tggggctgag	gtgaagaagc	ctggggcctc	agtgaaggtc	60
tctctgtcagg	cttctggata	caccttcagc	gattactata	ttcactgggt	gcgacagacc	120
cctggacaag	ggtttgagt	gatgggatgg	gtcaaccctg	acactgggtg	cacaagatac	180
gcgcagaagt	ttcagggctg	ggtcacaatg	accagggaca	tgtccaacac	cacagcctac	240
atggagctgc	ccaggctgag	agacgaogac	acggccgtat	attactgtgc	gagagatcta	300
actggatttg	atccttttga	tatctggggc	caggggaacc	tggtcacctg	ctcctca	357

<210> 87

<211> 327

<212> DNA

<213> Homo sapiens

<400> 87

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acctgtgggg	gaaacaactt	tcgaaataaa	agagtacact	ggatatcagca	gaggccaggg	120
caggcccctg	tcctgggtcat	ctattatgat	tcagaccggc	cctcagggat	ccctgagcga	180
ttctctgggt	cccgtctctg	gaacacgggc	accctgacca	tcagcagggt	cgaggccggg	240
gatgaggccg	acttttactg	tcagggtgtg	gatagtagta	ctgatcgtec	gctgttcggc	300
ggagggacca	agctgacctg	cctaggt				327

<210> 88

<211> 741

<212> DNA

<213> Homo sapiens

<400> 88

gaagtgcagc	tggtgcagtc	tggggctgag	gtgaagaagc	ctggggcctc	agtgaaggtc	60
tctctgtcagg	cttctggata	caccttcagc	gattactata	ttcactgggt	gcgacagacc	120
cctggacaag	ggtttgagt	gatgggatgg	gtcaaccctg	acactgggtg	cacaagatac	180
gcgcagaagt	ttcagggctg	ggtcaccatg	accagggaca	tgtccaacac	cacagcctac	240

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atggagctgc ccaggctgag agacgacgac acggccgtat attactgtgc gagagatcta	300
actggatttg atccttttga tatctggggc cagggaaccc tggtcaccgt ctogagtgga	360
ggcggcggtt caggcggagg tggctctggc ggtggcgga gtgcacagtc tgtgctgact	420
cagccaccct cagtgtcagt ggccccagga aagacggcca cgattacctg tgggggaaac	480
aactttcgaa ataaaagagt aacttggtat cagcagaggc caggccaggc ccctgtcctg	540
gtcatctatt atgattcaga ccggccctca gggatccctg agcgattctc tggctccgcg	600
tctgggaaca cggccaccct gaccatcagc agggctcagg ccggggatga ggccgacttt	660
tactgtcagg tgtgggatag tagtactgat cgtccgctgt tcggcggagg gaccaagctg	720
accgtcctag gtgcggcgcg a	741

<210> 89
 <211> 15
 <212> DNA
 <213> Homo sapiens

<400> 89	
gattactata ttcac	15

<210> 90
 <211> 51
 <212> DNA
 <213> Homo sapiens

<400> 90	
tgggtcaacc ctgacactgg tggcacaaga tacgcgcaga agtttcaggg c	51

<210> 91
 <211> 30
 <212> DNA
 <213> Homo sapiens

<400> 91	
gatctaactg gatttgatcc ttttgatata	30

<210> 92
 <211> 33
 <212> DNA
 <213> Homo sapiens

<400> 92	
gggggaaaca actttcgaaa taaaagagta cac	33

<210> 93
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 93
 tatgattcag accggccctc a

21

<210> 94
 <211> 33
 <212> DNA
 <213> Homo sapiens

<400> 94
 caggtgtggg atagtagtac tgatcgccg ctg

33

<210> 95
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 95
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45

Gly Trp Ile Asn Pro Tyr Thr Gly Gly Ala Phe Tyr Ala Gln Lys Phe
 50 55 60

Arg Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Asn Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Arg Leu Gly Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Glu Pro Glu Lys Phe Asp Phe Trp Gly Gly Asp Asn Trp Gly
 100 105 110

Arg Gly Thr Met Val Thr Val Ser Ser
 115 120

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<210> 96
<211> 112
<212> PRT
<213> Homo sapiens

<400> 96
Gln Ala Val Leu Thr Gln Pro Ser Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Gly Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85 90 95

Leu Ser Gly Tyr Val Phe Gly Thr Gly Thr Gln Leu Thr Val Leu Gly
100 105 110

<210> 97
<211> 252
<212> PRT
<213> Homo sapiens

<400> 97
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Asn Pro Tyr Thr Gly Gly Ala Phe Tyr Ala Gln Lys Phe
50 55 60

Arg Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Asn Thr Ala Tyr
65 70 75 80

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Met Glu Leu Ser Arg Leu Gly Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Pro Glu Lys Phe Asp Phe Trp Gly Gly Asp Asn Trp Gly
100 105 110

Arg Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Ala Val Leu Thr Gln Pro
130 135 140

Ser Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr
145 150 155 160

Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Gly Val His Trp Tyr Gln
165 170 175

Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Gly Asn Ser Asn
180 185 190

Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr
195 200 205

Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp
210 215 220

Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser Leu Ser Gly Tyr Val Phe Gly
225 230 235 240

Thr Gly Thr Gln Leu Thr Val Leu Ser Ala Ala Ala
245 250

<210> 98

<211> 5

<212> PRT

<213> Homo sapiens

<400> 98

Asp Tyr Tyr Met His

1

5

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<210> 99
<211> 17
<212> PRT
<213> Homo sapiens

<400> 99
Trp Ile Asn Pro Tyr Thr Gly Gly Ala Phe Tyr Ala Gln Lys Phe Arg
1 5 10 15

Gly

<210> 100
<211> 12
<212> PRT
<213> Homo sapiens

<400> 100
Glu Pro Glu Lys Phe Asp Phe Trp Gly Gly Asp Asn
1 5 10

<210> 101
<211> 14
<212> PRT
<213> Homo sapiens

<400> 101
Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Gly Val His
1 5 10

<210> 102
<211> 7
<212> PRT
<213> Homo sapiens

<400> 102
Gly Asn Ser Asn Arg Pro Ser
1 5

<210> 103
<211> 11
<212> PRT
<213> Homo sapiens

<400> 103
Gln Ser Tyr Asp Ser Ser Leu Ser Gly Tyr Val
1 5 10

<210> 104
<211> 363
<212> DNA
<213> Homo sapiens

<400> 104
 cagggtccagc tgggtgcagtc tggggctgag gtgaagaagc ctgggggcctc agtgaaggtc 60
 tcctgcaagg cttctggata caccttcacc gactactata tgcactgggt gcgacaggcc 120
 cctggacaag ggcttgagtg ggtgggatgg atcaaccctt atactgggtg cgcattctat 180
 gcacagaagt ttgggggcag ggtcacaatg accagggaca cgtccatcaa cacagcctac 240
 atggagctga gcagactggg atctgacgac acggccgtgt attattgtgc gagagaacct 300
 gaaaaattcg atttttgggg gggtgacaac tggggccggg ggacaatggg caccgtctcc 360
 tca 363

<210> 105
 <211> 336
 <212> DNA
 <213> Homo sapiens

<400> 105
 caggctgtgc tgaactcagcc gtcctcagtg tctggggccc cagggcagag ggtcaccatc 60
 tcctgcactg ggagcagctc caacatcggg gcagggttatg gtgtacactg gtaccaacag 120
 cttccaggaa cagcccccaa actcctcacc tatggtaaca gcaatcggcc ctcaggggtc 180
 cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
 caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttat 300
 gtcttcggaa ctgggaccca gtcaccgtc ctagg 336

<210> 106
 <211> 756
 <212> DNA
 <213> Homo sapiens

<400> 106
 cagggtccagc tgggtgcagtc tggggctgag gtgaagaagc ctgggggcctc agtgaaggtc 60
 tcctgcaagg cttctggata caccttcacc gactactata tgcactgggt gcgacaggcc 120
 cctggacaag ggcttgagtg ggtgggatgg atcaaccctt atactgggtg cgcattctat 180
 gcacagaagt ttgggggcag ggtcaccatg accagggaca cgtccatcaa cacagcctac 240
 atggagctga gcagactggg atctgacgac acggccgtgt attattgtgc gagagaacct 300
 gaaaaattcg atttttgggg gggtgacaac tggggccggg ggacaatggg caccgtctcg 360
 agtggaggcg gcgggttcagg cggaggtggc tctggcggtg gcggaagtgc acaggctgtg 420
 ctgactcagc cgtcctcagt gtctggggcc ccagggcaga gggtcaccat ctctgcact 480

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gggagcagct ccaacatcgg ggcaggttat ggtgtacact ggtaccaaca gcttccagga 540
acagccccc aactcctcat ctatggtaac agcaatcggc cctcaggggt ccctgaccga 600
ttctctgggt ccaagtctgg cacctcagcc tccctggcca tcaactgggt ccaggctgag 660
gatgaggctg attattactg ccagtcctat gacagcagcc tgagtgggta tgtcttcgga 720
actgggaccc agctcaccgt ttaagtgcg gccgca 756

<210> 107
<211> 15
<212> DNA
<213> Homo sapiens

<400> 107
gactactata tgcac 15

<210> 108
<211> 51
<212> DNA
<213> Homo sapiens

<400> 108
tggatcaacc cttatactgg tggcgcatte tatgcacaga agtttcgggg c 51

<210> 109
<211> 36
<212> DNA
<213> Homo sapiens

<400> 109
gaacctgaaa aattcgattt ttgggggggt gacaac 36

<210> 110
<211> 42
<212> DNA
<213> Homo sapiens

<400> 110
actgggagca gctccaacat cggggcaggt tatggtgtac ac 42

<210> 111
<211> 21
<212> DNA
<213> Homo sapiens

<400> 111
ggtaacagca atcgccctc a 21

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<210> 112
<211> 33
<212> DNA
<213> Homo sapiens

<400> 112
cagtcctatg acagcagcct gagtggttat gtc

33

<210> 113
<211> 119
<212> PRT
<213> Homo sapiens

<400> 113
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Thr Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Ile Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Leu Trp Val Trp Asp Pro Leu Asp Tyr Trp Gly Arg Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 114
<211> 108
<212> PRT
<213> Homo sapiens

<400> 114
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Ile Gly
1 5 10 15

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Gly Ile Tyr His Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Ser Leu Ala Ser Gly Ala Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Phe Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Glu Phe Ala Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 115

<211> 246

<212> PRT

<213> Homo sapiens

<400> 115

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Thr Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Ile Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Leu Trp Val Trp Asp Pro Leu Asp Tyr Trp Gly Arg Gly
100 105 110

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Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr
130 135 140

Leu Ser Ala Ser Ile Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145 150 155 160

Glu Gly Ile Tyr His Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
165 170 175

Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser Ser Leu Ala Ser Gly Ala
180 185 190

Pro Ser Arg Phe Ser Gly Ser Gly Phe Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Tyr Ser Glu Phe Ala Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
225 230 235 240

Lys Arg Ala Ala Ala His
245

<210> 116
<211> 5
<212> PRT
<213> Homo sapiens

<400> 116
Asp Tyr Tyr Met Ser
1 5

<210> 117
<211> 17
<212> PRT
<213> Homo sapiens

<400> 117
Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 118
 <211> 10
 <212> PRT
 <213> Homo sapiens

<400> 118
 Gly Leu Trp Val Trp Asp Pro Leu Asp Tyr
 1 5 10

<210> 119
 <211> 11
 <212> PRT
 <213> Homo sapiens

<400> 119
 Arg Ala Ser Glu Gly Ile Tyr His Trp Leu Ala
 1 5 10

<210> 120
 <211> 7
 <212> PRT
 <213> Homo sapiens

<400> 120
 Lys Ala Ser Ser Leu Ala Ser
 1 5

<210> 121
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 121
 Gln Gln Tyr Ser Glu Phe Ala Trp Thr
 1 5

<210> 122
 <211> 357
 <212> DNA
 <213> Homo sapiens

<400> 122
 gaggtgcagc tgggtggagtc tgggggaggc ttggtcacgc ctggaggggc cctgagactc 60
 tcctgtgcag cctctggatt caccttcagt gactactaca tgagctgggt ccgccaggct 120
 ccagggaggg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gatcaccatc tccagagaca acgccaagaa ctactgtat 240
 ctgcaaata ggcgcctgag atctgaggac acggccgtgt attactgtgc gagagggctt 300

tgggttttggg atcctcttga ctactggggc agaggaaccc tggtcaccgt ctctca 357

<210> 123

<211> 324

<212> DNA

<213> Homo sapiens

<400> 123

gacatccaga tgaccacagtc tccttccacc ctgtctgcat ctattggaga cagagtcacc 60

atcacctgcc gggccagtga gggatatttat cactgggttg cctggatatca gcagaagcca 120

gggaaagccc ctaaaactcct gatctataag gcctctagtt tagccagtgg ggccccatca 180

agggttcagcg gcagtggatt tgggaccgat ttcactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaacaa tacagcgagt tcgcctggac cttcggcgga 300

gggaccaagc tggagatcaa acgt 324

<210> 124

<211> 738

<212> DNA

<213> Homo sapiens

<400> 124

gaggtgcagc tgggtggagtc tgggggaggc ttgggtcacgc ctggagggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt gactactaca tgagctgggt ccgccagget 120

ccagggaggg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggcgc gatcaccatc tccagagaca acgccaagaa ctactgtat 240

ctgcaaatga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagggctt 300

tgggttttggg atcctcttga ctactggggc agaggaaccc tggtcaccgt ctcttcaggt 360

gggggocggtt caggcggagg tggcagcggc ggtggcggat cggacatcca gatgaccag 420

tccccttcca ccctgtctgc atctattgga gacagagtca ccatcacctg ccgggccagt 480

gagggtatth atcactgggtt ggcctgggtat cagcagaagc cagggaaagc ccctaaactc 540

ctgatctata aggcccttag tttagccagt ggggccccat caagggttcag cggcagtgga 600

tttgggacag atttcaactct caccatcagc agcctgcagc ctgatgattt tgcaacttat 660

tactgccaac aatacagcga gttcgcttg accttcggcg gagggaccaaa gctggagatc 720

aaacgtgcgg ccgcacat 738

<210> 125
 <211> 15
 <212> DNA
 <213> Homo sapiens

<400> 125
 gactactaca tgagc 15

<210> 126
 <211> 51
 <212> DNA
 <213> Homo sapiens

<400> 126
 gctatttagtg gtagtggtag tagcacatac tacgcagact ccgtgaaggg c 51

<210> 127
 <211> 30
 <212> DNA
 <213> Homo sapiens

<400> 127
 gggctttggg tttgggatcc tcttgactac 30

<210> 128
 <211> 33
 <212> DNA
 <213> Homo sapiens

<400> 128
 cgggccagtg aggggtattta tcaactgggtg gcc 33

<210> 129
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 129
 aaggcctcta gtttagccag t 21

<210> 130
 <211> 27
 <212> DNA
 <213> Homo sapiens

<400> 130
 caacaatata gogagttegc ctggacc 27

<210> 131
 <211> 119
 <212> PRT
 <213> Homo sapiens

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<400> 131

Gln Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Val Ser Ala Tyr Thr Gly Asn Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Gly Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Gly Tyr Tyr Asp Ala Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 132

<211> 108

<212> PRT

<213> Homo sapiens

<400> 132

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Ile Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Gly Ile Tyr His Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Ser Leu Ala Ser Gly Ala Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Phe Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Met Gly Glu Tyr Asn Ala
85 90 95

Thr Ile Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 133

<211> 246

<212> PRT

<213> Homo sapiens

<400> 133

Gln Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Val Ser Ala Tyr Thr Gly Asn Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Gly Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Gly Tyr Tyr Asp Ala Tyr Asp Ile Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr
130 135 140

Leu Ser Ala Ser Ile Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145 150 155 160

Glu Gly Ile Tyr His Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
165 170 175

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Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser Ser Leu Ala Ser Gly Ala
180 185 190

Pro Ser Arg Phe Ser Gly Ser Gly Phe Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Met Gly Glu Tyr Asn Ala Thr Ile Gly Gly Gly Thr Lys Leu Glu Ile
225 230 235 240

Lys Arg Ala Ala Ala His
245

<210> 134
<211> 5
<212> PRT
<213> Homo sapiens

<400> 134
Ser Tyr Gly Ile Ser
1 5

<210> 135
<211> 17
<212> PRT
<213> Homo sapiens

<400> 135
Trp Val Ser Ala Tyr Thr Gly Asn Thr Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 136
<211> 10
<212> PRT
<213> Homo sapiens

<400> 136
Asp Arg Gly Tyr Tyr Asp Ala Phe Asp Ile
1 5 10

<210> 137
 <211> 11
 <212> PRT
 <213> Homo sapiens

<400> 137
 Arg Ala Ser Glu Gly Ile Tyr His Trp Leu Ala
 1 5 10

<210> 138
 <211> 7
 <212> PRT
 <213> Homo sapiens

<400> 138
 Lys Ala Ser Ser Leu Ala Ser
 1 5

<210> 139
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 139
 Gln Gln Met Gly Glu Tyr Asn Ala Thr
 1 5

<210> 140
 <211> 357
 <212> DNA
 <213> Homo sapiens

<400> 140
 cagggtgcagc tgggtggagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
 tcctgcaagg cttctgggta cacctttacc agttatggta tcagctgggt gcgacaggcc 120
 cctggacaag ggcttgagtg gatgggatgg gtcagcgctt acaactggtaa cacaaactat 180
 gcacagaagt tccagggcag agtcaccatg accacagaca catccacgag cacagcctac 240
 atggaactga ggggcctgag atctgacgac acggccgtgt attactgtgc gagagatcgt 300
 ggatactatg atgcttttga tatctggggc caaggcaccc tggtcaccgt ctctca 357

<210> 141
 <211> 324
 <212> DNA
 <213> Homo sapiens

<400> 141
 gacatccaga tgaccagtc tccttcacc ctgtctgcat ctattggaga cagagtcacc 60
 atcacctgcc gggccagtg gggatatttat cactgggttg cctggatatca gcagaagcca 120

gggaaagccc ctaaactcct gatctataag gcctctagtt tagccagtgg ggccccatca 180
 aggttcagcg gcagtggatt tgggacagat ttcactctca ccatcagcag cctgcagcct 240
 gatgattttg caacttatta ctgccaaaca atgggcgagt acaacgccac catcggcgga 300
 gggaccaagc tggagatcaa acgt 324

<210> 142
 <211> 738
 <212> DNA
 <213> Homo sapiens

<400> 142
 cagggtgcagc tgggtggagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
 tcttgcaggc cttctgggta cacctttacc agttatggta tcagctgggt gcgacaggcc 120
 cctggacaag ggcttgagtg gatgggatgg gtcagcgctt aacttggtta cacaactat 180
 gcacagaagt tccagggcag agtcaccatg accacagaca catccacgag cacagcctac 240
 atggaactga ggggcctgag atctgacgac acggccgtgt attactgtgc gagagatcgt 300
 ggatactatg atgcttatga tatctggggc caaggcacc cgggtcacgt ctctcaggt 360
 ggaggcggtt caggcggagg tggcagcggc ggtggcggtt cggacatcca gatgaccag 420
 tctccttcca cctgtctgc atctattgga gacagagtca ccatcacctg cggggccagt 480
 gagggtatct atcactgggt ggccctggat cagcagaagc cagggaagc ccctaaactc 540
 ctgatctata aggcctctag tttagccagt ggggccccat caagggttcag cggcagtgga 600
 tttgggacag atttcactct caccatcagc agcctgcagc ctgatgattt tgcaacttat 660
 tactgccaac aaatgggcga gtacaacgcc accatcggcg gagggacca gctggagatc 720
 aaacgtgcgg ccgcacat 738

<210> 143
 <211> 15
 <212> DNA
 <213> Homo sapiens

<400> 143
 agttatggta tcagc 15

<210> 144
 <211> 51
 <212> DNA
 <213> Homo sapiens

<400> 144
 tgggtcagcg cttacactgg taacacaaac tatgcacaga agttccaggg c 51

<210> 145
 <211> 30
 <212> DNA
 <213> Homo sapiens

<400> 145
 gatcgtggat actatgatgc ttttgatata 30

<210> 146
 <211> 33
 <212> DNA
 <213> Homo sapiens

<400> 146
 cgggccagtg aggggtattta tcaactgggtg gcc 33

<210> 147
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 147
 aaggcctcta gtttagccag t 21

<210> 148
 <211> 27
 <212> DNA
 <213> Homo sapiens

<400> 148
 caacaaatgg gcgagtacaa cgccacc 27

<210> 149
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 149
 Gln Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

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Gly Trp Ile Ser Ala Tyr Thr Gly Asn Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Gly Tyr Tyr Asp Ala Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 150

<211> 108

<212> PRT

<213> Homo sapiens

<400> 150

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Ile Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Gly Ile Tyr His Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Ser Leu Ala Ser Gly Ala Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Phe Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Met Gly Glu Trp Lys Ala
85 90 95

Ala Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 151

<211> 246

<212> PRT

<213> Homo sapiens

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<400> 151

Gln Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Ser Ala Tyr Thr Gly Asn Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Gly Tyr Tyr Asp Ala Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr
130 135 140

Leu Ser Ala Ser Ile Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145 150 155 160

Glu Gly Ile Tyr His Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
165 170 175

Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser Ser Leu Ala Ser Gly Ala
180 185 190

Pro Ser Arg Phe Ser Gly Ser Gly Phe Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

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Met Gly Glu Trp Lys Ala Ala Phe Gly Gly Gly Thr Lys Leu Glu Ile
225 230 235 240

Lys Arg Ala Ala Ala His
245

<210> 152
<211> 5
<212> PRT
<213> Homo sapiens

<400> 152
Ser Tyr Gly Ile Ser
1 5

<210> 153
<211> 17
<212> PRT
<213> Homo sapiens

<400> 153
Trp Ile Ser Ala Tyr Thr Gly Asn Thr Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 154
<211> 10
<212> PRT
<213> Homo sapiens

<400> 154
Asp Arg Gly Tyr Tyr Asp Ala Phe Asp Ile
1 5 10

<210> 155
<211> 11
<212> PRT
<213> Homo sapiens

<400> 155
Arg Ala Ser Glu Gly Ile Tyr His Trp Leu Ala
1 5 10

<210> 156
<211> 7
<212> PRT
<213> Homo sapiens

<400> 156
 Lys Ala Ser Ser Leu Ala Ser
 1 5

<210> 157
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 157
 Gln Gln Met Gly Glu Trp Lys Ala Ala
 1 5

<210> 158
 <211> 357
 <212> DNA
 <213> Homo sapiens

<400> 158
 cagggtgcagc tgggtggagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc 60
 tcttgcaagg cttctgggta cacctttacc agttatggta tcagctgggt gcgacaggcc 120
 cctggacaag ggcttgagtg gatgggatgg atcagcgctt aacttggtaa cacaaactat 180
 gcacagaagt tccagggcag agtcaccatg accacagaca catccacgag cacagcctac 240
 atggaactga ggagcctgag atctgacgac acggccgtgt attactgtgc gagagatcgt 300
 ggatactatg atgctttcga tatctggggc caaggcaccc tggtcaccgt ctctctca 357

<210> 159
 <211> 324
 <212> DNA
 <213> Homo sapiens

<400> 159
 gacatccaga tgaccacgac tcttccacc ctgtctgcat ctattggaga cagagtcacc 60
 atcacctgcc gggccagtga gggatattat cactgggttg cctgggtatca gcagaagcca 120
 gggaaagccc ctaaactcct gatctataag gcctctagtt tagccagtgg ggccccatca 180
 aggttcagcg gcagtggatt tgggacagat ttcactctca ccatcagcag cctgcagcct 240
 gatgattttg caacttatta ctgccaacaa atgggggagt ggaaggcggc cttcgggcga 300
 gggaccaagc tggagatcaa acgt 324

<210> 160
 <211> 738
 <212> DNA
 <213> Homo sapiens

<400> 160
caggtgcagc tgggtggagtc tggagctgag gtgaagaagc ctgggggcctc agtgaaggtc 60
tcctgcaagg cttctgggta cacctttacc agttatggta tcagctgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggatgg atcagcgctt acactggtaa cacaaactat 180
gcacagaagt tccagggcag agtcaccatg accacagaca catccacgag cacagcctac 240
atggaactga ggagcctgag atctgacgac acggccgtgt attactgtgc gagagatcgt 300
ggatactatg atgctttcga tatctggggc caaggcacc cggtcaccgt ctctcaggt 360
gggggcgggt caggcggagg tggcagcggc ggtggcggat cggacatcca gatgaccag 420
tctccttcca ccctgtctgc atctattgga gacagagtca ccacacctg ccgggccagt 480
gagggtatct atcactgggt ggccctggat cagcagaagc cagggaagc ccctaaactc 540
ctgatctata aggcctctag tttagccagt ggggccccat caaggttcag cggcagtggg 600
tttgggacag atttcactct caccatcagc agcctgcagc ctgatgattt tgcaacttat 660
tactgccaac aaatggggga gtggaaggcg gccttcggcg gagggaccaa gctggagatc 720
aaacgtgcgg ccgcacat 738

<210> 161
<211> 15
<212> DNA
<213> Homo sapiens

<400> 161
agttatggta tcagc 15

<210> 162
<211> 51
<212> DNA
<213> Homo sapiens

<400> 162
tggatcagcg cttacactgg taacacaaac tatgcacaga agttccaggg c 51

<210> 163
<211> 30
<212> DNA
<213> Homo sapiens

<400> 163
gatcgtggat actatgatgc tttcgatata 30

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<210> 164
<211> 33
<212> DNA
<213> Homo sapiens

<400> 164
cgggccagtg aggggtattta tcaactgggtg gcc

33

<210> 165
<211> 21
<212> DNA
<213> Homo sapiens

<400> 165
aaggcctcta gtttagccag t

21

<210> 166
<211> 27
<212> DNA
<213> Homo sapiens

<400> 166
caacaaatgg gggagtggaa ggcggcc

27

<210> 167
<211> 5
<212> PRT
<213> Homo sapiens

<400> 167
Asp Tyr Gly Met Asn
1 5

<210> 168
<211> 111
<212> PRT
<213> Homo sapiens

<400> 168
Gln Ala Val Leu Thr Gln Pro Ser Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

Ser Ile Thr Ile Ser Cys Thr Gly Ala Ser Gly Asp Val Gly Ala Tyr
20 25 30

Asn Phe Val Ser Trp Tyr Gln Gln His Pro Gly Lys Thr Pro Lys Leu
35 40 45

Ile Ile Tyr Asp Val Asn Lys Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

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Ser Gly Ser Lys Ser Ser Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ser Asp Tyr Tyr Cys Ser Ser Tyr Thr Ser Thr
85 90 95

Phe Ser Val Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly
100 105 110

<210> 169

<211> 252

<212> PRT

<213> Homo sapiens

<400> 169

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Val Asn Trp Asn Gly Gly Thr Arg Asp Tyr Ala Ala Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Arg Gly Trp Tyr Ser Gly Ala Ala Trp Asn Met Gly Tyr Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Ala Val Leu Thr Gln Pro
130 135 140

Ser Ser Val Ser Gly Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr
145 150 155 160

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Gly Ala Ser Gly Asp Val Gly Ala Tyr Asn Phe Val Ser Trp Tyr Gln
165 170 175

Gln His Pro Gly Lys Thr Pro Lys Leu Ile Ile Tyr Asp Val Asn Lys
180 185 190

Arg Pro Ser Gly Val Ser Asn Arg Phe Ser Gly Ser Lys Ser Ser Asn
195 200 205

Thr Ala Ser Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ser Asp
210 215 220

Tyr Tyr Cys Ser Ser Tyr Thr Ser Thr Phe Ser Val Val Phe Gly Gly
225 230 235 240

Gly Thr Lys Val Thr Val Leu Gly Ala Ala Ala His
245 250

<210> 170
<211> 5
<212> PRT
<213> Homo sapiens

<400> 170
Asp Tyr Gly Met Asn
1 5

<210> 171
<211> 17
<212> PRT
<213> Homo sapiens

<400> 171
Gly Val Asn Trp Asn Gly Gly Thr Arg Asp Tyr Ala Ala Ser Val Lys
1 5 10 15

Gly

<210> 172
<211> 12
<212> PRT
<213> Homo sapiens

<400> 172
Gly Trp Tyr Ser Gly Ala Ala Trp Asn Met Gly Tyr
1 5 10

<210> 173
 <211> 14
 <212> PRT
 <213> Homo sapiens

<400> 173
 Thr Gly Ala Ser Gly Asp Val Gly Ala Tyr Asn Phe Val Ser
 1 5 10

<210> 174
 <211> 7
 <212> PRT
 <213> Homo sapiens

<400> 174
 Asp Val Asn Lys Arg Pro Ser
 1 5

<210> 175
 <211> 10
 <212> PRT
 <213> Homo sapiens

<400> 175
 Ser Ser Tyr Thr Ser Thr Phe Ser Val Val
 1 5 10

<210> 176
 <211> 363
 <212> DNA
 <213> Homo sapiens

<400> 176
 gaggtgcagc tgggtggagtc cgggggaggt gtggtacggc ctgggggggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttgac gattatggca tgaactgggt ccgccaagct 120
 ccaggggaagg ggctggagtg ggtctctggt gttaattgga atggtggtac cagagattat 180
 gcagcctcog tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
 ctgcaaatga acagtctgag agccgaggac acggccttgt attactgtgc gagaggatgg 300
 tatagtgggg ccgcgtggaa catgggctac tggggccgag gaaccctgggt caccgtctcc 360
 tca 363

<210> 177
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 177

cagggtgtgc tgactcagcc gtccctccgtg tctgggtctc ctggacagtc gatcaccatc	60
tccctgcactg gagccagcgg tgacgttggg gcttataact ttgtctcctg gtaccaacaa	120
caccagggca aaacccccaa actcataatt tatgatgtca ataagcggcc ctcaggggtt	180
tctaatoctt tctctggctc caagtctagc aacacggcct ccttgaccat ctctgggctc	240
caggccgagg acgagtctga ttattactgc agctcatata caagcacctt ctctgtggta	300
tttggcggag ggaccaaggt caccgtccta ggt	333

<210> 178

<211> 757

<212> DNA

<213> Homo sapiens

<400> 178

cgaggtgcag ctggtggagt cggggggagg tgtggtacgg cctgggggggt cctgagact	60
ctcctgtgca gcctctggat tcacctttga cgattatggc atgaactggg tccgccaaagc	120
tccaggggaag gggctggagt gggctctctg tgttaattgg aatgggtggta ccagagatta	180
tgcagcctcc gtgaagggcc gattcaccat ctccagagac aacgcccaaga actccctgta	240
tctgcaaatg aacagtctga gagccgagga cacggccttg tattactgtg cgagaggatg	300
gtatagtggg gccgcgtgga acatgggcta ctggggccga ggaaccctgg tcaccgtctc	360
gagtggaggc gggcggttcag gcggaggtgg ctctggcggt ggcgggaagtg cacaggctgt	420
gctgactcag ccgtccctccg tgtctgggtc tcctggacag tcgatcacca tctcctgcac	480
tggagccagc ggtgacgttg gtgcttataa ctttgtctcc tggtaaccaac aacacccagg	540
caaaaccccc aaactcataa tttatgatgt caataagcgg ccctcagggg tttctaactg	600
cttctctggc tccaagtcta gcaacacggc ctccctgacc atctctgggc tccaggccga	660
ggacgagtct gattattact gcagctcata tacaagcacc ttctctgtgg tatttggcgg	720
agggaccaag gtcaccgtcc taggtgcggc cgcacat	757

<210> 179

<211> 15

<212> DNA

<213> Homo sapiens

<400> 179

gattatggca tgaac

15

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<210> 180
<211> 51
<212> DNA
<213> Homo sapiens

<400> 180
gggtgtaatt ggaatgggtg taccagagat tatgcagcct ccgtgaaggg c 51

<210> 181
<211> 36
<212> DNA
<213> Homo sapiens

<400> 181
ggatgggtata gtggggccgc gtggaacatg ggctac 36

<210> 182
<211> 42
<212> DNA
<213> Homo sapiens

<400> 182
actggagcca gcggtgacgt tgggtgcttat aactttgtct cc 42

<210> 183
<211> 21
<212> DNA
<213> Homo sapiens

<400> 183
gatgtcaata agcggccctc a 21

<210> 184
<211> 30
<212> DNA
<213> Homo sapiens

<400> 184
agctcatata caagcacctt ctctgtggta 30

<210> 185
<211> 121
<212> PRT
<213> Homo sapiens

<400> 185
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

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Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Val Asn Trp Asn Gly Gly Thr Arg Asp Tyr Ala Ala Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Arg Gly Trp Tyr Ser Gly Ser Pro Trp Ser Leu Gly His Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 186

<211> 111

<212> PRT

<213> Homo sapiens

<400> 186

Gln Ala Val Leu Thr Gln Pro Ser Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

Ser Val Thr Ile Ser Cys Thr Gly Ala Ser Gly Asp Val Gly Ala Tyr
20 25 30

Asn Phe Val Ser Trp Tyr Gln Gln His Pro Gly Lys Thr Pro Lys Leu
35 40 45

Ile Ile Tyr Asp Val Asn Lys Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Arg Leu
65 70 75 80

Gln Ala Glu Asp Glu Ser Asp Tyr Tyr Cys Ser Ser Tyr Thr Ser Arg
85 90 95

Tyr Thr Thr Glu Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly
100 105 110

<210> 187
 <211> 271
 <212> PRT
 <213> Homo sapiens

<400> 187

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Val Asn Trp Asn Gly Gly Thr Arg Asp Tyr Ala Ala Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95

Ala Arg Gly Trp Tyr Ser Gly Ser Pro Trp Ser Leu Gly His Trp Gly
 100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
 115 120 125

Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly
 130 135 140

Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Ala Val Leu
 145 150 155 160

Thr Gln Pro Ser Ser Val Ser Gly Ser Pro Gly Gln Ser Val Thr Ile
 165 170 175

Ser Cys Thr Gly Ala Ser Gly Asp Val Gly Ala Tyr Asn Phe Val Ser
 180 185 190

Trp Tyr Gln Gln His Pro Gly Lys Thr Pro Lys Leu Ile Ile Tyr Asp
 195 200 205

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Val Asn Lys Arg Pro Ser Gly Val Ser Asn Arg Phe Ser Gly Ser Lys
210 215 220

Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Arg Leu Gln Ala Glu Asp
225 230 235 240

Glu Ser Asp Tyr Tyr Cys Ser Ser Tyr Thr Ser Arg Tyr Thr Thr Glu
245 250 255

Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Ala Ala Ala His
260 265 270

<210> 188
<211> 5
<212> PRT
<213> Homo sapiens

<400> 188
Asp Tyr Gly Met Asn
1 5

<210> 189
<211> 17
<212> PRT
<213> Homo sapiens

<400> 189
Gly Val Asn Trp Asn Gly Gly Thr Arg Asp Tyr Ala Ala Ser Val Lys
1 5 10 15

Gly

<210> 190
<211> 12
<212> PRT
<213> Homo sapiens

<400> 190
Gly Trp Tyr Ser Gly Ser Pro Trp Ser Leu Gly His
1 5 10

<210> 191
<211> 14
<212> PRT
<213> Homo sapiens

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<400> 191

Thr Gly Ala Ser Gly Asp Val Gly Ala Tyr Asn Phe Val Ser
1 5 10

<210> 192

<211> 7

<212> PRT

<213> Homo sapiens

<400> 192

Asp Val Asn Lys Arg Pro Ser
1 5

<210> 193

<211> 10

<212> PRT

<213> Homo sapiens

<400> 193

Ser Ser Tyr Thr Ser Arg Tyr Thr Thr Glu
1 5 10

<210> 194

<211> 363

<212> DNA

<213> Homo sapiens

<400> 194

gaggtgcagc tggtaggagtc cgggggaggt gtggtacggc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttgac gattatggca tgaactgggt ccgccaagct 120
ccaggggaagg ggctggagtg ggtctctggt gttaattgga atgggtggtag cagagattat 180
gcagcctccg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaataa acagtctgag agccgaggac acggccttgt attactgtgc gagaggatgg 300
tatagtggga gcccgtagtc gctggggccac tggggccgag gaaccctggt caccgtctcc 360
tca 363

<210> 195

<211> 333

<212> DNA

<213> Homo sapiens

<400> 195

caggctgtgc tgactcagcc gtccctccgtg tctgggtctc ctggacagtc ggtcaccatc 60
tcctgcactg gagccagcgg tgacgttggg gcttataact ttgtctctctg gtaccaacaa 120
caccagga aaacccccaa actcataatt tatgatgtca ataagcggcc ctcagggtt 180

66/206

tctaatacgt tctctggctc caagtctggc aacacggcct ccctgaccat ctctaggctc 240
caggccgagg acgagtctga ttattactgc agctcatata catcgaggta caccgacgag 300
tttggcggag ggaccaaggt caccgtccta ggt 333

<210> 196
<211> 813
<212> DNA
<213> Homo sapiens

<400> 196
gaggtgcagc tgggtggagtc cgggggaggt gtggtacggc ctgggggggtc cctgagactc 60
tctctgtcag cctctggatt cacctttgac gattatggca tgaactgggt ccgccaagct 120
ccagggaagg ggctggagtg ggtctctggt gttaattgga atgggtggtac cagagattat 180
gcagcctccg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaata acagtctgag agccgaggac acggccttgt attactgtgc gagaggatgg 300
tatagtggga gcccggtggt gctgggccac tggggccgag gaaccctggt caccgtctcg 360
agtggaggcg gcggttcagg cggaggtggc tctggcggta gcggaggtgg ctctggcggt 420
agcggaggtg gctctagcgg aggtggctct gcgggtggcg gaagtgcaca ggctgtgctg 480
actcagccgt cctccgtgtc tgggtctcct ggacagtcgg tcaccatctc ctgcactgga 540
gccagcgggt acgttggtgc ttataacttt gtctcctggt accaacaaca ccaggcaaa 600
acccccaaac tcataattta tgatgtcaat aagcgccct caggggtttc taatcgcttc 660
tctggctcca agtctggcaa caccgctcc ctgaccatct ctaggctcca ggccgaggac 720
gagtctgatt attactgcag ctcatatata tcgaggtaca cgaccgagtt tggcggaggg 780
accaaggtca ccgtcctagg tgcggccgca cat 813

<210> 197
<211> 15
<212> DNA
<213> Homo sapiens

<400> 197
gattatggca tgaac 15

<210> 198
<211> 51
<212> DNA
<213> Homo sapiens

<400> 198
ggtgttaatt ggaatgggtg taccagagat tatgcagcct ccgtgaaggg c 51

<210> 199
 <211> 36
 <212> DNA
 <213> Homo sapiens

<400> 199
 ggatggtata gtgggagccc gtggtcgctg ggccac 36

<210> 200
 <211> 42
 <212> DNA
 <213> Homo sapiens

<400> 200
 actggagcca gcggtgacgt tgggtgcttat aactttgtot cc 42

<210> 201
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 201
 gatgtcaata agcggccctc a 21

<210> 202
 <211> 30
 <212> DNA
 <213> Homo sapiens

<400> 202
 agctcatata catcgaggta caccgaccgag 30

<210> 203
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 203
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Val Asn Trp Asn Gly Gly Thr Arg Asp Tyr Ala Ala Ser Val
 50 55 60

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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Arg Gly Trp Tyr Ser Gly Ala Ala Trp Asn Met Gly Tyr Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 204

<211> 111

<212> PRT

<213> Homo sapiens

<400> 204

Gln Ala Val Leu Thr Gln Pro Ser Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

Ser Ile Thr Ile Ser Cys Thr Gly Ala Ser Gly Asp Val Gly Ala Tyr
20 25 30

Asn Phe Val Ser Trp Tyr Gln Gln His Pro Gly Lys Thr Pro Lys Leu
35 40 45

Ile Ile Tyr Asp Val Asn Lys Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ser Asp Tyr Tyr Cys Ala Ser Leu Val Ser Asp
85 90 95

Phe Ser Val Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly
100 105 110

<210> 205

<211> 256

<212> PRT

<213> Homo sapiens

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<400> 205

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Val Asn Trp Asn Gly Gly Thr Arg Asp Tyr Ala Ala Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Arg Gly Trp Tyr Ser Gly Ala Ala Trp Asn Met Gly Tyr Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Ala Gln Ala Val Leu Thr Gln Pro Ser Ser
145 150 155 160

Val Ser Gly Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Ala
165 170 175

Ser Gly Asp Val Gly Ala Tyr Asn Phe Val Ser Trp Tyr Gln Gln His
180 185 190

Pro Gly Lys Thr Pro Lys Leu Ile Ile Tyr Asp Val Asn Lys Arg Pro
195 200 205

Ser Gly Val Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala
210 215 220

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Ser Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ser Asp Tyr Tyr
225 230 235 240

Cys Ala Ser Leu Val Ser Asp Phe Ser Val Val Phe Gly Gly Gly Thr
245 250 255

Lys Val Thr Val Leu Gly Ala Ala Ala His
260 265

<210> 206
<211> 5
<212> PRT
<213> Homo sapiens

<400> 206
Asp Tyr Gly Met Asn
1 5

<210> 207
<211> 17
<212> PRT
<213> Homo sapiens

<400> 207
Gly Val Asn Trp Asn Gly Gly Thr Arg Asp Tyr Ala Ala Ser Val Lys
1 5 10 15

Gly

<210> 208
<211> 12
<212> PRT
<213> Homo sapiens

<400> 208
Gly Trp Tyr Ser Gly Ala Ala Trp Asn Met Gly Tyr
1 5 10

<210> 209
<211> 14
<212> PRT
<213> Homo sapiens

<400> 209
Thr Gly Ala Ser Gly Asp Val Gly Ala Tyr Asn Phe Val Ser
1 5 10

<210> 210
 <211> 7
 <212> PRT
 <213> Homo sapiens

<400> 210
 Asp Val Asn Lys Arg Pro Ser
 1 5

<210> 211
 <211> 10
 <212> PRT
 <213> Homo sapiens

<400> 211
 Ala Ser Leu Val Ser Asp Phe Ser Val Val
 1 5 10

<210> 212
 <211> 363
 <212> DNA
 <213> Homo sapiens

<400> 212
 gaggtgcagc tgggtggagtc cgggggaggt gtggtacggc ctgggggggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttgac gattatggca tgaactgggt ccgccaagct 120
 ccaggggaagg ggctggagtg ggtctctggt gttaattgga atggtgggtac cagagattat 180
 gcagcctccg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
 ctgcaaatga acagtctgag agccgaggac acggccttgt attactgtgc gagaggatgg 300
 tatagtgggg ccgcgtggaa catgggctac tggggccgag gaaccctggt caccgtctcc 360
 tca 363

<210> 213
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 213
 caggctgtgc tgactcagcc gtctctccgtg totgggtccc ctggacagtc gatcaccatc 60
 tcctgcactg gagccagcgg tgacgttgggt gcttataact ttgtctcctg gtaccaacaa 120
 caccaggca aaacccccaa actcataatt tatgatgtca ataagcggcc ctcagggggt 180
 tctaactcgt tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc 240
 caggccgagg acgagtctga ttattactgc gctccctcg tctccgactt ctctgtggta 300
 tttggcggag ggaccaaggt caccgtccta ggt 333

<210> 214
 <211> 798
 <212> DNA
 <213> Homo sapiens

<400> 214
 gaggtgcagc tgggtggagtc cggggggaggt gtggtacggc ctgggggggtc cctgagactc 60
 tectgtgcag cctctggatt cacctttgac gattatggca tgaactgggt ccgccaagct 120
 ccagggaagg ggctggagtg ggtctctggt gtttaattgga atggtggtac cagagattat 180
 gcagcctccg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
 ctgcaaataa acagtctgag agccgaggac acggccttgt attactgtgc gagaggatgg 300
 tatagtgggg ccgcgtggaa catgggctac tggggccgag gaaccttgggt caccgtctcg 360
 agtggaggcg gcggttcagg cggagggtgg tctggtggtg gcggagggtg ctctggcggg 420
 ggcgagggtg gctctggcgg tggcggaagt gcacaggctg tgctgactca gccgtcctcc 480
 gtgtctgggt cccttggaac gtcgatcacc atctctctgca ctggagccag cggtgacggt 540
 ggtgcttata actttgtctc ctggtaccaa caacaccag gcaaaacccc caaactcata 600
 atttatgatg tcaataagcg gccctcaggg gtttctaatc gcttctctgg ctccaagtct 660
 ggcaacacgg cctccctgac catctctggg ctccaggccg aggacgagtc tgattattac 720
 tgcgcctccc tcgtctccga cttctctgtg gtatttggcg gagggaccaa ggtcaccgtc 780
 ctaggtgcgg ccgcacat 798

<210> 215
 <211> 15
 <212> DNA
 <213> Homo sapiens

<400> 215
 gattatggca tgaac 15

<210> 216
 <211> 51
 <212> DNA
 <213> Homo sapiens

<400> 216
 ggtgttaatt ggaatggtgg taccagagat tatgcagcct ccgtgaaggg c 51

<210> 217
 <211> 36
 <212> DNA
 <213> Homo sapiens

<400> 217
 ggatggtata gtggggccgc gtggaacatg ggctac 36

<210> 218
 <211> 42
 <212> DNA
 <213> Homo sapiens

<400> 218
 actggagcca gcggtgacgt tggcgcttat aactttgtct cc 42

<210> 219
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 219
 gatgtcaata agcggccctc a 21

<210> 220
 <211> 30
 <212> DNA
 <213> Homo sapiens

<400> 220
 gcctccctcg tctccgactt ctctgtggta 30

<210> 221
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 221
 Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Thr Phe Ser Asp Tyr
 20 25 30

Tyr Ile His Trp Val Arg Gln Thr Pro Gly Gln Gly Phe Glu Trp Met
 35 40 45

Gly Trp Val Asn Pro Asp Thr Gly Gly Thr Arg Tyr Ala Gln Lys Phe
 50 55 60

74/206

Gln Gly Trp Val Thr Met Thr Arg Asp Met Ser Asn Thr Thr Ala Tyr
65 70 75 80

Met Glu Leu Pro Arg Leu Arg Asp Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Leu Thr Gly Phe Asp Pro Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 222
<211> 109
<212> PRT
<213> Homo sapiens

<400> 222
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Lys
1 5 10 15

Thr Ala Thr Ile Thr Cys Gly Gly Asn Asn Phe Arg Asn Lys Arg Val
20 25 30

His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

Tyr Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Arg Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80

Asp Glu Ala Asp Phe Tyr Cys Gln Val Trp Asp Leu Phe Asn Asp Asn
85 90 95

Gly Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105

<210> 223
<211> 248
<212> PRT
<213> Homo sapiens

<400> 223
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Thr Phe Ser Asp Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Thr Pro Gly Gln Gly Phe Glu Trp Met
35 40 45

Gly Trp Val Asn Pro Asp Thr Gly Gly Thr Arg Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Trp Val Thr Met Thr Arg Asp Met Ser Asn Thr Thr Ala Tyr
65 70 75 80

Met Glu Leu Pro Arg Leu Arg Asp Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Leu Thr Gly Phe Asp Pro Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Ala Gln Ser Val Leu Thr Gln Pro Pro Ser
130 135 140

Val Ser Val Ala Pro Gly Lys Thr Ala Thr Ile Thr Cys Gly Gly Asn
145 150 155 160

Asn Phe Arg Asn Lys Arg Val His Trp Tyr Gln Gln Arg Pro Gly Gln
165 170 175

Ala Pro Val Leu Val Ile Tyr Tyr Asp Ser Asp Arg Pro Ser Gly Ile
180 185 190

Pro Glu Arg Phe Ser Gly Ser Arg Ser Gly Asn Thr Ala Thr Leu Thr
195 200 205

Ile Ser Arg Val Glu Ala Gly Asp Glu Ala Asp Phe Tyr Cys Gln Val
210 215 220

Trp Asp Leu Phe Asn Asp Asn Gly Val Phe Gly Gly Gly Thr Lys Leu
225 230 235 240

Thr Val Leu Gly Ala Ala Ala His
245

<210> 224
<211> 5
<212> PRT
<213> Homo sapiens

<400> 224
Asp Tyr Tyr Ile His
1 5

<210> 225
<211> 17
<212> PRT
<213> Homo sapiens

<400> 225
Trp Val Asn Pro Asp Thr Gly Gly Thr Arg Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 226
<211> 10
<212> PRT
<213> Homo sapiens

<400> 226
Asp Leu Thr Gly Phe Asp Pro Phe Asp Ile
1 5 10

<210> 227
<211> 11
<212> PRT
<213> Homo sapiens

<400> 227
Gly Gly Asn Asn Phe Arg Asn Lys Arg Val His
1 5 10

<210> 228
<211> 7
<212> PRT
<213> Homo sapiens

<400> 228
Tyr Asp Ser Asp Arg Pro Ser
1 5

<210> 229
 <211> 11
 <212> PRT
 <213> Homo sapiens

<400> 229
 Gln Val Trp Asp Leu Phe Asn Asp Asn Gly Val
 1 5 10

<210> 230
 <211> 357
 <212> DNA
 <213> Homo sapiens

<400> 230
 gaggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
 tcctgtcagg cttctggata caccttcagc gattactata ttcactgggt gcgacagacc 120
 cctggacaag ggtttgagt gatgggatgg gtcaaccctg aactgggtgg cacaagatac 180
 gcgcagaagt ttcagggctg ggtcacaatg accagggaca tgtccaacac cacagcctac 240
 atggagctgc ccaggctgag agacgacgac acggccgtat attactgtgc gagagatcta 300
 actggatttg atccttttga tatctggggc caggggaaccc tggtcaccgt ctcctca 357

<210> 231
 <211> 327
 <212> DNA
 <213> Homo sapiens

<400> 231
 cagtctgtgc tgactcagcc accctcagtg tcagtggccc caggaaagac ggccacgatt 60
 acctgtgggg gaaacaactt tcgaaataaa agagtacact ggtatcagca gaggccaggc 120
 cagggcccctg tcctgggtcat ctattatgac tcagaccggc cctcagggat ccctgagcga 180
 ttctctggct cccgctctgg gaacacggcc accctgacca tcagcagggt cgaggccggg 240
 gatgaggcgg acttttactg tcaggtgtgg gatctcttca acgacaacgg cgtgttcggc 300
 ggagggacca agctgaccgt cctaggt 327

<210> 232
 <211> 744
 <212> DNA
 <213> Homo sapiens

<400> 232
 gaagtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
 tcctgtcagg cttctggata caccttcagc gattactata ttcactgggt gcgacagacc 120

cctggacaag ggtttgagtg gatgggatgg gtcaaccctg acactggtgg cacaagatac	180
gcgcagaagt ttcagggctg ggtcacaatg accagggaca tgtccaacac cacagcctac	240
atggagctgc ccaggctgag agacgacgac acggccgtat attactgtgc gagagatcta	300
actggatttg atccttttga tatctggggc caggggaacco tggtcaccgt ctcgagtgga	360
ggcggcagtt caggtggagg tggctctggc ggtggcggaa gtgcacagtc tgtgctgact	420
cagccaccct cagtgtcagt ggccccagga aagacggcca cgattacctg tgggggaaac	480
aactttcgaa ataaaagagt acaactggtat cagcagagggc caggccaggc ccctgtcctg	540
gtcatctatt atgattcaga ccggccctca gggatccctg agcgattctc tggtcccgcc	600
tctgggaaca cggccaccct gaccatcagc agggctcgagg ccggggatga ggccgacttt	660
tactgtcagg tgtgggatct cttcaacgac aacggcgtgt tcggcggagg gaccaagctg	720
accgtcctag gtgcggccgc acat	744

<210> 233
 <211> 15
 <212> DNA
 <213> Homo sapiens

<400> 233	
gattactata ttcac	15

<210> 234
 <211> 51
 <212> DNA
 <213> Homo sapiens

<400> 234	
tgggtcaacc ctgacactgg tggcacaaga tacgcgcaga agtttcaggg c	51

<210> 235
 <211> 30
 <212> DNA
 <213> Homo sapiens

<400> 235	
gatctaactg gatttgatcc ttttgatata	30

<210> 236
 <211> 33
 <212> DNA
 <213> Homo sapiens

<400> 236	
gggggaaaca actttcgaaa taaaagagta cac	33

<210> 237
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 237
 tatgactcag accggcctc a

21

<210> 238
 <211> 33
 <212> DNA
 <213> Homo sapiens

<400> 238
 caggtgtggg atctcttcaa cgacaacggc gtg

33

<210> 239
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 239
 Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Thr Phe Ser Asp Tyr
 20 25 30

Tyr Ile His Trp Val Arg Gln Thr Pro Gly Gln Gly Phe Glu Trp Met
 35 40 45

Gly Trp Val Asn Pro Asp Thr Gly Gly Thr Arg Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Trp Val Thr Met Thr Arg Asp Met Ser Asn Thr Thr Ala Tyr
 65 70 75 80

Met Glu Leu Pro Arg Leu Arg Asp Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Leu Thr Gly Phe Asp Pro Phe Asp Ile Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

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<210> 240
<211> 109
<212> PRT
<213> Homo sapiens

<400> 240
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Lys
1 5 10 15
Thr Ala Thr Ile Thr Cys Gly Gly Asn Asn Phe Arg Asn Lys Arg Val
20 25 30
His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45
Tyr Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60
Arg Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80
Asp Glu Ala Asp Phe Tyr Cys Gln Val Trp Asp Phe Leu Thr Asp Ser
85 90 95
Gly Ser Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105

<210> 241
<211> 248
<212> PRT
<213> Homo sapiens

<400> 241
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Thr Phe Ser Asp Tyr
20 25 30
Tyr Ile His Trp Val Arg Gln Thr Pro Gly Gln Gly Phe Glu Trp Met
35 40 45
Gly Trp Val Asn Pro Asp Thr Gly Gly Thr Arg Tyr Ala Gln Lys Phe
50 55 60
Gln Gly Trp Val Thr Met Thr Arg Asp Met Ser Asn Thr Thr Ala Tyr
65 70 75 80

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Met Glu Leu Pro Arg Leu Arg Asp Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Leu Thr Gly Phe Asp Pro Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Ala Gln Ser Val Leu Thr Gln Pro Pro Ser
130 135 140

Val Ser Val Ala Pro Gly Lys Thr Ala Thr Ile Thr Cys Gly Gly Asn
145 150 155 160

Asn Phe Arg Asn Lys Arg Val His Trp Tyr Gln Gln Arg Pro Gly Gln
165 170 175

Ala Pro Val Leu Val Ile Tyr Tyr Asp Ser Asp Arg Pro Ser Gly Ile
180 185 190

Pro Glu Arg Phe Ser Gly Ser Arg Ser Gly Asn Thr Ala Thr Leu Thr
195 200 205

Ile Ser Arg Val Glu Ala Gly Asp Glu Ala Asp Phe Tyr Cys Gln Val
210 215 220

Trp Asp Phe Leu Thr Asp Ser Gly Ser Phe Gly Gly Gly Thr Lys Leu
225 230 235 240

Thr Val Leu Gly Ala Ala Ala His
245

<210> 242
<211> 5
<212> PRT
<213> Homo sapiens

<400> 242
Asp Tyr Tyr Ile His
1 5

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<210> 243
<211> 17
<212> PRT
<213> Homo sapiens

<400> 243
Trp Val Asn Pro Asp Thr Gly Gly Thr Arg Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 244
<211> 10
<212> PRT
<213> Homo sapiens

<400> 244
Asp Leu Thr Gly Phe Asp Pro Phe Asp Ile
1 5 10

<210> 245
<211> 11
<212> PRT
<213> Homo sapiens

<400> 245
Gly Gly Asn Asn Phe Arg Asn Lys Arg Val His
1 5 10

<210> 246
<211> 7
<212> PRT
<213> Homo sapiens

<400> 246
Tyr Asp Ser Asp Arg Pro Ser
1 5

<210> 247
<211> 11
<212> PRT
<213> Homo sapiens

<400> 247
Gln Val Trp Asp Phe Leu Thr Asp Ser Gly Ser
1 5 10

<210> 248
<211> 357
<212> DNA
<213> Homo sapiens

<400> 248
gaggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tctgtcagg cttctggata caccttcagc gattactata ttcaactgggt gcgacagacc 120
cctggacaag ggtttgagtg gatgggatgg gtcaaccctg acactgggtg cacaagatac 180
gcgcagaagt ttcagggctg ggtcacaatg accagggaca tgtccaacac cacagcctac 240
atggagctgc ccaggctgag agacgacgac acggccgtat attactgtgc gagagatcta 300
actggatttg atccttttga tatctggggc cagggaaacc tggtcaccgt ctctca 357

<210> 249
<211> 327
<212> DNA
<213> Homo sapiens

<400> 249
cagtctgtgc tgactcagcc accctcagtg tcagtggccc caggaaagac ggccacaatt 60
acctgtgggg gaaacaactt tcgaaataaa agagtacact ggtatcagca gaggccaggc 120
caggcgctg tcttggtcat ctattatgat tcagaccggc cctcagggat ccctgagcga 180
ttctctggct ccgctctgg gaacacggcc accctgacca tcagcagggg cgaggccggg 240
gatgaggccg acttttactg tcagggtgtgg gatttctca ccgactcggg gtcgttcggc 300
ggagggacca agctgaccgt cctaggt 327

<210> 250
<211> 744
<212> DNA
<213> Homo sapiens

<400> 250
gaagtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tctgtcagg cttctggata caccttcagc gattactata ttcaactgggt gcgacagacc 120
cctggacaag ggtttgagtg gatgggatgg gtcaaccctg acactgggtg cacaagatac 180
gcgcagaagt ttcagggctg ggtcacaatg accagggaca tgtccaacac cacagcctac 240
atggagctgc ccaggctgag agacgacgac acggccgtat attactgtgc gagagatcta 300
actggatttg atccttttga tatctggggc cagggaaacc tggtcaccgt ctgagtgga 360
ggcggcggtt caggcggagg tggctctggc ggtggcggaa gtgcacagtc tgtgctgact 420
cagccaccct cagtgtcagt ggccccagga aagacggcca caattacctg tgggggaaac 480
aactttcgaa ataaaagagt acactgggtat cagcagaggc caggccaggc gcctgtcctg 540

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gtcatctatt atgattcaga cgggcoctca gggatccctg agcgattctc tggetcccgc 600
tctgggaaca cggccaccct gaccatcagc agggctcgagg ccggggatga ggccgacttt 660
tactgtcagg tgtgggattt cctcacogac tcggggtcgt tcggcgagg gaccaagctg 720
accgtcctag gtgcggccgc acat 744

<210> 251
<211> 15
<212> DNA
<213> Homo sapiens

<400> 251
gattactata ttcac 15

<210> 252
<211> 51
<212> DNA
<213> Homo sapiens

<400> 252
tgggtcaacc ctgacactgg tggcacaaga tacgcgcaga agtttcaggg c 51

<210> 253
<211> 30
<212> DNA
<213> Homo sapiens

<400> 253
gatctaactg gatttgatcc ttttgatatc 30

<210> 254
<211> 33
<212> DNA
<213> Homo sapiens

<400> 254
gggggaaaca actttcgaaa taaaagagta cac 33

<210> 255
<211> 21
<212> DNA
<213> Homo sapiens

<400> 255
tatgattcag accggccctc a 21

<210> 256
<211> 33
<212> DNA
<213> Homo sapiens

<400> 256

caggtgtggg atttcctcac cgactcgggg tcg

33

<210> 257

<211> 119

<212> PRT

<213> Homo sapiens

<400> 257

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Thr Phe Ser Asp Tyr
 20 25 30

Tyr Ile His Trp Val Arg Gln Thr Pro Gly Gln Gly Phe Glu Trp Met
 35 40 45

Gly Trp Val Asn Pro Asp Thr Gly Gly Thr Arg Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Trp Val Thr Met Thr Arg Asp Met Ser Asn Thr Thr Ala Tyr
 65 70 75 80

Met Glu Leu Pro Arg Leu Arg Asp Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Leu Thr Gly Tyr Asp Tyr Tyr Asp Arg Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 258

<211> 108

<212> PRT

<213> Homo sapiens

<400> 258

Gln Ser Val Leu Thr Gln Pro Pro Ser Met Ser Val Ala Pro Gly Lys
 1 5 10 15

Thr Ala Thr Ile Thr Cys Gly Gly Asn Asn Phe Arg Asn Lys Arg Val
 20 25 30

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His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

Tyr Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Arg Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80

Asp Glu Ala Asp Phe Tyr Cys Gln Val Trp Asp Phe Leu Ala Asp Glu
85 90 95

Ala Met Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 259

<211> 262

<212> PRT

<213> Homo sapiens

<400> 259

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Thr Phe Ser Asp Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Thr Pro Gly Gln Gly Phe Glu Trp Met
35 40 45

Gly Trp Val Asn Pro Asp Thr Gly Gly Thr Arg Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Trp Val Thr Met Thr Arg Asp Met Ser Asn Thr Thr Ala Tyr
65 70 75 80

Met Glu Leu Pro Arg Leu Arg Asp Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Leu Thr Gly Tyr Asp Tyr Tyr Asp Arg Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

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Ser Gly Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Ala Gln Ser Val Leu Thr Gln Pro Pro Ser Met Ser
145 150 155 160

Val Ala Pro Gly Lys Thr Ala Thr Ile Thr Cys Gly Gly Asn Asn Phe
165 170 175

Arg Asn Lys Arg Val His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro
180 185 190

Val Leu Val Ile Tyr Tyr Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu
195 200 205

Arg Phe Ser Gly Ser Arg Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser
210 215 220

Arg Val Glu Ala Gly Asp Glu Ala Asp Phe Tyr Cys Gln Val Trp Asp
225 230 235 240

Phe Leu Ala Asp Glu Ala Met Phe Gly Gly Gly Thr Lys Leu Thr Val
245 250 255

Leu Gly Ala Ala Ala His
260

<210> 260
<211> 5
<212> PRT
<213> Homo sapiens

<400> 260
Asp Tyr Tyr Ile His
1 5

<210> 261
<211> 17
<212> PRT
<213> Homo sapiens

<400> 261
Trp Val Asn Pro Asp Thr Gly Gly Thr Arg Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 262
 <211> 10
 <212> PRT
 <213> Homo sapiens

<400> 262
 Asp Leu Thr Gly Tyr Asp Tyr Tyr Asp Arg
 1 5 10

<210> 263
 <211> 11
 <212> PRT
 <213> Homo sapiens

<400> 263
 Gly Gly Asn Asn Phe Arg Asn Lys Arg Val His
 1 5 10

<210> 264
 <211> 7
 <212> PRT
 <213> Homo sapiens

<400> 264
 Tyr Asp Ser Asp Arg Pro Ser
 1 5

<210> 265
 <211> 11
 <212> PRT
 <213> Homo sapiens

<400> 265
 Gln Val Trp Asp Phe Leu Ala Asp Glu Ala Met
 1 5 10

<210> 266
 <211> 357
 <212> DNA
 <213> Homo sapiens

<400> 266
 gaggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
 tctgtcagg cttctggata caccttcagc gattactata ttcactgggt gcgacagacc 120
 cctggacaag ggtttgagtg gatgggatgg gtcaaccctg acactgggtg cacaagatac 180
 ggcgagaagt ttcagggtg ggtcacatg accaggggaca tgtccaacac cacagcctac 240
 atggagctgc ccaggctgag agacgacgac acgggcggtat attactgtgc gagagatcta 300

actggatacg actactacga ccggtggggc caggggaaccc tggtcaccgt ctctca 357

<210> 267

<211> 327

<212> DNA

<213> Homo sapiens

<400> 267

cagtctgtgc tgactcagcc gccctcaatg tcagtggccc caggaaagac ggccacgatt 60

acctgtgggg gaaacaactt tcgaaataaa agagtacact ggtatcagca gaggccagggc 120

caggccccctg tccttggtcat ctattatgat tcagaccggc cctcagggat ccttgagcga 180

ttctctgggt cccgctctgg gaacacggcc accctgacca tcagcagggt cgaggccggg 240

gatgaggccg acttttactg tcaggtgtgg gatttcctcg ccgacgaggc gatgttcggc 300

ggagggacca agctgaccgt cctaggt 327

<210> 268

<211> 786

<212> DNA

<213> Homo sapiens

<400> 268

gaagtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgtcagg cttctggata caccttcagc gattactata ttcactgggt gcgacagacc 120

cctggacaag gggttgagtg gatgggatgg gtcaacctg acactgggtg cacaagatac 180

gcgcagaagt ttcagggtg ggtcacaatg accagggaca tgtccaacac cacagcctac 240

atggagctgc ccaggctgag agacgacgac acggccgtat attactgtgc gagagatcta 300

actggatacg actactacga ccggtggggc caggggaaccc tggtcaccgt ctcgagtggg 360

ggcggcggtt caggcgagg tggctctggc ggtggtggag gtggctctgg cgggtggcgg 420

ggtggctctg gcgggtggcg aagtgcacag tctgtgctga ctgagccgcc ctcaatgtca 480

gtggccccag gaaagacggc cacgattacc tgtgggggaa acaactttcg aaataaaaga 540

gtacactggt atcagcagag gccaggccag gccctgtcc tggtcattcta ttatgattca 600

gaccggccct cagggatccc tgagcgattc tctggctccc gctctgggaa cacggccacc 660

ctgaccatca gcagggtcga ggccggggat gaggccgact tttactgtca ggtgtgggat 720

ttcctcgccg acgaggcgat gttcggcgga gggaccaagc tgacogtcct aggtgcggcc 780

gcacat 786

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<211> 15
<212> DNA
<213> Homo sapiens

<400> 269
gattactata ttcac

15

<210> 270
<211> 51
<212> DNA
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<400> 270
tgggtcaacc ctgacactgg tggcacaaga tacgcgcaga agtttcaggg c

51

<210> 271
<211> 30
<212> DNA
<213> Homo sapiens

<400> 271
gatctaactg gatacgacta ctacgaccgg

30

<210> 272
<211> 33
<212> DNA
<213> Homo sapiens

<400> 272
gggggaaaca actttcgaaa taaaagagta cac

33

<210> 273
<211> 21
<212> DNA
<213> Homo sapiens

<400> 273
tatgattcag accggccctc a

21

<210> 274
<211> 33
<212> DNA
<213> Homo sapiens

<400> 274
cagggtgtggg atttcctcgc cgacgaggcg atg

33

<210> 275
<211> 119
<212> PRT
<213> Homo sapiens

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<400> 275

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Thr Phe Ser Asp Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Thr Pro Gly Gln Gly Phe Glu Trp Met
35 40 45

Gly Trp Val Asn Pro Asp Thr Gly Gly Thr Arg Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Trp Val Thr Met Thr Arg Asp Met Ser Asn Thr Thr Ala Tyr
65 70 75 80

Met Glu Leu Pro Gly Leu Arg Asp Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Leu Thr Gly Tyr Asp Gln Tyr Thr Ala Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 276

<211> 109

<212> PRT

<213> Homo sapiens

<400> 276

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Lys
1 5 10 15

Thr Ala Thr Ile Thr Cys Gly Gly Asn Asn Phe Arg Asn Lys Arg Val
20 25 30

His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

Tyr Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Arg Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80

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Asp Glu Ala Asp Phe Tyr Cys Ser Thr Phe Asp Pro Phe Thr Asp Arg
85 90 95

Pro Leu Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105

<210> 277

<211> 248

<212> PRT

<213> Homo sapiens

<400> 277

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Thr Phe Ser Asp Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Thr Pro Gly Gln Gly Phe Glu Trp Met
35 40 45

Gly Trp Val Asn Pro Asp Thr Gly Gly Thr Arg Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Trp Val Thr Met Thr Arg Asp Met Ser Asn Thr Thr Ala Tyr
65 70 75 80

Met Glu Leu Pro Gly Leu Arg Asp Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Leu Thr Gly Tyr Asp Gln Tyr Thr Ala Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Ala Gln Ser Val Leu Thr Gln Pro Pro Ser
130 135 140

Val Ser Val Ala Pro Gly Lys Thr Ala Thr Ile Thr Cys Gly Gly Asn
145 150 155 160

Asn Phe Arg Asn Lys Arg Val His Trp Tyr Gln Gln Arg Pro Gly Gln
165 170 175

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Ala Pro Val Leu Val Ile Tyr Tyr Asp Ser Asp Arg Pro Ser Gly Ile
180 185 190

Pro Glu Arg Phe Ser Gly Ser Arg Ser Gly Asn Thr Ala Thr Leu Thr
195 200 205

Ile Ser Arg Val Glu Ala Gly Asp Glu Ala Asp Phe Tyr Cys Ser Thr
210 215 220

Phe Asp Pro Phe Thr Asp Arg Pro Leu Phe Gly Gly Gly Thr Lys Leu
225 230 235 240

Thr Val Leu Gly Ala Ala Ala His
245

<210> 278
<211> 5
<212> PRT
<213> Homo sapiens

<400> 278
Asp Tyr Tyr Ile His
1 5

<210> 279
<211> 17
<212> PRT
<213> Homo sapiens

<400> 279
Trp Val Asn Pro Asp Thr Gly Gly Thr Arg Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 280
<211> 10
<212> PRT
<213> Homo sapiens

<400> 280
Asp Leu Thr Gly Tyr Asp Gln Tyr Thr Ala
1 5 10

<210> 281
 <211> 11
 <212> PRT
 <213> Homo sapiens

<400> 281
 Gly Gly Asn Asn Phe Arg Asn Lys Arg Val His
 1 5 10

<210> 282
 <211> 7
 <212> PRT
 <213> Homo sapiens

<400> 282
 Tyr Asp Ser Asp Arg Pro Ser
 1 5

<210> 283
 <211> 11
 <212> PRT
 <213> Homo sapiens

<400> 283
 Ser Thr Phe Asp Pro Phe Thr Asp Arg Pro Leu
 1 5 10

<210> 284
 <211> 357
 <212> DNA
 <213> Homo sapiens

<400> 284
 gaggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
 tcctgtcagg cttctggata caccttcagc gattactata ttactgggt gcgacagacc 120
 ccaggacaag ggttttgagt gatgggatgg gtcaacctg aacttgggtg cagcagatac 180
 gcgcagaagt ttcagggctg ggtcacaatg accagggaca tgtccaacac cacagcctac 240
 atggagctgc cggggctgag agacgacgac acggccgtat attactgtgc gagagatcta 300
 actgggtacg accagtacac ggcttggggc cagggaaacc tggtcaccgt ctctca 357

<210> 285
 <211> 327
 <212> DNA
 <213> Homo sapiens

<400> 285
 cagtctgtgc tgactcagcc accctcagtg tcagtggccc caggaaagac ggccacgatt 60
 acctgtgggg gaaacaactt tcgaaataaa agagtacact ggtatcagca gaggccaggc 120

caggccccctg	tccctggatcat	ctattatgat	tcagaccggc	cctcagggat	ccctgagcga	180
ttctctggct	cccgtctctgg	gaacacggcc	accctgacca	tcagcagggg	cgaggccggg	240
gatgagggcg	acttttactg	tagcaccttc	gaccccttca	ctgatcgccc	gctgttcggc	300
ggagggacca	agctgaccgt	cctaggt				327

<210> 286

<211> 744

<212> DNA

<213> Homo sapiens

<400> 286

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tccctgtcagg	cttctggata	caccttcagc	gattactata	ttcactgggt	gcgacagacc	120
ccaggacaag	ggtttgagtg	gatgggatgg	gtcaaccctg	acactgggtg	cacgagatac	180
gcgcagaagt	ttcagggctg	ggtcacaatg	accagggaca	tgtccaacac	cacagcctac	240
atggagctgc	ccgggctgag	agacgacgac	acggccgtat	attactgtgc	gagagatcta	300
actgggtacg	accagtacac	ggcctggggc	caggggaacc	tggtcacctg	ctcgagtggg	360
ggcggcggtt	caggcggagg	tggctctggc	ggtggcgga	gtgcacagtc	tgtgctgact	420
cagccaccct	cagtgtcagt	ggccccagga	aagacggcca	cgattacctg	tgggggaaac	480
aactttcgaa	ataaaagagt	acactgggtat	cagcagaggc	caggccaggc	ccctgtcctg	540
gtcatctatt	atgattcaga	ccggccctca	gggatccctg	agcgattctc	tggctcccgc	600
tctgggaaca	cgccaccctt	gaccatcagc	agggctcagg	ccggggatga	ggccgacttt	660
tactgtagca	ccttcgaccc	cttcactgat	cgtccgctgt	tcggcggagg	gaccaagctg	720
accgtcctag	gtgcggccgc	acat				744

<210> 287

<211> 15

<212> DNA

<213> Homo sapiens

<400> 287

gattactata	ttcac	15

<210> 288

<211> 51

<212> DNA

<213> Homo sapiens

<400> 288
 tgggtcaacc ctgacactgg tggcacgaga tacgcgcaga agtttcaggg c 51

<210> 289
 <211> 30
 <212> DNA
 <213> Homo sapiens

<400> 289
 gatctaactg ggtacgacca gtacacggcc 30

<210> 290
 <211> 33
 <212> DNA
 <213> Homo sapiens

<400> 290
 gggggaaaca actttcgaaa taaaagagta cac 33

<210> 291
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 291
 tatgattcag accggccctc a 21

<210> 292
 <211> 33
 <212> DNA
 <213> Homo sapiens

<400> 292
 agcaccttcg accccttcac tgatcgctccg ctg 33

<210> 293
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 293
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Lys Lys Pro Gly Ala Ser
 1 5 10 15

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr
 20 25 30

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val Gly
 35 40 45

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Trp Ile Asn Pro Tyr Thr Gly Gly Ala Phe Tyr Ala Gln Lys Phe Arg
50 55 60

Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Asn Thr Ala Tyr Met
65 70 75 80

Glu Leu Ser Arg Leu Gly Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Glu Pro Glu Arg Phe Gly Asp Ser Thr Gly Gln Val Trp Gly Arg
100 105 110

Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 294
<211> 113
<212> PRT
<213> Homo sapiens

<400> 294
Gln Ala Val Leu Thr Gln Pro Ser Ser Val Ser Gly Ala Pro Arg Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Gly Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Tyr His Trp Asp Lys Glu
85 90 95

Gln Ser Gly Tyr Val Phe Gly Thr Gly Thr Gln Leu Thr Val Leu Ser
100 105 110

Ala

98/206

<210> 295
<211> 249
<212> PRT
<213> Homo sapiens

<400> 295
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Lys Lys Pro Gly Ala Ser
1 5 10 15

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr
20 25 30

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val Gly
35 40 45

Trp Ile Asn Pro Tyr Thr Gly Gly Ala Phe Tyr Ala Gln Lys Phe Arg
50 55 60

Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Asn Thr Ala Tyr Met
65 70 75 80

Glu Leu Ser Arg Leu Gly Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Glu Pro Glu Arg Phe Gly Asp Ser Thr Gly Gln Val Trp Gly Arg
100 105 110

Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Ser Arg Ser Ala Gln Ala Val Leu Thr Gln Pro Ser
130 135 140

Ser Val Ser Gly Ala Pro Arg Gln Arg Val Thr Ile Ser Cys Thr Gly
145 150 155 160

Ser Ser Ser Asn Ile Gly Ala Gly Tyr Gly Val His Trp Tyr Gln Gln
165 170 175

Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Gly Asn Ser Asn Arg
180 185 190

Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser
195 200 205

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Ala Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr
210 215 220

Tyr Cys Tyr His Trp Asp Lys Glu Gln Ser Gly Tyr Val Phe Gly Thr
225 230 235 240

Gly Thr Gln Leu Thr Val Leu Ser Ala
245

<210> 296
<211> 5
<212> PRT
<213> Homo sapiens

<400> 296
Asp Tyr Tyr Met His
1 5

<210> 297
<211> 17
<212> PRT
<213> Homo sapiens

<400> 297
Trp Ile Asn Pro Tyr Thr Gly Gly Ala Phe Tyr Ala Gln Lys Phe Arg
1 5 10 15

Gly

<210> 298
<211> 12
<212> PRT
<213> Homo sapiens

<400> 298
Glu Pro Glu Arg Phe Gly Asp Ser Thr Gly Gln Val
1 5 10

<210> 299
<211> 14
<212> PRT
<213> Homo sapiens

<400> 299
Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Gly Val His
1 5 10

<210> 300
 <211> 7
 <212> PRT
 <213> Homo sapiens

<400> 300
 Gly Asn Ser Asn Arg Pro Ser
 1 5

<210> 301
 <211> 11
 <212> PRT
 <213> Homo sapiens

<400> 301
 Tyr His Trp Asp Lys Glu Gln Ser Gly Tyr Val
 1 5 10

<210> 302
 <211> 363
 <212> DNA
 <213> Homo sapiens

<400> 302
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 tcttgcaagg cttctggata caccttcacc gactactata tgcactgggt gcgacaggcc 120
 cctggacaag ggcttgagtg ggtgggatgg atcaaccctt atactgggtg cgcattctat 180
 gcacagaagt ttctggggcag ggtcacaatg accagggaca cgtccatcaa cacagcctac 240
 atggagctaa gcagactggg atctgacgac acggccgtgt attattgtgc gagagaacct 300
 gaaagattcg gcgactccac ggggcaggtc tggggccggg ggacaatggg caccgtctcg 360
 agt 363

<210> 303
 <211> 339
 <212> DNA
 <213> Homo sapiens

<400> 303
 cagggtgtgc tgactcagcc gtcttcagtg tctggggccc caaggcagag ggtcaccatc 60
 tcttgcaactg ggagcagctc caacatcggg gcagggttatg gtgtacactg gtaccaacag 120
 cttccaggaa cagcccccaa actcctcatc tatggtaaca gcaatcggcc ctgaggggtc 180
 cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
 cagggtgagg atgaggctga ttattactgc taccactggg acaaggagca gagtgggtat 300
 gtcttcggaa ctgggaccca gctcaccgtt ttaagtgcg 339

<210> 304
 <211> 750
 <212> DNA
 <213> Homo sapiens

<400> 304
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 tcttgcaagg cttctggata caccttcacc gactactata tgcactgggt gcgacaggcc 120
 cctggacaag ggcttgagtg ggtgggatgg atcaaccctt atactgggtg cgcattctat 180
 gcacagaagt ttcggggcag ggtcacaatg accagggaca cgtccatcaa cacagcctac 240
 atggagctaa gcagactggg atctgacgac acggcctgtg attattgtgc gagagaacct 300
 gaaagattcg gcgactccac ggggcaggtc tggggccggg ggacaatggg caccgtctcg 360
 agtgggggcg gcggttcagg cggaggtggc tctggcggtg gcagaagtgc acaggctgtg 420
 ctgactcagc cgtcctcagt gtctggggcc ccaaggcaga gggtcaccat ctctgcact 480
 gggagcagct ccaacatcgg ggcaggttat ggtgtacact ggtaccaaca gcttcagga 540
 acagccccc aactcctcat ctatggtaac agcaatcggc cctcaggggt ccctgaccga 600
 ttctctggct ccaagtctgg cacctcagcc tccctggcca tcaactgggt ccaggctgag 660
 gatgaggctg attattactg ctaccactgg gacaaggagc agagtgggta tgtcttcgga 720
 actgggaccc agctcacgt ttttaagtgcg 750

<210> 305
 <211> 15
 <212> DNA
 <213> Homo sapiens

<400> 305
 gactactata tgcac 15

<210> 306
 <211> 51
 <212> DNA
 <213> Homo sapiens

<400> 306
 tggatcaacc cttatactgg tggcgcatte tatgcacaga agtttcgggg c 51

<210> 307
 <211> 36
 <212> DNA
 <213> Homo sapiens

102/206

<400> 307
gaacctgaaa gattcggcga ctccacgggg caggtc 36

<210> 308
<211> 42
<212> DNA
<213> Homo sapiens

<400> 308
actgggagca gctccaacat cggggcaggt tatgggtgtac ac 42

<210> 309
<211> 21
<212> DNA
<213> Homo sapiens

<400> 309
ggtaacagca atcggccctc a 21

<210> 310
<211> 33
<212> DNA
<213> Homo sapiens

<400> 310
taccactggg acaaggagca gagtgggttat gtc 33

<210> 311
<211> 121
<212> PRT
<213> Homo sapiens

<400> 311
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Asn Pro Tyr Thr Gly Ser Ala Phe Tyr Ala Gln Lys Phe
50 55 60

Arg Gly Arg Ala Thr Met Thr Arg Asn Thr Ser Ile Asn Thr Ala Tyr
65 70 75 80

103/206

Met Glu Leu Ser Arg Leu Gly Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Pro Glu Lys Phe Gly Glu Ser Ser Gly Gln Leu Trp Gly
100 105 110

Arg Gly Thr Met Val Thr Ile Ser Ser
115 120

<210> 312
<211> 113
<212> PRT
<213> Homo sapiens

<400> 312
Gln Ala Val Leu Thr Gln Pro Ser Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Pro Gly
20 25 30

Tyr Gly Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Gly Asp Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Gly
85 90 95

Leu Ser Gly Tyr Val Phe Gly Thr Gly Thr Gln Leu Thr Val Leu Ser
100 105 110

Ala

<210> 313
<211> 250
<212> PRT
<213> Homo sapiens

<400> 313
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

104/206

Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Asn Pro Tyr Thr Gly Ser Ala Phe Tyr Ala Gln Lys Phe
50 55 60

Arg Gly Arg Ala Thr Met Thr Arg Asn Thr Ser Ile Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Gly Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Pro Glu Lys Phe Gly Glu Ser Ser Gly Gln Leu Trp Gly
100 105 110

Arg Gly Thr Met Val Thr Ile Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Ser Gly Ser Ala Gln Ala Val Leu Thr Gln Pro
130 135 140

Ser Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr
145 150 155 160

Gly Ser Ser Ser Asn Ile Gly Pro Gly Tyr Gly Val His Trp Tyr Gln
165 170 175

Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Gly Asp Ser Asn
180 185 190

Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr
195 200 205

Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp
210 215 220

Tyr Tyr Cys Gln Ser Tyr Asp Ser Gly Leu Ser Gly Tyr Val Phe Gly
225 230 235 240

105/206

Thr Gly Thr Gln Leu Thr Val Leu Ser Ala
245 250

<210> 314
<211> 5
<212> PRT
<213> Homo sapiens

<400> 314
Asp Tyr Tyr Met His
1 5

<210> 315
<211> 17
<212> PRT
<213> Homo sapiens

<400> 315
Trp Ile Asn Pro Tyr Thr Gly Ser Ala Phe Tyr Ala Gln Lys Phe Arg
1 5 10 15

Gly

<210> 316
<211> 12
<212> PRT
<213> Homo sapiens

<400> 316
Glu Pro Glu Lys Phe Gly Glu Ser Ser Gly Gln Leu
1 5 10

<210> 317
<211> 14
<212> PRT
<213> Homo sapiens

<400> 317
Thr Gly Ser Ser Ser Asn Ile Gly Pro Gly Tyr Gly Val His
1 5 10

<210> 318
<211> 7
<212> PRT
<213> Homo sapiens

<400> 318
Gly Asp Ser Asn Arg Pro Ser
1 5

<210> 319
 <211> 11
 <212> PRT
 <213> Homo sapiens

<400> 319
 Gln Ser Tyr Asp Ser Gly Leu Ser Gly Tyr Val
 1 5 10

<210> 320
 <211> 363
 <212> DNA
 <213> Homo sapiens

<400> 320
 gaagtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
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 cctggacaag ggcttgagtg ggtgggggtgg atcaaccctt atactggtag cgcattctat 180
 gcacagaagt ttctggggcag ggccacaatg accaggaaca cgtccatcaa cacagcctac 240
 atggagctga gcagactggg atctgacgac acggcctgtg attattgtgc gagagaacct 300
 gaaaaattcg gcgagtcag cgccagttg tggggccggg ggacaatggt caccatctcg 360
 agt 363

<210> 321
 <211> 339
 <212> DNA
 <213> Homo sapiens

<400> 321
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 cttccaggaa cagcccccaa actcctcatc tatgggtgaca gcaatcggcc ctccaggggtc 180
 cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
 caggccgagg atgaggctga ttattactgc cagtcctatg acagcggcct gagtggttat 300
 gtcttcggaa ctggggacca gctcaccgtt ttaagtgcg 339

<210> 322
 <211> 750
 <212> DNA
 <213> Homo sapiens

<400> 322
 gaagtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

107/206

tccctgtcagg cttctggata caccttcacc gactactata tgcactgggt gcgacaggcc 120
cctggacaag ggcttgagtg ggtgggggtg atcaaccctt atactggtag cgcattctat 180
gcacagaagt ttcggggcag ggccacaatg accaggaaca cgtccatcaa cacagcctac 240
atggagctga gcagactggg atctgacgac acggccgtgt attattgtgc gagagaacct 300
gaaaaattcg gcgagtccag cggccagttg tggggccggg ggacaatggg caccatctcg 360
agtggaggcg gcggttcagg cggaggtggc tctggcggtg gcggaagtgc acaggctgtg 420
ctgactcagc cgctctcagt gtctggggcc ccagggcaga gggtcaccat ctctgcact 480
gggagcagct ccaacatcgg ggcaggttat ggtgtacact ggtaccaaca gcttcagga 540
acagccccc aactcctcat ctatggtgac agcaatcggc cctcaggggt ccctgaccga 600
ttctctggct ccaagtctgg cacctcagcc tccctggcca tcaactgggt ccaggccgag 660
gatgaggctg attattactg ccagtcctat gacagcggcc tgagtgggta tgtcttcgga 720
actgggaccc agctcaccgt tttaagtgcg 750

<210> 323
<211> 15
<212> DNA
<213> Homo sapiens

<400> 323
gactactata tgcac 15

<210> 324
<211> 51
<212> DNA
<213> Homo sapiens

<400> 324
tggatcaacc cttatactgg tagcgcatc tatgcacaga agtttcggg c 51

<210> 325
<211> 36
<212> DNA
<213> Homo sapiens

<400> 325
gaacctgaaa aattcggcga gtccagcggc cagttg 36

<210> 326
<211> 42
<212> DNA
<213> Homo sapiens

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<400> 326
actgggagca gctccaacat cggggcaggt tatggtgtac ac 42

<210> 327
<211> 21
<212> DNA
<213> Homo sapiens

<400> 327
ggtgacagca atcggcctc a 21

<210> 328
<211> 33
<212> DNA
<213> Homo sapiens

<400> 328
cagtcctatg acagcggcct gattggttat gtc 33

<210> 329
<211> 121
<212> PRT
<213> Homo sapiens

<400> 329
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr His Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Asn Pro Tyr Thr Gly Gly Ala Phe Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Gly Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Pro Glu Lys Phe Asp Ser Pro Asn Ala Glu Ile Trp Gly
100 105 110

Arg Gly Thr Met Val Thr Ile Ser Ser
115 120

109/206

<210> 330
<211> 113
<212> PRT
<213> Homo sapiens

<400> 330
Gln Ala Val Leu Thr Gln Pro Ser Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Gly Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85 90 95

Leu Ser Gly Tyr Val Phe Gly Thr Gly Thr Gln Leu Thr Val Leu Ser
100 105 110

Ala

<210> 331
<211> 250
<212> PRT
<213> Homo sapiens

<400> 331
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr His Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

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Gly Trp Ile Asn Pro Tyr Thr Gly Gly Ala Phe Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Gly Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Pro Glu Lys Phe Asp Ser Pro Asn Ala Glu Ile Trp Gly
100 105 110

Arg Gly Thr Met Val Thr Ile Ser Ser Glu Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Ser Gly Ser Ala Gln Ala Val Leu Thr Gln Pro
130 135 140

Ser Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr
145 150 155 160

Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Gly Val His Trp Tyr Gln
165 170 175

Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Gly Asn Ser Asn
180 185 190

Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr
195 200 205

Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp
210 215 220

Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser Leu Ser Gly Tyr Val Phe Gly
225 230 235 240

Thr Gly Thr Gln Leu Thr Val Leu Ser Ala
245 250

<210> 332

<211> 5

<212> PRT

<213> Homo sapiens

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<400> 332
His Tyr Tyr Met His
1 5

<210> 333
<211> 17
<212> PRT
<213> Homo sapiens

<400> 333
Trp Ile Asn Pro Tyr Thr Gly Gly Ala Phe Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 334
<211> 12
<212> PRT
<213> Homo sapiens

<400> 334
Glu Pro Glu Lys Phe Asp Ser Pro Asn Ala Glu Ile
1 5 10

<210> 335
<211> 14
<212> PRT
<213> Homo sapiens

<400> 335
Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Gly Val His
1 5 10

<210> 336
<211> 7
<212> PRT
<213> Homo sapiens

<400> 336
Gly Asn Ser Asn Arg Pro Ser
1 5

<210> 337
<211> 11
<212> PRT
<213> Homo sapiens

<400> 337
Gln Ser Tyr Asp Ser Ser Leu Ser Gly Tyr Val
1 5 10

<210> 338
 <211> 363
 <212> DNA
 <213> Homo sapiens

<400> 338
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 tcttgcaagg cttctggata caccttcacc cactactata tgcactgggt gcgacaggcc 120
 cctggacaag ggcttgagtg ggtgggatgg atcaaccctt atactgggtg cgcattctat 180
 gcacagaagt ttcagggcag ggtcacaatg accagggaca cgtccatcaa cacagcctac 240
 atggagctga gcagactggg atctgacgac acggccgtgt attattgtgc gagagaacct 300
 gaaaaattcg actcgccgaa cgccgagatc tggggccggg ggacaatggt caccatctcg 360
 agt 363

<210> 339
 <211> 339
 <212> DNA
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<400> 339
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 tcttgcaactg ggagcagctc caacatcggg gcaggttatg gtgtacactg gtaccaacag 120
 cttccaggaa cagcccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc 180
 cctgaccgat tctctggctc caagtctggc acctcagcct ccttggccat cactgggtc 240
 caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggtat 300
 gtcttcggaa ccgggaccca gctcaccgtt ttaagtgcg 339

<210> 340
 <211> 750
 <212> DNA
 <213> Homo sapiens

<400> 340
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 tcttgcaagg cttctggata caccttcacc cactactata tgcactgggt gcgacaggcc 120
 cctggacaag ggcttgagtg ggtgggatgg atcaaccctt atactgggtg cgcattctat 180
 gcacagaagt ttcagggcag ggtcacaatg accagggaca cgtccatcaa cacagcctac 240
 atggagctga gcagactggg atctgacgac acggccgtgt attattgtgc gagagaacct 300
 gaaaaattcg actcgccgaa cgccgagatc tggggccggg ggacaatggt caccatctcg 360

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agtgaaggcg gcggttcagg cggaggtggc tctggcggtg gcggaagtgc acaggctgtg 420
ctgactcagc cgtcctcagt gtctggggcc ccagggcaga gggtcaccat ctctgcact 480
gggagcagct ccaacatcgg ggcaggttat ggtgtacact ggtaccaaca gcttcaggga 540
acagccccc aactcctcat ctatggtaac agcaatcggc cctcaggggt cctgaccga 600
ttctctggct ccaagtctgg cacctcagcc tccctggcca tcaactgggt ccaggctgag 660
gatgaggctg attattactg ccagtcctat gacagcagcc tgagtgggta tgtcttcgga 720
accgggaccc agctcacogt ttttaagtgcg 750

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<211> 15
<212> DNA
<213> Homo sapiens

<400> 341
cactactata tgcac 15

<210> 342
<211> 51
<212> DNA
<213> Homo sapiens

<400> 342
tggatcaacc cttatactgg tggcgcatte tatgcacaga agtttcaggg c 51

<210> 343
<211> 36
<212> DNA
<213> Homo sapiens

<400> 343
gaacctgaaa aattcgacte gccgaacgcc gagate 36

<210> 344
<211> 42
<212> DNA
<213> Homo sapiens

<400> 344
actgggagca gctccaacat cggggcaggt tatgggtgtac ac 42

<210> 345
<211> 21
<212> DNA
<213> Homo sapiens

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<400> 345
ggtaacagca atcgccctc a

21

<210> 346
<211> 33
<212> DNA
<213> Homo sapiens

<400> 346
cagtcctatg acagcagcct gagtgggttat gtc

33

<210> 347
<211> 121
<212> PRT
<213> Homo sapiens

<400> 347
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Asn Pro Tyr Thr Gly Ser Ala Phe Tyr Ala Gln Lys Phe
50 55 60

Arg Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Gly Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Pro Glu Lys Phe Asp Ser Asp Asp Ser Asp Val Trp Gly
100 105 110

Arg Gly Thr Met Val Thr Val Ser Gly
115 120

<210> 348
<211> 112
<212> PRT
<213> Homo sapiens

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<400> 348

Gln Ala Val Leu Thr Pro Pro Ser Val Ser Gly Ala Pro Gly Gln Arg
1 5 10 15

Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr
20 25 30

Gly Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Ile
35 40 45

Ile Tyr Gly Asp Ser Ser Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65 70 75 80

Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Asn Ser Leu
85 90 95

Ser Gly Tyr Val Phe Gly Thr Gly Thr Gln Leu Thr Val Leu Ser Ala
100 105 110

<210> 349

<211> 249

<212> PRT

<213> Homo sapiens

<400> 349

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Asn Pro Tyr Thr Gly Ser Ala Phe Tyr Ala Gln Lys Phe
50 55 60

Arg Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Gly Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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Ala Arg Glu Pro Glu Lys Phe Asp Ser Asp Asp Ser Asp Val Trp Gly
100 105 110

Arg Gly Thr Met Val Thr Val Ser Gly Gly Gly Gly Ser Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Ser Gly Ser Ala Gln Ala Val Leu Thr Pro Pro
130 135 140

Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly
145 150 155 160

Ser Ser Ser Asn Ile Gly Ala Gly Tyr Gly Val His Trp Tyr Gln Gln
165 170 175

Leu Pro Gly Thr Ala Pro Lys Leu Ile Ile Tyr Gly Asp Ser Ser Arg
180 185 190

Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser
195 200 205

Ala Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr
210 215 220

Tyr Cys Gln Ser Tyr Asp Asn Ser Leu Ser Gly Tyr Val Phe Gly Thr
225 230 235 240

Gly Thr Gln Leu Thr Val Leu Ser Ala .
245

<210> 350
<211> 5
<212> PRT
<213> Homo sapiens

<400> 350
Asn Tyr Tyr Met His
1 5

<210> 351
<211> 17
<212> PRT
<213> Homo sapiens

117/206

<400> 351

Trp Ile Asn Pro Tyr Thr Gly Ser Ala Phe Tyr Ala Gln Lys Phe Arg
1 5 10 15

Gly

<210> 352

<211> 12

<212> PRT

<213> Homo sapiens

<400> 352

Glu Pro Glu Lys Phe Asp Ser Asp Asp Ser Asp Val
1 5 10

<210> 353

<211> 14

<212> PRT

<213> Homo sapiens

<400> 353

Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Gly Val His
1 5 10

<210> 354

<211> 8

<212> PRT

<213> Homo sapiens

<400> 354

Gly Asp Ser Ser Arg Pro Ser Gly
1 5

<210> 355

<211> 11

<212> PRT

<213> Homo sapiens

<400> 355

Gln Ser Tyr Asp Asn Ser Leu Ser Gly Tyr Val
1 5 10

<210> 356

<211> 363

<212> DNA

<213> Homo sapiens

<400> 356

cagggttcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tctctgcaagg cttctgggata caccttcaac aactactata tgcactgggt gcgacaggcc 120

cctggacagg ggcttgagtg ggtgggatgg atcaaccctt atactggtag cgcattctat	180
gcacagaagt ttcggggcag ggttacaatg accagggaca cgtccatcaa cacagcctac	240
atggagctga gcagactggg atctgacgac acggccgtgt attattgtgc gagagaacct	300
gaaaaattcg actccgacga ctccgacgtc tggggccgcg ggacaatggg caccgtctcg	360
ggt	363

<210> 357
 <211> 339
 <212> DNA
 <213> Homo sapiens

<400> 357	
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tctgcactg ggagcagctc caacatcggg gcaggttatg gtgtacactg gtaccaacag	120
cttcaggaa cagccccaa actcatcatc tatggtgaca gcagtcggcc ctcaggggtc	180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc	240
caggctgagg atgaggctga ttattactgc cagtcctatg acaacagcct gagcggttat	300
gtcttcggaa ctgggaccca gctcaccgtt ttaagtgcg	339

<210> 358
 <211> 750
 <212> DNA
 <213> Homo sapiens

<400> 358	
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tcttgcaagg cttctggata caccttcacc aactactata tgcactgggt gcgacaggcc	120
cctggacagg ggcttgagtg ggtgggatgg atcaaccctt atactggtag cgcattctat	180
gcacagaagt ttcggggcag ggttacaatg accagggaca cgtccatcaa cacagcctac	240
atggagctga gcagactggg atctgacgac acggccgtgt attattgtgc gagagaacct	300
gaaaaattcg actccgacga ctccgacgtc tggggccgcg ggacaatggg caccgtctcg	360
ggtggaggcg gcagttcagg cggagggtggc tctggcggta gcggaagtgc acaggctgtg	420
ctgactcagc cgccctcagt gtctggggcc ccagggcaga gggtcaccat ctctgcact	480
gggagcagct ccaacatcgg ggcagggttat ggtgtacact ggtaccaaca gcttcaggga	540
acagccccca aactcatcat ctatggtgac agcagtcggc cctcaggggt ccctgaccga	600
ttctctggct ccaagtctgg cacctcagcc tcctggcca tcactgggct ccaggctgag	660

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gatgaggctg attattactg ccagtcctat gacaacagcc tgagcgggta tgtcttcgga 720
actgggaccc agctcacccg ttttaagtgcg 750

<210> 359
<211> 15
<212> DNA
<213> Homo sapiens

<400> 359
aactactata tgcac 15

<210> 360
<211> 51
<212> DNA
<213> Homo sapiens

<400> 360
tggatcaacc cttatactgg tagcgcattc tatgcacaga agtttcgggg c 51

<210> 361
<211> 36
<212> DNA
<213> Homo sapiens

<400> 361
gaacctgaaa aattcgactc cgacgactcc gacgtc 36

<210> 362
<211> 42
<212> DNA
<213> Homo sapiens

<400> 362
actgggagca gctccaacat cggggcaggt tatggtgtac ac 42

<210> 363
<211> 24
<212> DNA
<213> Homo sapiens

<400> 363
ggtgacagca gtcggccctc aggg 24

<210> 364
<211> 33
<212> DNA
<213> Homo sapiens

<400> 364
cagtcctatg acaacagcct gagcgggttat gtc 33

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<210> 365
<211> 119
<212> PRT
<213> Homo sapiens

<400> 365
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30
Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Ile Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Gly Leu Trp Val Trp Asp Pro Leu Asp Tyr Trp Gly Arg Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
115

<210> 366
<211> 108
<212> PRT
<213> Homo sapiens

<400> 366
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Gly Ile Tyr His Trp
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

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Tyr Lys Ala Ser Ser Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Asn Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 367

<211> 243

<212> PRT

<213> Homo sapiens

<400> 367

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Ile Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Leu Trp Val Trp Asp Pro Leu Asp Tyr Trp Gly Arg Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr
130 135 140

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Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145 150 155 160

Glu Gly Ile Tyr His Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
165 170 175

Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser Ser Leu Ala Ser Gly Val
180 185 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Tyr Ser Asn Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
225 230 235 240

Lys Arg Ala

<210> 368
<211> 5
<212> PRT
<213> Homo sapiens

<400> 368
Asp Tyr Tyr Met Ser
1 5

<210> 369
<211> 17
<212> PRT
<213> Homo sapiens

<400> 369
Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 370
<211> 10
<212> PRT
<213> Homo sapiens

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<400> 370

Gly Leu Trp Val Trp Asp Pro Leu Asp Tyr
1 5 10

<210> 371

<211> 11

<212> PRT

<213> Homo sapiens

<400> 371

Arg Ala Ser Glu Gly Ile Tyr His Trp Leu Ala
1 5 10

<210> 372

<211> 7

<212> PRT

<213> Homo sapiens

<400> 372

Lys Ala Ser Ser Leu Ala Ser
1 5

<210> 373

<211> 9

<212> PRT

<213> Homo sapiens

<400> 373

Gln Gln Tyr Ser Asn Tyr Pro Leu Thr
1 5

<210> 374

<211> 357

<212> DNA

<213> Homo sapiens

<400> 374

caagtgcagc	tggtggagtc	tgggggaggc	ttggtcaagc	ctggaggggc	cctgagactc	60
tcctgtgcag	cctctggatt	caccttcagt	gactactaca	tgagctggat	ccgccaggct	120
ccaggggaagg	ggctggagtg	ggtctcagct	attagtggta	gtggtggtag	cacatactac	180
gcagactccg	tgaagggccg	gatcaccatc	tccagagaca	acgccaagaa	ctcactgtat	240
ctgcaaata	acagcctgag	agctgaggac	acggccgtgt	attactgtgc	gagagggctt	300
tggggtttggg	atcctcttga	ctactggggc	agaggaaccc	tggtcacccg	ctcttca	357

<210> 375

<211> 324

<212> DNA

<213> Homo sapiens

<400> 375
gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgttggaga cagagtcacc 60
atcacctgcc gggccagtga gggatatttat cactgggttg cctgggtatca gcagaagcca 120
gggaaagccc ctaaactcct gatctataag gcctctagtt tagccagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagag ttcaactctca ccatcagcag cctgcagcct 240
gatgattttg caacttatta ctgccaacaa tatagtaatt atccgctcac ttccggcgga 300
gggaccaagg tggagatcaa acgt 324

<210> 376
<211> 729
<212> DNA
<213> Homo sapiens

<400> 376
caagtgcagc tgggtggagtc tgggggagge ttggtcaagc ctggaggggc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt gactactaca tgagctggat ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggttag cacatactac 180
gcagactccg tgaagggccg gatcaccatc tccagagaca acgccaagaa ctcaactgtat 240
ctgcaaatga acagcctgag agctgaggac acggccgtgt attactgtgc gagagggctt 300
tgggttttggg atcctcttga ctactggggc agaggaaccc tggtcaccgt ctcttcaggt 360
ggaggcggtt caggcggagg tggcagcggc ggtggcggat cggacatcca gatgaccag 420
tctccttcca ccctgtctgc atctgttggg gacagagtca ccatcacctg ccggggcagt 480
gagggtatct atcaactggtt ggcctgggtat cagcagaagc cagggaaagc ccctaaactc 540
ctgatctata aggctcttag ttttagccagt ggggtcccat caaggttcag cggcagtgga 600
tctgggacag atttcactct caccatcagc agcctgcagc ctgatgattt tgcaacttat 660
tactgccaac aatatagtaa ttatccgctc actttcggcg gagggaccaa ggtggagatc 720
aaacgtgctg 729

<210> 377
<211> 15
<212> DNA
<213> Homo sapiens

<400> 377
gactactaca tgagc 15

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<210> 378
<211> 51
<212> DNA
<213> Homo sapiens

<400> 378
gctattagtg gtagtggtgg tagcacatac tacgcagact ccgtgaaggg c 51

<210> 379
<211> 30
<212> DNA
<213> Homo sapiens

<400> 379
gggctttggg tttgggatcc ttttgactac 30

<210> 380
<211> 33
<212> DNA
<213> Homo sapiens

<400> 380
cgggccagtg aggggtattta tcaactggttg gcc 33

<210> 381
<211> 21
<212> DNA
<213> Homo sapiens

<400> 381
aaggcctcta gtttagccag t 21

<210> 382
<211> 27
<212> DNA
<213> Homo sapiens

<400> 382
caacaatata gtaattatcc gtcact 27

<210> 383
<211> 5
<212> PRT
<213> Homo sapiens

<400> 383
Ser Tyr Gly Ile Ser
1 5

126/206

<210> 384
<211> 108
<212> PRT
<213> Homo sapiens

<400> 384
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Gly Ile Tyr His Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Ser Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Asn Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 385
<211> 243
<212> PRT
<213> Homo sapiens

<400> 385
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Ser Ala Tyr Thr Gly Asn Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Gly Tyr Tyr Asp Ala Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr
130 135 140

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145 150 155 160

Glu Gly Ile Tyr His Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
165 170 175

Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser Ser Leu Ala Ser Gly Val
180 185 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
195 200 205

Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Tyr Ser Asn Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
225 230 235 240

Lys Arg Ala

<210> 386

<211> 5

<212> PRT

<213> Homo sapiens

<400> 386

Ser Tyr Gly Ile Ser

1

5

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<210> 387
<211> 17
<212> PRT
<213> Homo sapiens

<400> 387
Trp Ile Ser Ala Tyr Thr Gly Asn Thr Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 388
<211> 10
<212> PRT
<213> Homo sapiens

<400> 388
Asp Arg Gly Tyr Tyr Asp Ala Phe Asp Ile
1 5 10

<210> 389
<211> 11
<212> PRT
<213> Homo sapiens

<400> 389
Arg Ala Ser Glu Gly Ile Tyr His Trp Leu Ala
1 5 10

<210> 390
<211> 7
<212> PRT
<213> Homo sapiens

<400> 390
Lys Ala Ser Ser Leu Ala Ser
1 5

<210> 391
<211> 9
<212> PRT
<213> Homo sapiens

<400> 391
Gln Gln Tyr Ser Asn Tyr Pro Leu Thr
1 5

<210> 392
<211> 357
<212> DNA
<213> Homo sapiens

<400> 392

caggtgcagc	tggtgcagtc	tggagctgag	gtgaagaagc	ctggggcctc	agtgaaggtc	60
tcttgcaagg	cttctgggta	cacctttacc	agttatggta	tcagctgggt	gcgacaggcc	120
cctggacaag	ggcttgagtg	gatgggatgg	atcagcgctt	acactggtaa	cacaaactat	180
gcacagaagt	tccagggcag	agtcaccatg	accacagaca	catccacgag	cacagcctac	240
atggaactga	ggagcctgag	atctgacgac	acggccgtgt	attactgtgc	gagagatcgt	300
ggatactatg	atgcttttga	tatctggggc	caaggcaccc	tggtcacctg	ctcctca	357

<210> 393

<211> 324

<212> DNA

<213> Homo sapiens

<400> 393

gacatccaga	tgacccagtc	tccttccacc	ctgtctgcat	ctgttggaga	cagagtcacc	60
atcacctgcc	gggccagtg	gggtatttat	cactgggttg	cctgggtatca	gcagaagcca	120
gggaaagccc	ctaaactcct	gatctataag	gcctctagtt	tagccagtgg	gggtcccatca	180
aggttcagcg	gcagtggatc	tgggacagag	ttcactctca	ccatcagcag	cctgcagcct	240
gatgatattg	caacttatta	ctgccaacaa	tatagtaatt	atccgctcac	tttcggcgga	300
gggaccaagg	tggagatcaa	acgt				324

<210> 394

<211> 729

<212> DNA

<213> Homo sapiens

<400> 394

caggtgcagc	tggtgcagtc	tggagctgag	gtgaagaagc	ctggggcctc	agtgaaggtc	60
tcttgcaagg	cttctgggta	cacctttacc	agttatggta	tcagctgggt	gcgacaggcc	120
cctggacaag	ggcttgagtg	gatgggatgg	atcagcgctt	acactggtaa	cacaaactat	180
gcacagaagt	tccagggcag	agtcaccatg	accacagaca	catccacgag	cacagcctac	240
atggaactga	ggagcctgag	atctgacgac	acggccgtgt	attactgtgc	gagagatcgt	300
ggatactatg	atgcttttga	tatctggggc	caaggcaccc	tggtcacctg	ctcctcaggt	360
ggaggcggtt	caggcgagg	tggcagcggc	ggtggcggt	cggacatcca	gatgaccag	420
tctccttcca	ccctgtctgc	atctgttga	gacagagtca	ccatcacctg	ccggggcagt	480
gagggtat	atcactgggt	ggcctgggt	cagcagaagc	cagggaagc	ccctaaactc	540

130/206

ctgatctata aggcctctag tttagccagt ggggtcccat caagggtcag cggcagtgga 600
tctgggacag agttcactct caccatcagc agcctgcagc ctgatgattt tgcaacttat 660
tactgccaac aatatagtaa ttatccgctc actttcggcg gagggaccaa ggtggagatc 720
aaacgtgcg 729

<210> 395
<211> 15
<212> DNA
<213> Homo sapiens

<400> 395
agttatggta tcagc 15

<210> 396
<211> 51
<212> DNA
<213> Homo sapiens

<400> 396
tggatcagcg cttacactgg taacacaaac tatgcacaga agttccaggg c 51

<210> 397
<211> 30
<212> DNA
<213> Homo sapiens

<400> 397
gatcgtggat actatgatgc ttttgatata 30

<210> 398
<211> 33
<212> DNA
<213> Homo sapiens

<400> 398
cgggccagtg agggatttta tcactgggtg gcc 33

<210> 399
<211> 21
<212> DNA
<213> Homo sapiens

<400> 399
aaggcctcta gtttagccag t 21

<210> 400
<211> 27
<212> DNA
<213> Homo sapiens

131/206

<400> 400
caacaatata gtaattatcc gctcact

27

<210> 401
<211> 119
<212> PRT
<213> Homo sapiens

<400> 401
Gln Met Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Gly Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala His Ile Trp Tyr Asp Gly Ser Asn Glu Lys Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Met Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Thr Glu Gln His Trp Ile Thr Ala Phe Asp Ile Trp Gly Lys Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 402
<211> 111
<212> PRT
<213> Homo sapiens

<400> 402
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
20 25 30

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Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Met Ile Tyr Glu Gly Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Thr Thr Arg
85 90 95

Ser Thr Arg Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 403

<211> 246

<212> PRT

<213> Homo sapiens

<400> 403

Gln Met Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Gly Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala His Ile Trp Tyr Asp Gly Ser Asn Glu Lys Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Met Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Thr Glu Gln His Trp Ile Thr Ala Phe Asp Ile Trp Gly Lys Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Ala Gly Gly
115 120 125

133/206

Ser Gly Gly Gly Gly Ser Gln Ser Ala Leu Thr Gln Pro Ala Ser Val
130 135 140

Ser Gly Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser
145 150 155 160

Ser Asp Val Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln Gln His Pro
165 170 175

Gly Lys Ala Pro Lys Leu Met Ile Tyr Glu Gly Ser Lys Arg Pro Ser
180 185 190

Gly Val Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser
195 200 205

Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
210 215 220

Ser Ser Tyr Thr Thr Arg Ser Thr Arg Val Phe Gly Gly Gly Thr Lys
225 230 235 240

Leu Thr Val Leu Gly Ala
245

<210> 404
<211> 5
<212> PRT
<213> Homo sapiens

<400> 404
Asn Tyr Gly Met Tyr
1 5

<210> 405
<211> 17
<212> PRT
<213> Homo sapiens

<400> 405
His Ile Trp Tyr Asp Gly Ser Asn Glu Lys Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 406
 <211> 10
 <212> PRT
 <213> Homo sapiens

<400> 406
 Glu Gln His Trp Ile Thr Ala Phe Asp Ile
 1 5 10

<210> 407
 <211> 14
 <212> PRT
 <213> Homo sapiens

<400> 407
 Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr Asn Tyr Val Ser
 1 5 10

<210> 408
 <211> 7
 <212> PRT
 <213> Homo sapiens

<400> 408
 Glu Gly Ser Lys Arg Pro Ser
 1 5

<210> 409
 <211> 10
 <212> PRT
 <213> Homo sapiens

<400> 409
 Ser Ser Tyr Thr Thr Arg Ser Thr Arg Val
 1 5 10

<210> 410
 <211> 357
 <212> DNA
 <213> Homo sapiens

<400> 410
 cagatgcagc tgggtggagtc tggggggaggc gtggtccagc ctgggaggtc cctgagactc 60
 tctgtgagc cctctggatt caccttcagt aactatggca tgtactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg ggtggcacat atttggatg atggaagtaa tgaaaagtat 180
 gcagactccg tgaagggccg aatgaccgtc tccagagaca attccaagaa caggttgat 240
 ttgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gacagagcaa 300
 cactggatta ctgcttttga tatctggggc aaaggaaccc tggtcaccgt ctctca 357

<210> 411
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 411
 cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc 60
 tcttgactg gaaccagcag tgacgttggt gggtataact atgtctcctg gtaccaacaa 120
 caccagggca aagcccccaa actcatgatt tatgagggca gtaagcggcc ctgaggggtt 180
 tctaategct tctctggctc caagtctggc aacacggcct cctgacaat ctctgggctc 240
 caggctgagg acgaggtctga ttactactgc agctcatata caaccaggag cactcgagtt 300
 ttggcgaggag ggaccaagct gaccgtccta ggt 333

<210> 412
 <211> 738
 <212> DNA
 <213> Homo sapiens

<400> 412
 cagatgcagc tgggtggagtc tgggggaggc gtgggtccagc ctgggaggtc cctgagactc 60
 tcctgtgcag cctctggatt caccttcagt aactatggca tgtactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg ggtggcacat atttggtatg atggaagtaa tgaaaagtat 180
 gcagactccg tgaagggccg aatgaccgtc tccagagaca attccaagaa caggttgtat 240
 ttgcaaatga acagcctgag agcggaggac acggtctgtt attactgtgc gacagagcaa 300
 cactggatta ctgcttttga tatctggggc aaaggcaccc tggtcaccgt ctctcaggt 360
 ggagggcggtt caggcgagcagg tggcagcggc ggtggcggat cacagtctgc gctgactcag 420
 cctgcctccg tgtctgggtc tcttgacag tcgataacca tctcctgcac tgggaaccagc 480
 agtgacgttg gtggttataa ctatgtctcc tgggtaccaac aacaccagg caaagcccc 540
 aaactcatga tttatgaggg cagtaagcgg ccctcagggg tttctaateg cttctctggc 600
 tccaagtctg gcaacacggc ctccctgaca atctctgggc tccaggctga ggacgaggct 660
 gattattact gcagctcata tacaaccagg agcactcgag ttttcggcgg agggaccaag 720
 ctgaccgtcc taggtgag 738

<210> 413
 <211> 15
 <212> DNA
 <213> Homo sapiens

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<400> 413
aactatggca tgtac 15

<210> 414
<211> 51
<212> DNA
<213> Homo sapiens

<400> 414
catatttggt atgatggaag taatgaaaag tatgcagact ccgtgaaggg c 51

<210> 415
<211> 30
<212> DNA
<213> Homo sapiens

<400> 415
gagcaacact ggattactgc ttttgatata 30

<210> 416
<211> 42
<212> DNA
<213> Homo sapiens

<400> 416
actggaacca gcagtgcagt tgggtggttat aactatgtct cc 42

<210> 417
<211> 21
<212> DNA
<213> Homo sapiens

<400> 417
gagggcagta agcggccctc a 21

<210> 418
<211> 30
<212> DNA
<213> Homo sapiens

<400> 418
agctcatata caaccaggag cactcgagtt 30

<210> 419
<211> 121
<212> PRT
<213> Homo sapiens

<400> 419
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly
1 5 10 15

137/206

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Val Asn Trp Asn Gly Gly Thr Arg Asp Tyr Ala Ala Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr His Cys
85 90 95

Ala Arg Gly Trp Tyr Ser Gly Ser Phe Tyr Tyr Phe Gly Tyr Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 420

<211> 111

<212> PRT

<213> Homo sapiens

<400> 420

Gln Ala Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

Ser Ile Thr Ile Ser Cys Thr Gly Ala Ser Gly Asp Val Gly Ala Tyr
20 25 30

Asn Phe Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Ile Ile Tyr Asp Val Asn Lys Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Thr Ser Thr
85 90 95

138/206

Phe Ser Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 421

<211> 249

<212> PRT

<213> Homo sapiens

<400> 421

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Val Asn Trp Asn Gly Gly Thr Arg Asp Tyr Ala Ala Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr His Cys
85 90 95

Ala Arg Gly Trp Tyr Ser Gly Ser Phe Tyr Tyr Phe Gly Tyr Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Ala Ala Leu Thr Gln Pro
130 135 140

Ala Ser Val Ser Gly Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr
145 150 155 160

Gly Ala Ser Gly Asp Val Gly Ala Tyr Asn Phe Val Ser Trp Tyr Gln
165 170 175

Gln His Pro Gly Lys Ala Pro Lys Leu Ile Ile Tyr Asp Val Asn Lys
180 185 190

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Arg Pro Ser Gly Val Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn
195 200 205

Thr Ala Ser Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp
210 215 220

Tyr Tyr Cys Ser Ser Tyr Thr Ser Thr Phe Ser Val Val Phe Gly Gly
225 230 235 240

Gly Thr Lys Leu Thr Val Leu Gly Ala
245

<210> 422
<211> 5
<212> PRT
<213> Homo sapiens

<400> 422
Asp Tyr Gly Met Asn
1 5

<210> 423
<211> 17
<212> PRT
<213> Homo sapiens

<400> 423
Gly Val Asn Trp Asn Gly Gly Thr Arg Asp Tyr Ala Ala Ser Val Lys
1 5 10 15

Gly

<210> 424
<211> 12
<212> PRT
<213> Homo sapiens

<400> 424
Gly Trp Tyr Ser Gly Ser Phe Tyr Tyr Phe Gly Tyr
1 5 10

<210> 425
<211> 14
<212> PRT
<213> Homo sapiens

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<400> 425

Thr Gly Ala Ser Gly Asp Val Gly Ala Tyr Asn Phe Val Ser
1 5 10

<210> 426

<211> 7

<212> PRT

<213> Homo sapiens

<400> 426

Asp Val Asn Lys Arg Pro Ser
1 5

<210> 427

<211> 10

<212> PRT

<213> Homo sapiens

<400> 427

Ser Ser Tyr Thr Ser Thr Phe Ser Val Val
1 5 10

<210> 428

<211> 363

<212> DNA

<213> Homo sapiens

<400> 428

gagggtgcagc tgggtggagag cggggggaggt gtggtacggc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttgac gattatggca tgaactgggt ccgccaagct 120
ccagggaagg ggctggagtg ggtctctggt gttaattgga atggtggtac cagagattat 180
gcagcctccg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaatga acagtctgag agccgaggac acggccttgt atcactgtgc gagaggatgg 300
tatagtggga gcttctacta ctttggttac tggggccgag gaaccctggt caccgtctcc 360
tca 363

<210> 429

<211> 333

<212> DNA

<213> Homo sapiens

<400> 429

caggctgcgc tgactcagcc ggcctccgtg tctgggtctc ctggacagtc gatcaccatc 60
tcctgcactg gagccagcgg tgacgttggt gcttataact ttgtctcctg gtaccaacaa 120
caccaggga aagcccccaa actcataatt tatgatgtca ataagcgcc ctcagggggt 180

141/206

tctaatacgct tctctggctc caagtctggc aacacggcct ccctgacat ctctgggctc	240
caggccgagg acgaggctga ttattactgc agctcatata caagcacctt ctctgtggta	300
tttggcggag ggaccaagct gaccgtccta ggt	333

<210> 430
 <211> 747
 <212> DNA
 <213> Homo sapiens

<400> 430	
gaggtgcagc tgggtggagtc cgggggagggt gtggtacggc ctgggggggtc cctgagactc	60
tcctgtgcag cctctggatt cacctttgac gattatggca tgaactgggt ccgccaagct	120
ccaggggaagg ggctggagtg ggtctctggt gttaattgga atgggtggtac cagagattat	180
gcagcctccg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat	240
ctgcaaatga acagtctgag agccgaggac acggccttgt atcactgtgc gagaggatgg	300
tatagtggga gcttctacta ctttggctac tggggccgag gaaccctggt caccgtctcg	360
agtggaggcg gcggttcagg cggagggtggc tctggcggtg gcggaagtgc acaggctgcg	420
ctgactcagc cggcctccgt gtctgggtct cctggacagt cgatcaccat ctctgcact	480
ggagccagcg gtgacgttgg tgcttataac tttgtctcct ggtaccaaca acacccaggc	540
aaagcccca aactcataat ttatgatgtc aataagcggc cctcaggggt ttctaatagc	600
ttctctggct ccaagtctgg caacacggcc tccctgacca tctctgggct ccaggccgag	660
gacgaggctg attattactg cagctcatat acaagcacct tctctgtggt atttggcgga	720
gggaccaagc tcaccgtcct aggtgcg	747

<210> 431
 <211> 15
 <212> DNA
 <213> Homo sapiens

<400> 431	
gattatggca tgaac	15

<210> 432
 <211> 51
 <212> DNA
 <213> Homo sapiens

<400> 432	
ggtgttaatt ggaatggtgg taccagagat tatgcagcct ccgtgaaggg c	51

142/206

<210> 433
<211> 36
<212> DNA
<213> Homo sapiens

<400> 433
ggatgggtata gtgggagctt ctactacttt ggctac

36

<210> 434
<211> 42
<212> DNA
<213> Homo sapiens

<400> 434
actggagcca gcggtgacgt tgggtgcttat aactttgtct cc

42

<210> 435
<211> 21
<212> DNA
<213> Homo sapiens

<400> 435
gatgtcaata agcggccctc a

21

<210> 436
<211> 30
<212> DNA
<213> Homo sapiens

<400> 436
agctcatata caagcacctt ctctgtggtgta

30

<210> 437
<211> 119
<212> PRT
<213> Homo sapiens

<400> 437
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asp Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Val Asn Pro Asp Thr Gly Gly Thr Arg Tyr Ala Gln Lys Phe
50 55 60

143/206

Gln Gly Arg Val Thr Met Thr Arg Asp Met Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Leu Thr Gly Phe Asp Pro Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 438
<211> 109
<212> PRT
<213> Homo sapiens

<400> 438
Ser Ser Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Lys
1 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Phe Arg Asn Lys Arg Val
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

Tyr Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Arg Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Thr Asp Arg
85 90 95

Pro Leu Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105

<210> 439
<211> 245
<212> PRT
<213> Homo sapiens

<400> 439
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

144/206

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asp Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Val Asn Pro Asp Thr Gly Gly Thr Arg Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Met Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Leu Thr Gly Phe Asp Pro Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Ala Ser Ser Val Leu Thr Gln Pro Pro Ser
130 135 140

Val Ser Val Ala Pro Gly Lys Thr Ala Arg Ile Thr Cys Gly Gly Asn
145 150 155 160

Asn Phe Arg Asn Lys Arg Val His Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ala Pro Val Leu Val Ile Tyr Tyr Asp Ser Asp Arg Pro Ser Gly Ile
180 185 190

Pro Glu Arg Phe Ser Gly Ser Arg Ser Gly Asn Thr Ala Thr Leu Thr
195 200 205

Ile Ser Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val
210 215 220

Trp Asp Ser Ser Thr Asp Arg Pro Leu Phe Gly Gly Gly Thr Lys Leu
225 230 235 240

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Thr Val Leu Gly Ala
245

<210> 440
<211> 5
<212> PRT
<213> Homo sapiens

<400> 440
Asp Tyr Tyr Ile His
1 5

<210> 441
<211> 17
<212> PRT
<213> Homo sapiens

<400> 441
Trp Val Asn Pro Asp Thr Gly Gly Thr Arg Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 442
<211> 10
<212> PRT
<213> Homo sapiens

<400> 442
Asp Leu Thr Gly Phe Asp Pro Phe Asp Ile
1 5 10

<210> 443
<211> 11
<212> PRT
<213> Homo sapiens

<400> 443
Gly Gly Asn Asn Phe Arg Asn Lys Arg Val His
1 5 10

<210> 444
<211> 7
<212> PRT
<213> Homo sapiens

<400> 444
Tyr Asp Ser Asp Arg Pro Ser
1 5

<210> 445
 <211> 11
 <212> PRT
 <213> Homo sapiens

<400> 445
 Gln Val Trp Asp Ser Ser Thr Asp Arg Pro Leu
 1 5 10

<210> 446
 <211> 357
 <212> DNA
 <213> Homo sapiens

<400> 446
 caggtccagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
 tcctgtaagg cttctggata caccttcagc gattactata ttcactgggt gcgacaggcc 120
 cctggacaag gggttgagtg gatgggatgg gtcaaccctg aactgggtgg cacaagatac 180
 gcgcagaagt ttcagggccg ggtcacaatg accagggaca tgtccatctc cacagcctac 240
 atggagctgt ccaggctgag aagcgacgac acggccgtat attactgtgc gagagatcta 300
 actggatttg atccttttga tatctggggc caggggaacc tggtcaccgt ctccctca 357

<210> 447
 <211> 327
 <212> DNA
 <213> Homo sapiens

<400> 447
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 acctgtgggg gaaacaactt tcgaaataaa agagtacact ggtatcagca gaagccaggc 120
 caggcccttg tcctggatcat ctattatgat tcagaccggc cctcagggat ccctgagcga 180
 ttctctggct cccgctctgg gaacacggcc accctgacca tcagcagggt cgaggccggg 240
 gatgaggccg actattactg tcagggtgtgg gatagtagta ctgatcgtec gctgttcggc 300
 ggagggacca agctgaccgt cctaggt 327

<210> 448
 <211> 735
 <212> DNA
 <213> Homo sapiens

<400> 448
 caagtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
 tcctgtaagg cttctggata caccttcagc gattactata ttcactgggt gcgacaggcc 120

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cctggacaag ggttggagtg gatgggatgg gtcaaccctg acactgggtg cacaagatac	180
gcgcagaagt ttcagggccg ggtcacaaatg accagggaca tgtccatctc cacagcctac	240
atggagctgt ccaggctgag aagcgacgac acggccgtat attactgtgc gagagatcta	300
actggatttg atccttttga tatctggggc cagggaaaccc tggtcaccgt ctcgagtggg	360
ggcggcggtt cagggcgagg tggctctggc ggtggcgga gtgcacgtc tgtgtgact	420
cagccaccct cagtgtcagt ggccccagga aagacggccc gcattacctg tgggggaaac	480
aactttcgaa ataaaagagt acactgggtat cagcagaagc cagggcaggc ccctgtcctg	540
gtcatctatt atgattcaga ccggccctca gggatccctg agcgattctc tgggtcccgc	600
tctgggaaca cggccaccct gaccatcagc agggctcagg ccggggatga ggccgactat	660
tactgtcagg tgtgggatag tagtactgat cgtccgctgt tcggcggagg gaccaagctg	720
accgtcctag gtgcg	735

<210> 449
 <211> 15
 <212> DNA
 <213> Homo sapiens

<400> 449 gattactata ttcac	15

<210> 450
 <211> 51
 <212> DNA
 <213> Homo sapiens

<400> 450 tgggtcaacc ctgacactgg tggcacaaga tacgcgaga agtttcaggg c	51

<210> 451
 <211> 30
 <212> DNA
 <213> Homo sapiens

<400> 451 gatctaactg gatttgatcc ttttgatata	30

<210> 452
 <211> 33
 <212> DNA
 <213> Homo sapiens

<400> 452 gggggaaaca actttcgaaa taaaagagta cac	33

<210> 453
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 453
 tatgattcag accggccctc a

21

<210> 454
 <211> 33
 <212> DNA
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<400> 454
 caggtgtggg atagtagtac tgatcgtccg ctg

33

<210> 455
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 455
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45

Gly Trp Ile Asn Pro Tyr Thr Gly Gly Ala Phe Tyr Ala Gln Lys Phe
 50 55 60

Arg Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Glu Pro Glu Lys Phe Asp Phe Trp Gly Gly Asp Asn Trp Gly
 100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser
 115 120

149/206

<210> 456
<211> 112
<212> PRT
<213> Homo sapiens

<400> 456
Gln Ala Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Gly Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85 90 95

Leu Ser Gly Tyr Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu Gly
100 105 110

<210> 457
<211> 250
<212> PRT
<213> Homo sapiens

<400> 457
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Asn Pro Tyr Thr Gly Gly Ala Phe Tyr Ala Gln Lys Phe
50 55 60

Arg Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

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Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Pro Glu Lys Phe Asp Phe Trp Gly Gly Asp Asn Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Ala Val Leu Thr Gln Pro
130 135 140

Pro Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr
145 150 155 160

Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Gly Val His Trp Tyr Gln
165 170 175

Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Gly Asn Ser Asn
180 185 190

Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr
195 200 205

Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp
210 215 220

Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser Leu Ser Gly Tyr Val Phe Gly
225 230 235 240

Gly Gly Thr Gln Leu Thr Val Leu Ser Ala
245 250

<210> 458

<211> 5

<212> PRT

<213> Homo sapiens

<400> 458

Asp Tyr Tyr Met His

1

5

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<210> 459
<211> 17
<212> PRT
<213> Homo sapiens

<400> 459
Trp Ile Asn Pro Tyr Thr Gly Gly Ala Phe Tyr Ala Gln Lys Phe Arg
1 5 10 15

Gly

<210> 460
<211> 12
<212> PRT
<213> Homo sapiens

<400> 460
Glu Pro Glu Lys Phe Asp Phe Trp Gly Gly Asp Asn
1 5 10

<210> 461
<211> 14
<212> PRT
<213> Homo sapiens

<400> 461
Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Gly Val His
1 5 10

<210> 462
<211> 7
<212> PRT
<213> Homo sapiens

<400> 462
Gly Asn Ser Asn Arg Pro Ser
1 5

<210> 463
<211> 11
<212> PRT
<213> Homo sapiens

<400> 463
Gln Ser Tyr Asp Ser Ser Leu Ser Gly Tyr Val
1 5 10

<210> 464
<211> 363
<212> DNA
<213> Homo sapiens

<400> 464

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caggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc      60
tcttgcaagg cttctggata caccttcacc gactactata tgcactgggt gcgacaggcc      120
cctggacaag ggcttgagtg ggtgggatgg atcaaccctt atactgggtg cgcattctat      180
gcacagaagt ttcggggcag ggtcacaatg accagggaca cgtccatcag cacagcctac      240
atggagctga gcagactgag atctgacgac acggccgtgt attattgtgc gagagaacct      300
gaaaaattcg atttttgggg ggggtgacaac tggggccggg ggacattggg caccgtctcc      360
tca                                     363

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<210> 465

<211> 336

<212> DNA

<213> Homo sapiens

<400> 465

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caggctgtgc tgactcagcc gccgtcagtg tctggggccc cagggcagag ggtcaccatc      60
tcttgacttg ggagcagctc caacatcggg gcaggttatg gtgtacactg gtaccaacag      120
cttcaggaa cagcccccaa actcctcacc tatggtaaca gcaatcggcc ctcaggggtc      180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc      240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttat      300
gtcttcggag gtgggaccca gctcacctgc ctaggt                                     336

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<210> 466

<211> 750

<212> DNA

<213> Homo sapiens

<400> 466

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tcttgcaagg cttctggata caccttcacc gactactata tgcactgggt gcgacaggcc      120
cctggacaag ggcttgagtg ggtgggatgg atcaaccctt atactgggtg cgcattctat      180
gcacagaagt ttcggggcag ggtcacaatg accagggaca cgtccatcag cacagcctac      240
atggagctga gcagactgag atctgacgac acggccgtgt attattgtgc gagagaacct      300
gaaaaattcg atttttgggg ggggtgacaac tggggccggg ggacattggg caccgtctcg      360
agtggaggcg gcggttcagg cggaggtggc tctggcggtg gcggaagtgc acaggctgtg      420
ctgactcagc cgccgtcagt gtctggggcc ccagggcaga gggtcacat ctcctgcact      480

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gggagcagct ccaacatcgg ggcagggttat ggtgtacact ggtaccaaca gcttccagga 540
acagccccc aactcctcat ctatggtaac agcaatcggc cctcaggggt ccctgaccga 600
ttctctgggt ccaagtctgg cacctcagcc tccctggcca tcaactgggt ccaggetgag 660
gatgaggctg attattactg ccagtcctat gacagcagcc tgagtgggta tgtcttcgga 720
ggtgggaccc agctcacggt ttttaagtgcg 750

<210> 467
<211> 15
<212> DNA
<213> Homo sapiens

<400> 467
gactactata tgcac 15

<210> 468
<211> 51
<212> DNA
<213> Homo sapiens

<400> 468
tggatcaacc cttatactgg tggcgcatto tatgcacaga agtttcgggg c 51

<210> 469
<211> 36
<212> DNA
<213> Homo sapiens

<400> 469
gaacctgaaa aattcgattt ttgggggggt gacaac 36

<210> 470
<211> 42
<212> DNA
<213> Homo sapiens

<400> 470
actgggagca gctccaacat cggggcaggt tatgggtgtac ac 42

<210> 471
<211> 21
<212> DNA
<213> Homo sapiens

<400> 471
ggtaacagca atcgccctc a 21

154/206

<210> 472
<211> 33
<212> DNA
<213> Homo sapiens

<400> 472
cagtcctatg acagcagcct gagtgggttat gtc

33

<210> 473
<211> 119
<212> PRT
<213> Homo sapiens

<400> 473
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Val Ser Ala Tyr Thr Gly Asn Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Gly Tyr Tyr Asp Ala Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 474
<211> 108
<212> PRT
<213> Homo sapiens

<400> 474
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Gly Ile Tyr His Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Ser Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Met Gly Glu Tyr Asn Ala
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 475

<211> 242

<212> PRT

<213> Homo sapiens

<400> 475

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Val Ser Ala Tyr Thr Gly Asn Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Gly Tyr Tyr Asp Ala Phe Asp Ile Trp Gly Gln Gly
100 105 110

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Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr
130 135 140

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145 150 155 160

Glu Gly Ile Tyr His Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
165 170 175

Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser Ser Leu Ala Ser Gly Val
180 185 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
195 200 205

Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Met Gly Glu Tyr Asn Ala Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
225 230 235 240

Lys Arg

<210> 476
<211> 5
<212> PRT
<213> Homo sapiens

<400> 476
Ser Tyr Gly Ile Ser
1 5

<210> 477
<211> 17
<212> PRT
<213> Homo sapiens

<400> 477
Trp Val Ser Ala Tyr Thr Gly Asn Thr Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

157/206

<210> 478
<211> 10
<212> PRT
<213> Homo sapiens

<400> 478
Asp Arg Gly Tyr Tyr Asp Ala Phe Asp Ile
1 5 10

<210> 479
<211> 11
<212> PRT
<213> Homo sapiens

<400> 479
Arg Ala Ser Glu Gly Ile Tyr His Trp Leu Ala
1 5 10

<210> 480
<211> 7
<212> PRT
<213> Homo sapiens

<400> 480
Lys Ala Ser Ser Leu Ala Ser
1 5

<210> 481
<211> 9
<212> PRT
<213> Homo sapiens

<400> 481
Gln Gln Met Gly Glu Tyr Asn Ala Thr
1 5

<210> 482
<211> 357
<212> DNA
<213> Homo sapiens

<400> 482
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tcctgcaagg cttctgggta cacctttacc agttatggta tcagctgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggatgg gtcagcgctt acaactggtaa cacaaactat 180
gcacagaagt tccagggcag agtcaccatg accacagaca catccacgag cacagcctac 240
atggaactga ggagcctgag atctgacgac acggccgtgt attactgtgc gagagatcgt 300

ggatactatg atgcttttga tatctggggc caaggcacc tggtcacctg ctccctca 357

<210> 483

<211> 324

<212> DNA

<213> Homo sapiens

<400> 483

gacatccaga tgaccagtc tccttccacc ctgtctgcat ctgttgaga cagagtcacc 60

atcacctgcc gggccagtga ggggtatttat cactgggtgg cctgggtatca gcagaagcca 120

gggaaagccc ctaaactcct gatctataag gcctctagtt tagccagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagag ttcactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaacaa atgggcgagt acaacgccac cttcggcgga 300

gggaccaagg tggagatcaa acgt 324

<210> 484

<211> 726

<212> DNA

<213> Homo sapiens

<400> 484

cagggtgcagc tgggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctgggta cacctttacc agttatggta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg gtcagcgctt aactggtaa cacaaactat 180

gcacagaagt tcaggggcag agtcaccatg accacagaca catccacgag cacagcctac 240

atggaactga ggagcctgag atctgacgac acggcctgtt attactgtgc gagagatcgt 300

ggatactatg atgcttttga tatctggggc caaggcacc tggtcacctg ctccctcaggt 360

ggaggcggtt caggcgagg tggcagcggc ggtggcggtt cggacatcca gatgaccag 420

tctccttcca cctgtctgc atctgttga gacagagtca ccatcacctg ccgggccagt 480

gagggtatct atcactggtt ggctggtat cagcagaagc cagggaagc ccctaaactc 540

ctgatctata aggcctctag tttagccagt ggggtcccat caagggtcag cggcagtggg 600

tctgggacag agttcactct caccatcagc agcctgcagc ctgatgattt tgcaacttat 660

tactgccaac aaatgggga gtacaacgcc accttcggcg gagggacca ggtggagatc 720

aaacgt 726

159/206

<210> 485
<211> 15
<212> DNA
<213> Homo sapiens

<400> 485
agttatggta tcagc

15

<210> 486
<211> 51
<212> DNA
<213> Homo sapiens

<400> 486
tgggtcagcg cttacactgg taacacaaac tatgcacaga agttccaggg c

51

<210> 487
<211> 30
<212> DNA
<213> Homo sapiens

<400> 487
gatcgtggat actatgatgc ttttgatato

30

<210> 488
<211> 33
<212> DNA
<213> Homo sapiens

<400> 488
cgggccagtg aggggtattta tcactgggtg gcc

33

<210> 489
<211> 21
<212> DNA
<213> Homo sapiens

<400> 489
aaggcctcta gtttagccag t

21

<210> 490
<211> 27
<212> DNA
<213> Homo sapiens

<400> 490
caacaaatgg gcgagtacaa cgccacc

27

<210> 491
<211> 121
<212> PRT
<213> Homo sapiens

160/206

<400> 491

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Val Asn Trp Asn Gly Gly Thr Arg Asp Tyr Ala Ala Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr His Cys
85 90 95

Ala Arg Gly Trp Tyr Ser Gly Ala Ala Trp Asn Met Gly Tyr Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 492

<211> 111

<212> PRT

<213> Homo sapiens

<400> 492

Gln Ala Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

Ser Ile Thr Ile Ser Cys Thr Gly Ala Ser Gly Asp Val Gly Ala Tyr
20 25 30

Asn Phe Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Ile Ile Tyr Asp Val Asn Lys Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

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Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Thr Ser Thr
85 90 95

Phe Ser Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 493

<211> 248

<212> PRT

<213> Homo sapiens

<400> 493

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Val Asn Trp Asn Gly Gly Thr Arg Asp Tyr Ala Ala Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr His Cys
85 90 95

Ala Arg Gly Trp Tyr Ser Gly Ala Ala Trp Asn Met Gly Tyr Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Ala Ala Leu Thr Gln Pro
130 135 140

Ala Ser Val Ser Gly Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr
145 150 155 160

Gly Ala Ser Gly Asp Val Gly Ala Tyr Asn Phe Val Ser Trp Tyr Gln
165 170 175

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Gln His Pro Gly Lys Ala Pro Lys Leu Ile Ile Tyr Asp Val Asn Lys
180 185 190

Arg Pro Ser Gly Val Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn
195 200 205

Thr Ala Ser Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp
210 215 220

Tyr Tyr Cys Ser Ser Tyr Thr Ser Thr Phe Ser Val Val Phe Gly Gly
225 230 235 240

Gly Thr Lys Leu Thr Val Leu Gly
245

<210> 494

<211> 5

<212> PRT

<213> Homo sapiens

<400> 494

Asp Tyr Gly Met Asn

1

5

<210> 495

<211> 17

<212> PRT

<213> Homo sapiens

<400> 495

Gly Val Asn Trp Asn Gly Gly Thr Arg Asp Tyr Ala Ala Ser Val Lys

1

5

10

15

Gly

<210> 496

<211> 12

<212> PRT

<213> Homo sapiens

<400> 496

Gly Trp Tyr Ser Gly Ala Ala Trp Asn Met Gly Tyr

1

5

10

163/206

<210> 497
<211> 14
<212> PRT
<213> Homo sapiens

<400> 497
Thr Gly Ala Ser Gly Asp Val Gly Ala Tyr Asn Phe Val Ser
1 5 10

<210> 498
<211> 7
<212> PRT
<213> Homo sapiens

<400> 498
Asp Val Asn Lys Arg Pro Ser
1 5

<210> 499
<211> 10
<212> PRT
<213> Homo sapiens

<400> 499
Ser Ser Tyr Thr Ser Thr Phe Ser Val Val
1 5 10

<210> 500
<211> 363
<212> DNA
<213> Homo sapiens

<400> 500
gaggtgcagc tgggtggagag cgggggaggt gtggtacggc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttgac gattatggca tgaactgggt ccgccaagct 120
ccaggggaagg ggctggagtg ggtctctggt gttaattgga atggtggtac cagagattat 180
gcagcctccg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaataga acagtctgag agccgaggac acggccttgt atcactgtgc gagaggatgg 300
tatagtgggg ccgcgtggaa catgggctac tggggccgag gaaccctggt caccgtctcc 360
tca 363

<210> 501
<211> 333
<212> DNA
<213> Homo sapiens

<400> 501
caggctgcgc tgactcagcc ggcctccgtg tctgggtctc ctggacagtc gatcaccatc 60

tcctgcactg gagccagcgg tgacgttggt gcttataact ttgtctcctg gtaccaacaa 120
 caccagggca aagcccccaa actcataatt tatgatgtca ataagcggcc ctccaggggtt 180
 tctaatacgt tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc 240
 caggccgagg acgaggctga ttattactgc agctcatata caagcacctt ctctgtggta 300
 tttggcggag ggaccaagct gaccgtccta ggt 333

<210> 502
 <211> 744
 <212> DNA
 <213> Homo sapiens

<400> 502
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 tcctgtgcag cctctggatt cacccttgac gattatggca tgaactgggt ccgccaagct 120
 ccagggaagg ggctggagtg ggtctctggt gttaattgga atggtggtac cagagattat 180
 gcagcctccg tgaagggccg attcaccatc tcagagaca acgccaagaa ctccctgtat 240
 ctgcaaataa acagtctgag agccgaggac acggccttgt atcactgtgc gagaggatgg 300
 tatagtgggg ccgcgtggaa catgggctac tggggccgag gaaccctggt caccgtctcc 360
 tcaggaggcg gcggttcagg cggaggtggc tctggcgggt gcggaagtgc acaggctgcg 420
 ctgactcagc cggcctccgt gtctgggtct cctggacagt cgatcaccat ctctgcact 480
 ggagccagcg gtgacgttgg tgcttataac tttgtctcct ggtaccaaca acaccaggc 540
 aaagcccca aactcataat ttatgatgtc aataagcggc cctcaggggt ttctaatacgc 600
 ttctctggct ccaagtctgg caacacggcc tcctgacca tctctgggct ccaggccgag 660
 gacgaggctg attattactg cagctcatat acaagcacct tctctgtggt atttggcgga 720
 gggaccaagc tgaccgtcct aggt 744

<210> 503
 <211> 15
 <212> DNA
 <213> Homo sapiens

<400> 503
 gattatggca tgaac 15

<210> 504
 <211> 51
 <212> DNA
 <213> Homo sapiens

<400> 504
ggtgttaatt ggaatggtgg taccagagat tatgcagcct ccgtgaaggg c 51

<210> 505
<211> 36
<212> DNA
<213> Homo sapiens

<400> 505
ggatgggtata gtgggggcgc gtggaacatg ggctac 36

<210> 506
<211> 42
<212> DNA
<213> Homo sapiens

<400> 506
actggagcca gcggtgacgt tgggtgcttat aactttgtct cc 42

<210> 507
<211> 21
<212> DNA
<213> Homo sapiens

<400> 507
gatgtcaata agcggccctc a 21

<210> 508
<211> 30
<212> DNA
<213> Homo sapiens

<400> 508
agtcacatata caagcacctt ctctgtggta 30

<210> 509
<211> 119
<212> PRT
<213> Homo sapiens

<400> 509
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asp Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

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Gly Trp Val Asn Pro Asp Thr Gly Gly Thr Arg Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Met Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Leu Thr Gly Phe Asp Pro Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 510

<211> 109

<212> PRT

<213> Homo sapiens

<400> 510

Ser Ser Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Lys
1 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Phe Arg Asn Lys Arg Val
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

Tyr Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Arg Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Leu Phe Asn Asp Asn
85 90 95

Gly Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105

167/206

<210> 511

<211> 244

<212> PRT

<213> Homo sapiens

<400> 511

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asp Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Val Asn Pro Asp Thr Gly Gly Thr Arg Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Met Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Leu Thr Gly Phe Asp Pro Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Ala Ser Ser Val Leu Thr Gln Pro Pro Ser
130 135 140

Val Ser Val Ala Pro Gly Lys Thr Ala Arg Ile Thr Cys Gly Gly Asn
145 150 155 160

Asn Phe Arg Asn Lys Arg Val His Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ala Pro Val Leu Val Ile Tyr Tyr Asp Ser Asp Arg Pro Ser Gly Ile
180 185 190

Pro Glu Arg Phe Ser Gly Ser Arg Ser Gly Asn Thr Ala Thr Leu Thr
195 200 205

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Ile Ser Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val
210 215 220

Trp Asp Leu Phe Asn Asp Asn Gly Val Phe Gly Gly Gly Thr Lys Leu
225 230 235 240

Thr Val Leu Gly

<210> 512
<211> 5
<212> PRT
<213> Homo sapiens

<400> 512
Asp Tyr Tyr Ile His
1 5

<210> 513
<211> 17
<212> PRT
<213> Homo sapiens

<400> 513
Trp Val Asn Pro Asp Thr Gly Gly Thr Arg Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 514
<211> 10
<212> PRT
<213> Homo sapiens

<400> 514
Asp Leu Thr Gly Phe Asp Pro Phe Asp Ile
1 5 10

<210> 515
<211> 11
<212> PRT
<213> Homo sapiens

<400> 515
Gly Gly Asn Asn Phe Arg Asn Lys Arg Val His
1 5 10

<210> 516
 <211> 7
 <212> PRT
 <213> Homo sapiens

<400> 516
 Tyr Asp Ser Asp Arg Pro Ser
 1 5

<210> 517
 <211> 11
 <212> PRT
 <213> Homo sapiens

<400> 517
 Gln Val Trp Asp Leu Phe Asn Asp Asn Gly Val
 1 5 10

<210> 518
 <211> 357
 <212> DNA
 <213> Homo sapiens

<400> 518
 caggtccagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
 tcctgttaagg cttctggata caccttcagc gattactata ttcaactgggt gcgacaggcc 120
 cctggacaag ggttggagtg gatgggatgg gtcaaccctg acactgggtg cacaagatac 180
 gcgcagaagt ttcaggggccg ggtcacaatg accaggggaca tgtccatctc cacagcctac 240
 atggagctgt ccaggctgag aagcgacgac acggccgtat attactgtgc gagagatcta 300
 actggatttg atccttttga tatctggggc cagggaaccc tggtcaccgt ctctca 357

<210> 519
 <211> 327
 <212> DNA
 <213> Homo sapiens

<400> 519
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 acctgtgggg gaaacaactt tcgaaataaa agagtacact ggtatcagca gaagccaggc 120
 caggcccctg tcctggatcat ctattatgat tcagaccgga cctcagggat cctgagcga 180
 ttctctggct cccgctcttg gaacacggcc accctgacca tcagcagggt cgaggccggg 240
 gatgaggccg actattactg tcagggtgtgg gatctcttca acgacaacgg cgtgttcggc 300
 ggagggacca agctgaccgt cctaggt 327

170/206

<210> 520
<211> 732
<212> DNA
<213> Homo sapiens

<400> 520
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tcctgtaagg cttctggata caccttcagc gattactata ttcactgggt gcgacaggcc 120
cctggacaag ggttggagtg gatgggatgg gtcaacctg acactgggtg cacaagatac 180
gcgcagaagt ttcagggccg ggtcacaatg accagggaca tgtccatctc cacagcctac 240
atggagctgt ccaggctgag aagcgacgac acggccgtat attactgtgc gagagatcta 300
actggatttg atccttttga tatctggggc cagggaaacc tggtcaccgt ctctcagga 360
ggcggcagtt caggtggagg tggctctggc ggtggcggaa gtgcatcgtc tgtgctgact 420
cagccaccct cagtgtcagt ggccccagga aagacggccc gcattacctg tgggggaaac 480
aactttcgaa ataaaagagt acactgggtat cagcagaagc cagggccaggc ccctgtcctg 540
gtcatctatt atgattcaga ccggccctca gggatccctg agcgattctc tggctcccgc 600
tctgggaaca cggccaccct gaccatcagc agggtcgagg ccggggatga ggccgactat 660
tactgtcagg tgtgggatct cttcaacgac aacggcgtgt tcggcggagg gaccaagctg 720
accgtcctag gt 732

<210> 521
<211> 15
<212> DNA
<213> Homo sapiens

<400> 521
gattactata ttcac 15

<210> 522
<211> 51
<212> DNA
<213> Homo sapiens

<400> 522
tgggtcaacc ctgacactgg tggcacaaga tacgcgcaga agtttcaggg c 51

<210> 523
<211> 30
<212> DNA
<213> Homo sapiens

<400> 523
gatctaactg gatttgatcc ttttgatata 30

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<210> 524
<211> 33
<212> DNA
<213> Homo sapiens

<400> 524
gggggaaaca actttcgaaa taaaagagta cac 33

<210> 525
<211> 21
<212> DNA
<213> Homo sapiens

<400> 525
tatgattcag accggccctc a 21

<210> 526
<211> 33
<212> DNA
<213> Homo sapiens

<400> 526
caggtgtggg atctcttcaa cgacaacggc gtg 33

<210> 527
<211> 119
<212> PRT
<213> Homo sapiens

<400> 527
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asp Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Val Asn Pro Asp Thr Gly Gly Thr Arg Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Met Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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Ala Arg Asp Leu Thr Gly Phe Asp Pro Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 528

<211> 109

<212> PRT

<213> Homo sapiens

<400> 528

Ser Ser Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Lys
1 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Phe Arg Asn Lys Arg Val
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

Tyr Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Arg Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Phe Leu Thr Asp Ser
85 90 95

Gly Ser Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105

<210> 529

<211> 244

<212> PRT

<213> Homo sapiens

<400> 529

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asp Tyr
20 25 30

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Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Val Asn Pro Asp Thr Gly Gly Thr Arg Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Met Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Leu Thr Gly Phe Asp Pro Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Ala Ser Ser Val Leu Thr Gln Pro Pro Ser
130 135 140

Val Ser Val Ala Pro Gly Lys Thr Ala Arg Ile Thr Cys Gly Gly Asn
145 150 155 160

Asn Phe Arg Asn Lys Arg Val His Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ala Pro Val Leu Val Ile Tyr Tyr Asp Ser Asp Arg Pro Ser Gly Ile
180 185 190

Pro Glu Arg Phe Ser Gly Ser Arg Ser Gly Asn Thr Ala Thr Leu Thr
195 200 205

Ile Ser Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val
210 215 220

Trp Asp Phe Leu Thr Asp Ser Gly Ser Phe Gly Gly Gly Thr Lys Leu
225 230 235 240

Thr Val Leu Gly

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<210> 530
<211> 5
<212> PRT
<213> Homo sapiens

<400> 530
Asp Tyr Tyr Ile His
1 5

<210> 531
<211> 17
<212> PRT
<213> Homo sapiens

<400> 531
Trp Val Asn Pro Asp Thr Gly Gly Thr Arg Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 532
<211> 10
<212> PRT
<213> Homo sapiens

<400> 532
Asp Leu Thr Gly Phe Asp Pro Phe Asp Ile
1 5 10

<210> 533
<211> 11
<212> PRT
<213> Homo sapiens

<400> 533
Gly Gly Asn Asn Phe Arg Asn Lys Arg Val His
1 5 10

<210> 534
<211> 7
<212> PRT
<213> Homo sapiens

<400> 534
Tyr Asp Ser Asp Arg Pro Ser
1 5

<210> 535
<211> 11
<212> PRT
<213> Homo sapiens

<400> 535
 Gln Val Trp Asp Phe Leu Thr Asp Ser Gly Ser
 1 5 10

<210> 536
 <211> 357
 <212> DNA
 <213> Homo sapiens

<400> 536
 caggtccagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
 tctgtgaagg ottctggata caccttcagc gattactata ttcactgggt gcgacaggcc 120
 cctggacaag ggttggagtg gatgggatgg gtcaaccctg aactgggtgg cacaagatac 180
 gcgcagaagt ttcaggggccg ggtcacaatg accaggggaca tgtccatctc cacagcctac 240
 atggagctgt ccaggctgag aagcgacgac acggccgtat attactgtgc gagagatcta 300
 actggatttg atccttttga tatctggggc cagggaaccc tggtcaccgt ctcctca 357

<210> 537
 <211> 327
 <212> DNA
 <213> Homo sapiens

<400> 537
 tcgtctgtgc tgactcagcc accctcagtg tcagtggccc caggaaagac ggcccgcatt 60
 acctgtgggg gaaacaactt tcgaaataaa agagtacact ggtatcagca gaagccaggc 120
 caggcccctg tctgtgtcat ctattatgat tcagacgggc cctcagggat ccctgagcga 180
 ttctctgggt cccgctcttg gaacacggcc accctgacca tcagcagggt cgaggccggg 240
 gatgaggccg actattactg tcagggtgtg gatttctca ccgactcggg gtcgttcggc 300
 ggagggacca agctgaccgt cctaggt 327

<210> 538
 <211> 732
 <212> DNA
 <213> Homo sapiens

<400> 538
 caggtccagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
 tctgtgaagg ottctggata caccttcagc gattactata ttcactgggt gcgacaggcc 120
 cctggacaag ggttggagtg gatgggatgg gtcaaccctg aactgggtgg cacaagatac 180
 gcgcagaagt ttcaggggccg ggtcacaatg accaggggaca tgtccatctc cacagcctac 240

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atggagctgt ccaggctgag aagcgacgac acggccgtat attactgtgc gagagatcta	300
actggatttg atccttttga tatctggggc caggggaaccc tggtcaccgt ctcttcagga	360
ggcggcggtt cagggcgagg tggctctggc ggtggcgga gtgcacgtc tgtgctgact	420
cagccaccct cagtgtcagt ggccccagga aagacggccc gcattacctg tgggggaaac	480
aactttcgaa ataaaagagt aacttggtat cagcagaagc cagggcaggc ccctgtcctg	540
gtcatctatt atgattcaga cggccctca gggatccctg agcgattctc tggctccgc	600
tctgggaaca cggccaccct gaccatcagc agggctcagg ccggggatga ggccgactat	660
tactgtcagg tgtgggattt cctcacgac tcggggtcgt tcggcgagg gaccaagctg	720
accgtcctag gt	732

<210> 539
 <211> 15
 <212> DNA
 <213> Homo sapiens

<400> 539 gattactata ttcac	15

<210> 540
 <211> 51
 <212> DNA
 <213> Homo sapiens

<400> 540 tgggtcaacc ctgacactgg tggcacaaga tacgcgaga agtttcaggg c	51

<210> 541
 <211> 30
 <212> DNA
 <213> Homo sapiens

<400> 541 gatctaactg gatttgatcc ttttgatata	30

<210> 542
 <211> 33
 <212> DNA
 <213> Homo sapiens

<400> 542 gggggaaaca actttcgaaa taaaagagta cac	33

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<210> 543
<211> 21
<212> DNA
<213> Homo sapiens

<400> 543
tatgattcag accggccctc a

21

<210> 544
<211> 33
<212> DNA
<213> Homo sapiens

<400> 544
caggtgtggg atttcttcac cgactcgggg tcg

33

<210> 545
<211> 121
<212> PRT
<213> Homo sapiens

<400> 545
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Asn Pro Tyr Thr Gly Gly Ala Phe Tyr Ala Gln Lys Phe
50 55 60

Arg Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Pro Glu Arg Phe Gly Asp Ser Thr Gly Gln Val Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser
115 120

178/206

<210> 546
<211> 112
<212> PRT
<213> Homo sapiens

<400> 546
Gln Ala Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Gly Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Tyr His Trp Asp Lys Glu
85 90 95

Gln Ser Gly Tyr Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu Gly
100 105 110

<210> 547
<211> 249
<212> PRT
<213> Homo sapiens

<400> 547
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Asn Pro Tyr Thr Gly Gly Ala Phe Tyr Ala Gln Lys Phe
50 55 60

Arg Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

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Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Pro Glu Arg Phe Gly Asp Ser Thr Gly Gln Val Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Ser Arg Ser Ala Gln Ala Val Leu Thr Gln Pro
130 135 140

Pro Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr
145 150 155 160

Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Gly Val His Trp Tyr Gln
165 170 175

Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Gly Asn Ser Asn
180 185 190

Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr
195 200 205

Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp
210 215 220

Tyr Tyr Cys Tyr His Trp Asp Lys Glu Gln Ser Gly Tyr Val Phe Gly
225 230 235 240

Gly Gly Thr Gln Leu Thr Val Leu Gly
245

<210> 548

<211> 5

<212> PRT

<213> Homo sapiens

<400> 548

Asp Tyr Tyr Met His

1

5

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<210> 549
<211> 17
<212> PRT
<213> Homo sapiens

<400> 549
Trp Ile Asn Pro Tyr Thr Gly Gly Ala Phe Tyr Ala Gln Lys Phe Arg
1 5 10 15

Gly

<210> 550
<211> 12
<212> PRT
<213> Homo sapiens

<400> 550
Glu Pro Glu Arg Phe Gly Asp Ser Thr Gly Gln Val
1 5 10

<210> 551
<211> 14
<212> PRT
<213> Homo sapiens

<400> 551
Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Gly Val His
1 5 10

<210> 552
<211> 7
<212> PRT
<213> Homo sapiens

<400> 552
Gly Asn Ser Asn Arg Pro Ser
1 5

<210> 553
<211> 11
<212> PRT
<213> Homo sapiens

<400> 553
Tyr His Trp Asp Lys Glu Gln Ser Gly Tyr Val
1 5 10

<210> 554
<211> 363
<212> DNA
<213> Homo sapiens

<400> 554
 caggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
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 cctggacaag ggcttgagtg ggtgggatgg atcaaccctt atactgggtg cgcattctat 180
 gcacagaagt ttcggggcag ggtcacaatg accagggaaca cgtccatcag cacagcctac 240
 atggagctga gcagactgag atctgacgac acggccgtgt attattgtgc gagagaacct 300
 gaaagattcg gcgactccac ggggcaggtc tggggccggg ggacattggt caccgtctcc 360
 tca 363

<210> 555
 <211> 336
 <212> DNA
 <213> Homo sapiens

<400> 555
 caggctgtgc tgactcagcc gccgtcagtg tctggggccc cagggcagag ggtcaccatc 60
 tcctgcaactg ggagcagctc caacatcggg gcagggttatg gtgtacactg gtaccaacag 120
 cttccaggaa cagcccccaa actcctcatc tatggtaaca gcaatcggcc ctccaggggtc 180
 cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
 caggctgagg atgaggctga ttattactgc taccactggg acaaggagca gagtggttat 300
 gtcttcggag gtgggaccca gctcacctgc ctaggt 336

<210> 556
 <211> 747
 <212> DNA
 <213> Homo sapiens

<400> 556
 caggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
 tcctgcaagg cttctggata caccttcacc gactactata tgcactgggt gcgacaggcc 120
 cctggacaag ggcttgagtg ggtgggatgg atcaaccctt atactgggtg cgcattctat 180
 gcacagaagt ttcggggcag ggtcacaatg accagggaaca cgtccatcag cacagcctac 240
 atggagctga gcagactgag atctgacgac acggccgtgt attattgtgc gagagaacct 300
 gaaagattcg gcgactccac ggggcaggtc tggggccggg ggacattggt caccgtctcc 360
 tcagggggcg gcggttcagg cggaggtggc tctggcggtg gcagaagtgc acaggctgtg 420
 ctgactcagc cgcctcagtc gtctggggcc ccagggcaga gggtcacat ctctgcaact 480

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gggagcagct ccaacatcgg ggcagggttat ggtgtacact ggtaccaaca gcttccagga 540
 acagccccc aactcctcat ctatggtaac agcaatcggc cctcaggggt ccctgaccga 600
 ttctctggct ccaagtctgg cacctcagcc tccctggcca tcaactgggt ccaggctgag 660
 gatgaggctg attattactg ctaccactgg gacaaggagc agagtgggta tgtcttcgga 720
 ggtgggaccc agctcacctg cctaggt 747

<210> 557
 <211> 15
 <212> DNA
 <213> Homo sapiens

<400> 557
 gactactata tgcac 15

<210> 558
 <211> 51
 <212> DNA
 <213> Homo sapiens

<400> 558
 tggatcaacc cttatactgg tggcgcatto tatgcacaga agtttcgggg c 51

<210> 559
 <211> 36
 <212> DNA
 <213> Homo sapiens

<400> 559
 gaacctgaaa gattcggcga ctccacgggg caggtc 36

<210> 560
 <211> 42
 <212> DNA
 <213> Homo sapiens

<400> 560
 actgggagca gctccaacat cggggcaggt tatggtgtac ac 42

<210> 561
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 561
 ggtaacagca atcgccctc a 21

183/206

<210> 562
<211> 33
<212> DNA
<213> Homo sapiens

<400> 562
taccactggg acaaggagca gagtggttat gtc

33

<210> 563
<211> 121
<212> PRT
<213> Homo sapiens

<400> 563
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Asn Pro Tyr Thr Gly Ser Ala Phe Tyr Ala Gln Lys Phe
50 55 60

Arg Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Pro Glu Lys Phe Gly Glu Ser Ser Gly Gln Leu Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 564
<211> 112
<212> PRT
<213> Homo sapiens

<400> 564
Gln Ala Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

184/206

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Gly Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Gly Asp Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Gly
85 90 95

Leu Ser Gly Tyr Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu Gly
100 105 110

<210> 565

<211> 249

<212> PRT

<213> Homo sapiens

<400> 565

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Asn Pro Tyr Thr Gly Ser Ala Phe Tyr Ala Gln Lys Phe
50 55 60

Arg Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Pro Glu Lys Phe Gly Glu Ser Ser Gly Gln Leu Trp Gly
100 105 110

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Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Ser Gly Ser Ala Gln Ala Val Leu Thr Gln Pro
130 135 140

Pro Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr
145 150 155 160

Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Gly Val His Trp Tyr Gln
165 170 175

Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Gly Asp Ser Asn
180 185 190

Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr
195 200 205

Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp
210 215 220

Tyr Tyr Cys Gln Ser Tyr Asp Ser Gly Leu Ser Gly Tyr Val Phe Gly
225 230 235 240

Gly Gly Thr Gln Leu Thr Val Leu Gly
245

<210> 566

<211> 5

<212> PRT

<213> Homo sapiens

<400> 566

Asp Tyr Tyr Met His

1

5

<210> 567

<211> 17

<212> PRT

<213> Homo sapiens

<400> 567

Trp Ile Asn Pro Tyr Thr Gly Ser Ala Phe Tyr Ala Gln Lys Phe Arg

1

5

10

15

Gly

186/206

<210> 568
<211> 12
<212> PRT
<213> Homo sapiens

<400> 568
Glu Pro Glu Lys Phe Gly Glu Ser Ser Gly Gln Leu
1 5 10

<210> 569
<211> 14
<212> PRT
<213> Homo sapiens

<400> 569
Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Gly Val His
1 5 10

<210> 570
<211> 7
<212> PRT
<213> Homo sapiens

<400> 570
Gly Asp Ser Asn Arg Pro Ser
1 5

<210> 571
<211> 11
<212> PRT
<213> Homo sapiens

<400> 571
Gln Ser Tyr Asp Ser Gly Leu Ser Gly Tyr Val
1 5 10

<210> 572
<211> 363
<212> DNA
<213> Homo sapiens

<400> 572
caggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcttgcaagg cttctggata caocttcacc gactactata tgcactgggt gcgacaggcc 120
cctggacaag ggcttgagtg ggtgggatgg atcaaccctt atactggtag cgctttctat 180
gcacagaagt ttcggggcag ggtcacaatg accagggaca cgtccatcag cacagcctac 240
atggagctga gcagactgag atctgacgac acggccgtgt attattgtgc gagagaacct 300

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gaaaaattcg gcgagtcag cgccagttg tggggccggg ggacattggt caccgtctcc 360

tca 363

<210> 573
<211> 336
<212> DNA
<213> Homo sapiens

<400> 573
caggctgtgc tgactcagcc gccgtcagtg totggggccc cagggcagag ggtcaccatc 60
tcttgactg ggagcagctc caacatcggg gcaggttatg gtgtacactg gtaccaacag 120
cttcaggaa cagcccccaa actcctcatc tatggtgaca gcaatcggcc ctgaggggtc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccttggccat cactgggctc 240
caggctgagg atgaggtga ttattactgc cagtcctatg acagcggcct gagtgggtat 300
gtcttcggag gtgggaccca gctcaccgtc ctaggt 336

<210> 574
<211> 747
<212> DNA
<213> Homo sapiens

<400> 574
cagggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcttgcaagg ctcttgata caccttcacc gactactata tgcactgggt gcgacaggcc 120
cctggacaag ggcttgagtg ggtgggatgg atcaaccctt atactggtag cgctttctat 180
gcacagaagt ttcggggcag ggtcacaatg accagggaca cgtccatcag cacagcctac 240
atggagctga gcagactgag atctgacgac acggccgtgt attattgtgc gagagaacct 300
gaaaaattcg gcgagtcag cgccagttg tggggccggg ggacattggt caccgtctcc 360
tcaggaggcg gcggttcagg cggaggtggc totggcggta gcggaagtgc acaggctgtg 420
ctgactcagc cgccgtcagt gtctggggcc ccagggcaga gggtcaccat ctctgcact 480
gggagcagct ccaacatcgg ggcaggttat ggtgtacact ggtaccaaca gcttcaggga 540
acagccccc aactcctcat ctatggtgac agcaatcggc cctcaggggt cctgaccga 600
ttctctgggt ccaagtctgg cacctcagcc tccttgcca tcaactgggt ccaggctgag 660
gatgaggctg attattactg ccagtcctat gacagcggcc tgagtggta tgtcttcgga 720
ggcgggaccc agctcaccgt cctaggt 747

188/206

<210> 575
<211> 15
<212> DNA
<213> Homo sapiens

<400> 575
gactactata tgcac

15

<210> 576
<211> 51
<212> DNA
<213> Homo sapiens

<400> 576
tggatcaacc cttatactgg tagcgctttc tatgcacaga agtttcgggg c

51

<210> 577
<211> 36
<212> DNA
<213> Homo sapiens

<400> 577
gaacctgaaa aattcggcga gtccagcggc cagttg

36

<210> 578
<211> 42
<212> DNA
<213> Homo sapiens

<400> 578
actgggagca gctccaacat cggggcaggt tatggtgtac ac

42

<210> 579
<211> 21
<212> DNA
<213> Homo sapiens

<400> 579
ggtgacagca atcggccctc a

21

<210> 580
<211> 33
<212> DNA
<213> Homo sapiens

<400> 580
cagtcctatg acagcggcct gagggttat gtc

33

<210> 581
<211> 121
<212> PRT
<213> Homo sapiens

189/206

<400> 581

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr His Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Asn Pro Tyr Thr Gly Gly Ala Phe Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Pro Glu Lys Phe Asp Ser Pro Asn Ala Glu Ile Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 582

<211> 112

<212> PRT

<213> Homo sapiens

<400> 582

Gln Ala Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Gly Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

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Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85 90 95

Leu Ser Gly Tyr Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu Gly
100 105 110

<210> 583

<211> 249

<212> PRT

<213> Homo sapiens

<400> 583

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr His Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Asn Pro Tyr Thr Gly Gly Ala Phe Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Pro Glu Lys Phe Asp Ser Pro Asn Ala Glu Ile Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser Glu Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Ser Gly Ser Ala Gln Ala Val Leu Thr Gln Pro
130 135 140

Pro Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr
145 150 155 160

Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Gly Val His Trp Tyr Gln
165 170 175

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Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Gly Asn Ser Asn
180 185 190

Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr
195 200 205

Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp
210 215 220

Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser Leu Ser Gly Tyr Val Phe Gly
225 230 235 240

Gly Gly Thr Gln Leu Thr Val Leu Gly
245

<210> 584

<211> 5

<212> PRT

<213> Homo sapiens

<400> 584

His Tyr Tyr Met His
1 5

<210> 585

<211> 17

<212> PRT

<213> Homo sapiens

<400> 585

Trp Ile Asn Pro Tyr Thr Gly Gly Ala Phe Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 586

<211> 12

<212> PRT

<213> Homo sapiens

<400> 586

Glu Pro Glu Lys Phe Asp Ser Pro Asn Ala Glu Ile
1 5 10

192/206

<210> 587
<211> 14
<212> PRT
<213> Homo sapiens

<400> 587
Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Gly Val His
1 5 10

<210> 588
<211> 7
<212> PRT
<213> Homo sapiens

<400> 588
Gly Asn Ser Asn Arg Pro Ser
1 5

<210> 589
<211> 11
<212> PRT
<213> Homo sapiens

<400> 589
Gln Ser Tyr Asp Ser Ser Leu Ser Gly Tyr Val
1 5 10

<210> 590
<211> 363
<212> DNA
<213> Homo sapiens

<400> 590
cagggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgcaagg cttctggata caccttcacc cactactata tgcactgggt gcgacaggcc 120
cctggacaag ggcttgagtg ggtgggatgg atcaaccctt atactgggtg cgcattctat 180
gcacagaagt ttcagggcag ggtcacaatg accagggaca cgtccatcag cacagcctac 240
atggagctga gcagactgag atctgacgac acggccgtgt attattgtgc gagagaacct 300
gaaaaattcg actcgccgaa cgccgagatc tggggccggg ggacattggt caccgtctcc 360
tca 363

<210> 591
<211> 336
<212> DNA
<213> Homo sapiens

<400> 591
caggctgtgc tgactcagcc gccgtcagtg tctggggccc cagggcagag ggtcaccatc 60

tcttgcaactg	ggagcagctc	caacatcggg	gcagggttatg	gtgtacactg	gtaccaacag	120
cttcacaggaa	cagcccccaa	actcctcatc	tatggtaaca	gcaatcggcc	ctcaggggtc	180
cctgaccgat	tctctggctc	caagtctggc	acctcagcct	ccctggccat	cactgggctc	240
caggctgagg	atgaggctga	ttattactgc	cagtcctatg	acagcagcct	gagtgggtat	300
gtcttcggag	gtgggaccca	gctcacgcgc	ctaggt			336

<210> 592
 <211> 747
 <212> DNA
 <213> Homo sapiens

<400> 592	
cagggtgcagc	tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcttgcaagg	cttctggata caccttcacc cactactata tgcactgggt gcgacaggcc 120
cctggacaag	ggcttgagtg ggtgggatgg atcaaccctt atactgggtg cgcattctat 180
gcacagaagt	ttcagggcag ggtcacaatg accagggaca cgtccatcag cacagcctac 240
atggagctga	gcagactgag atctgacgac acggccgtgt attattgtgc gagagaacct 300
gaaaaattcg	actcgccgaa cgccgagatc tggggccggg ggacattgggt caccgtctcc 360
tcagaaggcg	gcggttcagg cggaggtggc tctggcggta gcggaagtgc acaggctgtg 420
ctgactcagc	cgccgtcagt gtctggggcc ccagggcaga gggtcacat ctctgcact 480
gggagcagct	ccaacatcgg ggcagggttat ggtgtacact ggtaccaaca gcttcagga 540
acagcccca	aactcctcat ctatggtaac agcaatcggc cctcaggggt cctgaccga 600
ttctctggct	ccaagtctgg cacctcagcc tccctggcca tcaactgggt ccaggctgag 660
gatgaggtg	attattactg ccagtcctat gacagcagcc tgagtgggta tgtcttcgga 720
ggtgggaccc	agctcacgt cctaggt 747

<210> 593
 <211> 15
 <212> DNA
 <213> Homo sapiens

<400> 593	
cactactata	tgcac 15

<210> 594
 <211> 51
 <212> DNA
 <213> Homo sapiens

<400> 594
 tggatcaacc cttatactgg tggcgcatc tatgcacaga agtttcaggg c 51

<210> 595
 <211> 36
 <212> DNA
 <213> Homo sapiens

<400> 595
 gaacctgaaa aattcgactc gccgaacgcc gagatc 36

<210> 596
 <211> 42
 <212> DNA
 <213> Homo sapiens

<400> 596
 actgggagca gctccaacat cggggcaggt tatggtgtac ac 42

<210> 597
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 597
 ggtaacagca atcggccctc a 21

<210> 598
 <211> 33
 <212> DNA
 <213> Homo sapiens

<400> 598
 cagtctatg acagcagcct gactgggttat gtc 33

<210> 599
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 599
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45

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Gly Trp Ile Asn Pro Tyr Thr Gly Ser Ala Phe Tyr Ala Gln Lys Phe
50 55 60

Arg Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Pro Glu Lys Phe Asp Ser Asp Asp Ser Asp Val Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 600

<211> 112

<212> PRT

<213> Homo sapiens

<400> 600

Gln Ala Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Gly Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Gly Asp Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Asn Ser
85 90 95

Leu Ser Gly Tyr Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu Gly
100 105 110

196/206

<210> 601
<211> 249
<212> PRT
<213> Homo sapiens

<400> 601

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Trp Ile Asn Pro Tyr Thr Gly Ser Ala Phe Tyr Ala Gln Lys Phe
50 55 60

Arg Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Pro Glu Lys Phe Asp Ser Asp Asp Ser Asp Val Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Ser Gly Ser Ala Gln Ala Val Leu Thr Gln Pro
130 135 140

Pro Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr
145 150 155 160

Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Gly Val His Trp Tyr Gln
165 170 175

Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Gly Asp Ser Asn
180 185 190

Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr
195 200 205

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Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp
210 215 220

Tyr Tyr Cys Gln Ser Tyr Asp Asn Ser Leu Ser Gly Tyr Val Phe Gly
225 230 235 240

Gly Gly Thr Gln Leu Thr Val Leu Gly
245

<210> 602
<211> 5
<212> PRT
<213> Homo sapiens

<400> 602
Asn Tyr Tyr Met His
1 5

<210> 603
<211> 17
<212> PRT
<213> Homo sapiens

<400> 603
Trp Ile Asn Pro Tyr Thr Gly Ser Ala Phe Tyr Ala Gln Lys Phe Arg
1 5 10 15

Gly

<210> 604
<211> 12
<212> PRT
<213> Homo sapiens

<400> 604
Glu Pro Glu Lys Phe Asp Ser Asp Asp Ser Asp Val
1 5 10

<210> 605
<211> 14
<212> PRT
<213> Homo sapiens

<400> 605
Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Gly Val His
1 5 10

<210> 606
 <211> 7
 <212> PRT
 <213> Homo sapiens

<400> 606
 Gly Asp Ser Asn Arg Pro Ser
 1 5

<210> 607
 <211> 11
 <212> PRT
 <213> Homo sapiens

<400> 607
 Gln Ser Tyr Asp Asn Ser Leu Ser Gly Tyr Val
 1 5 10

<210> 608
 <211> 363
 <212> DNA
 <213> Homo sapiens

<400> 608
 caggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
 tcttgcaagg cttctggata caccttcacc aactactata tgcactgggt ggcacaggcc 120
 cctggacaag ggcttgagtg ggtgggatgg atcaaccott atactggtag cgcattctat 180
 gcacagaagt ttcgggggcag ggtcacaatg accaggggaca cgtccatcag cacagcctac 240
 atggagctga gcagactgag atctgaacgac acggccgtgt attattgtgc gagagaacct 300
 gaaaaattcg actccgacga ctccgacgtc tggggccgcg ggacattggt caccgtctcc 360
 tca 363

<210> 609
 <211> 336
 <212> DNA
 <213> Homo sapiens

<400> 609
 caggctgtgc tgactcagcc gcggtcagtg tctggggccc cagggcagag ggtcaccatc 60
 tcttgcaactg ggagcagctc caacatcggtg gcagggttatg gtgtacactg gtaccaacag 120
 cttccaggaa cagcccccaa actcctcctc tatggtgaca gcaatcggcc ctccaggggtc 180
 cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
 caggctgagg atgaggctga ttattactgc cagtcctatg acaacagcct gagcgggttat 300
 gtcttcggag gtgggaccca gctcaccgtc ctagggt 336

<210> 610
 <211> 747
 <212> DNA
 <213> Homo sapiens

<400> 610
 caggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
 tcctgcaagg cttctggata caccttcacc aactactata tgcactgggt gcgacaggcc 120
 cctggacaag ggcttgagtg ggtgggatgg atcaaccctt atactggtag cgcattctat 180
 gcacagaagt ttcggggcag ggtcacaatg accagggaca cgtccatcag cacagcctac 240
 atggagctga gcagactgag atctgacgac acggccgtgt attattgtgc gagagaacct 300
 gaaaaattcg actccgacga ctccgacgtc tggggccgcg ggacattggt caccgtctcc 360
 tcaggaggcg gcagttcagg cggaggtggc tctggcggta gcggaagtgc acaggctgtg 420
 ctgactcagc cgccgtcagt gtctggggcc ccagggcaga gggtcacat ctctgcact 480
 gggagcagct ccaacatcgg ggcaggttat ggtgtacact ggtaccaaca gcttccagga 540
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 ttctctggt ccaagtctgg caccctcagc tccttgccca tcaactgggt ccaggctgag 660
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 ggtgggaccc agctcacctg cctaggt 747

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<400> 616
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<213> Homo sapiens

<400> 617
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1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Val Asn Trp Asn Gly Gly Thr Arg Asp Tyr Ala Ala Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

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Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr His Cys
85 90 95

Ala Arg Gly Trp Tyr Ser Gly Ala Ala Trp Asn Met Gly Tyr Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 618
<211> 110
<212> PRT
<213> Homo sapiens

<400> 618
Gln Ala Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

Ser Ile Thr Ile Ser Cys Thr Gly Ala Ser Gly Asp Val Gly Ala Tyr
20 25 30

Asn Phe Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Ile Ile Tyr Asp Val Asn Lys Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ser Leu Val Ser Asp
85 90 95

Phe Ser Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

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<400> 619
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1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

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Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Val Asn Trp Asn Gly Gly Thr Arg Asp Tyr Ala Ala Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr His Cys
85 90 95

Ala Arg Gly Trp Tyr Ser Gly Ala Ala Trp Asn Met Gly Tyr Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Ala Gln Ala Ala Leu Thr Gln Pro Ala Ser
145 150 155 160

Val Ser Gly Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Ala
165 170 175

Ser Gly Asp Val Gly Ala Tyr Asn Phe Val Ser Trp Tyr Gln Gln His
180 185 190

Pro Gly Lys Ala Pro Lys Leu Ile Ile Tyr Asp Val Asn Lys Arg Pro
195 200 205

Ser Gly Val Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala
210 215 220

Ser Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr
225 230 235 240

Cys Ala Ser Leu Val Ser Asp Phe Ser Val Val Phe Gly Gly Gly Thr
245 250 255

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Lys Leu Thr Val Leu
260

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Asp Tyr Gly Met Asn
1 5

<210> 621
<211> 17
<212> PRT
<213> Homo sapiens

<400> 621
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1 5 10 15

Gly

<210> 622
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1 5 10

<210> 623
<211> 16
<212> PRT
<213> Homo sapiens

<400> 623
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1 5 10 15

<210> 624
<211> 7
<212> PRT
<213> Homo sapiens

<400> 624
Asp Val Asn Lys Arg Pro Ser
1 5

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<210> 625
<211> 10
<212> PRT
<213> Homo sapiens

<400> 625
Ala Ser Leu Val Ser Asp Phe Ser Val Val
1 5 10

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<213> Homo sapiens

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ccaggcaagg gcctggagtg ggtgtccggc gtgaactgga acggcggcac cagagactac 180
gccgcctctg tgaagggcag attcaccatc agccgggaca acgccaagaa cagcctgtac 240
ctgcagatga acagcctgag agccgaggac accgccctgt accactgcgc cagaggctgg 300
tacagcggag ccgcctggaa catgggctac tggggcagag gcaccctggt gaccgtgtcc 360
agc 363

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<213> Homo sapiens

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caccocggca agggcccca gctgatcatc tacgacgtga acaagagacc cagcggcgtg 180
tccaacagat tcagcggcag caagagcggc aacaccgcca gcctgaccat cagcggactg 240
caggccgagg acgaggccga ctactactgc gccagcctgg tgtccgactt cagcgtggtg 300
ttcggcggag gcaccaagct gaccgtgctg 330

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<213> Homo sapiens

<400> 628
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ccaggcaagg gcctggagtg ggtgtccggc gtgaactgga acggcggcac cagagactac	180
gccgcctctg tgaagggcag attcaccatc agccgggaca acgccaagaa cagcctgtac	240
ctgcagatga acagcctgag agccgaggac accgccctgt accactgcgc cagaggctgg	300
tacagcggag ccgcctggaa catgggctac tggggcagag gcaccctggt gaccgtgtcc	360
agcggaggcg gcgggttcagg cggagggtggc tctggtggta gcggagggtg ctctggcggt	420
ggcggagggtg gctctggcgg tggcggaagt gcacaggccg ccctgaccca gcccgccagc	480
gtgtctggca gcccaggcca gagcatcacc atcagctgca ccggcgccag cggcgatgtg	540
ggcgctaca acttcgtgtc ctggtatcag cagcaccocg gcaaggcccc caagctgato	600
atctacgacg tgaacaagag acccagcggc gtgtccaaca gattcagcgg cagcaagagc	660
ggcaacaccg ccagcctgac catcagcggc ctgcaggccg aggacgaggc cgactactac	720
tgcgccagcc tgggtgtccga cttcagcgtg gtgttcggcg gaggcaccaa gctgaccgtg	780
ctg	783

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<400> 629	
gactacggca tgaac	15

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 <212> DNA
 <213> Homo sapiens

<400> 630	
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<210> 631
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 <212> DNA
 <213> Homo sapiens

<400> 631	
ggctggtaca gcggagccgc ctggaacatg ggctac	36

<210> 632
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 <212> DNA
 <213> Homo sapiens

<400> 632
accggcgcca gcggcgatgt gggcgccctac aacttcgtgt cc 42

<210> 633
<211> 21
<212> DNA
<213> Homo sapiens

<400> 633
gacgtgaaca agagaccag c 21

<210> 634
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<400> 634
gccagcctgg tgtccgactt cagcgtggtg 30

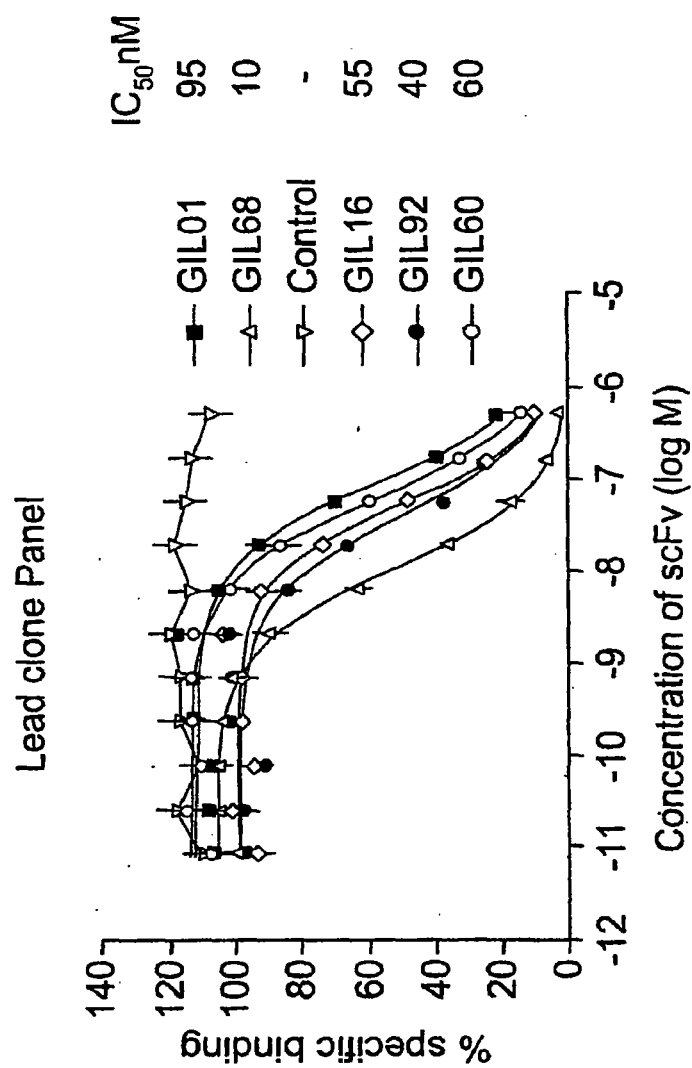


FIG. 1



163163



G00002

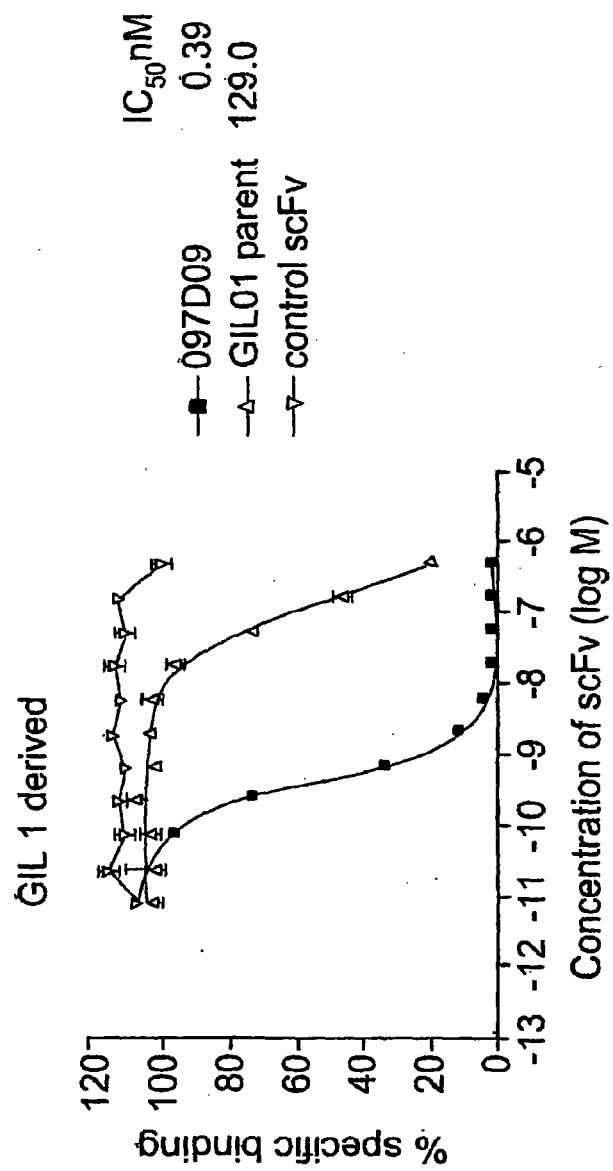


FIG. 2A

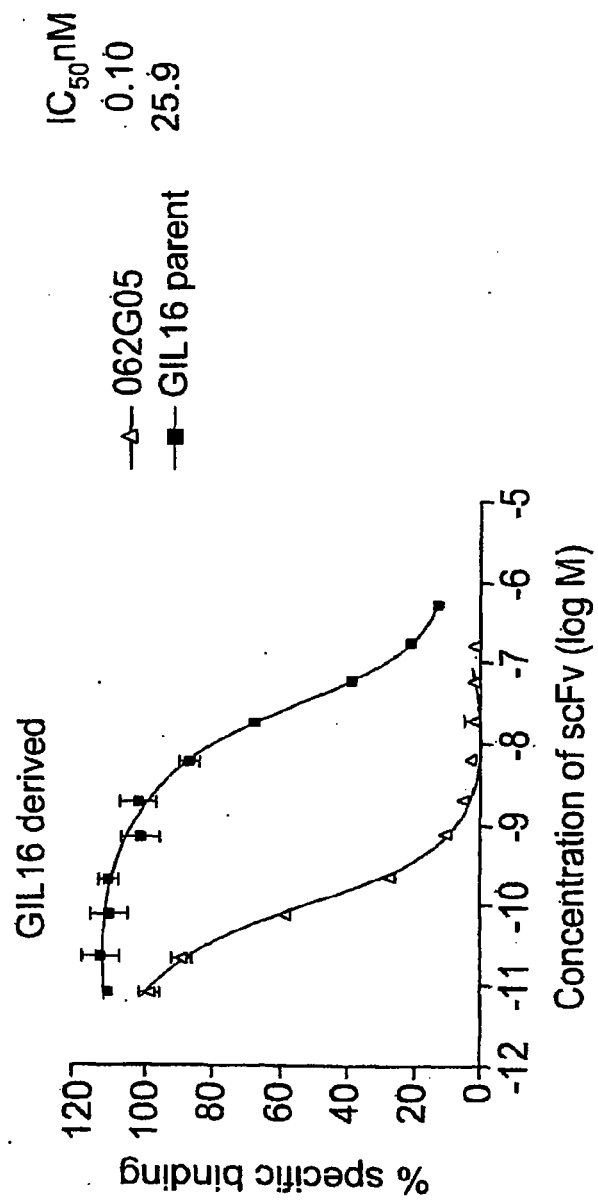


FIG. 2B

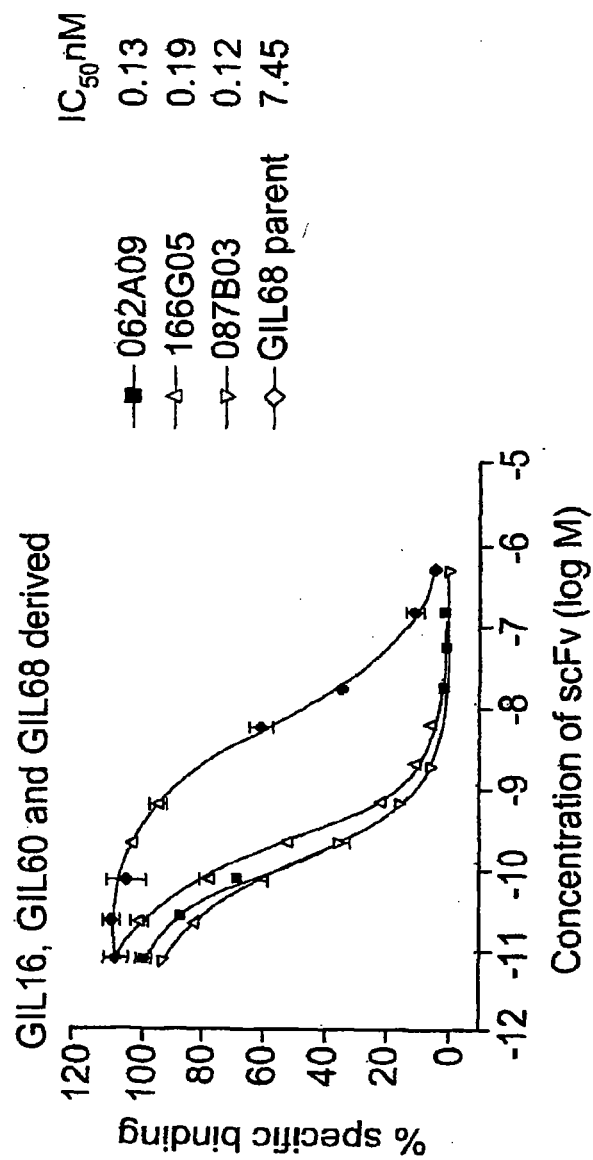


FIG. 2C

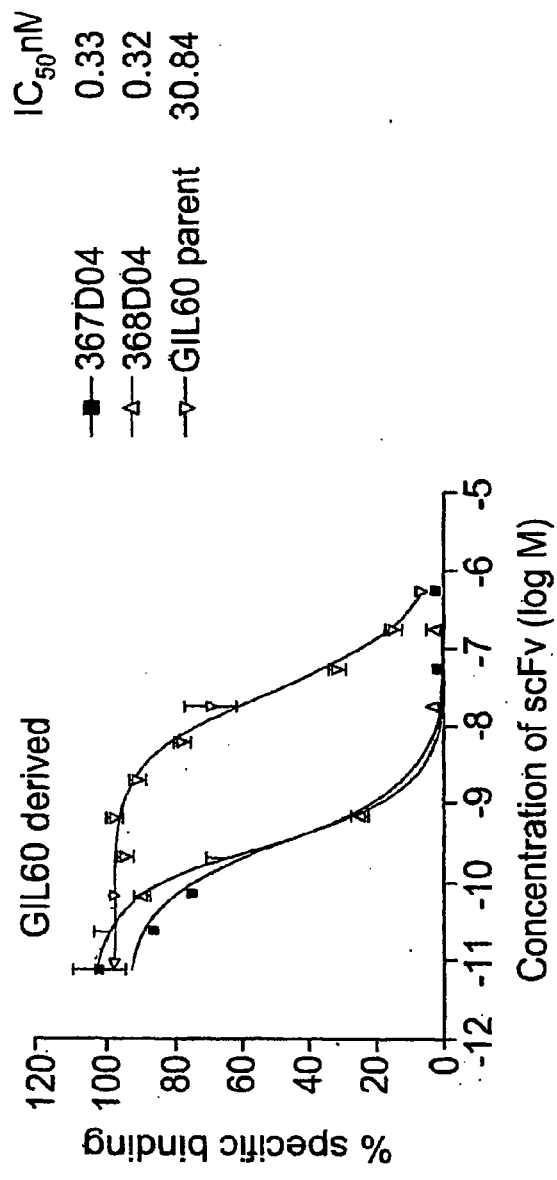


FIG. 2D

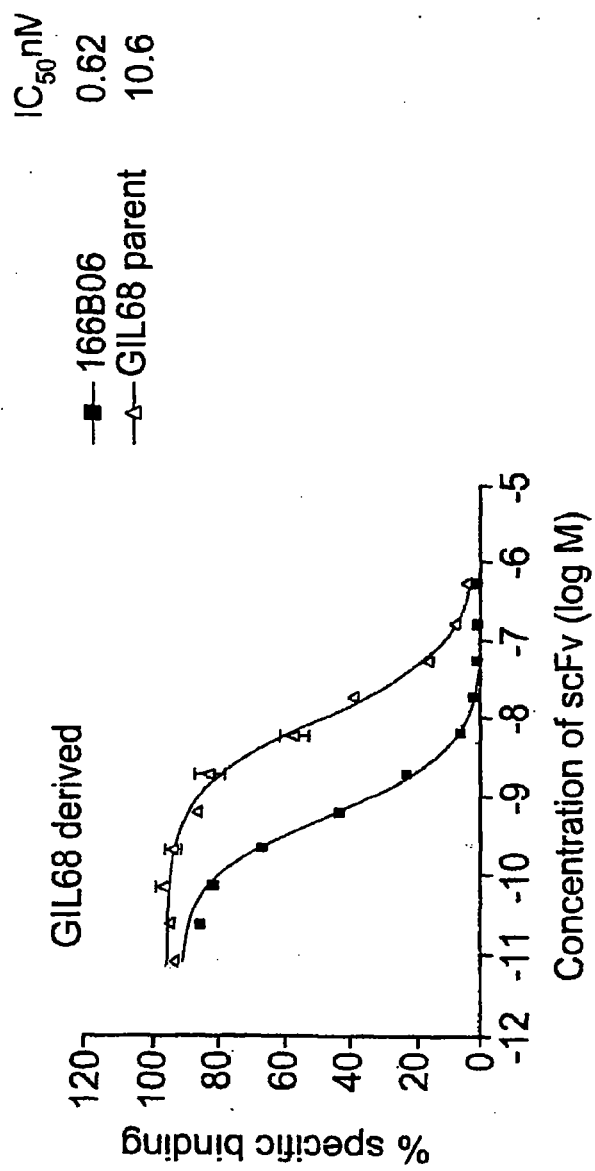


FIG. 2E

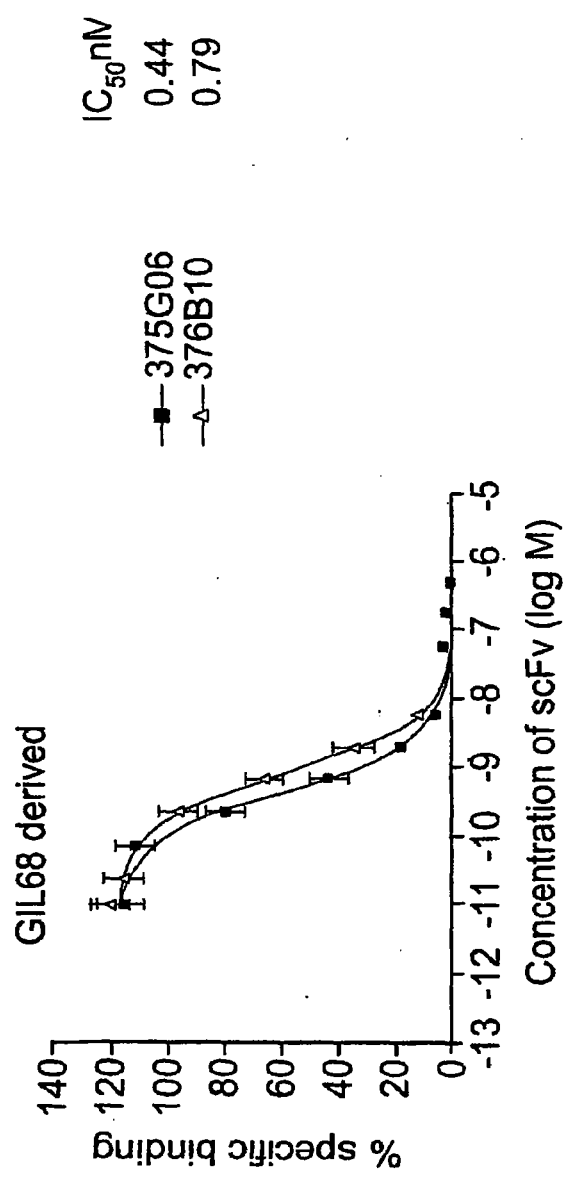


FIG. 2F

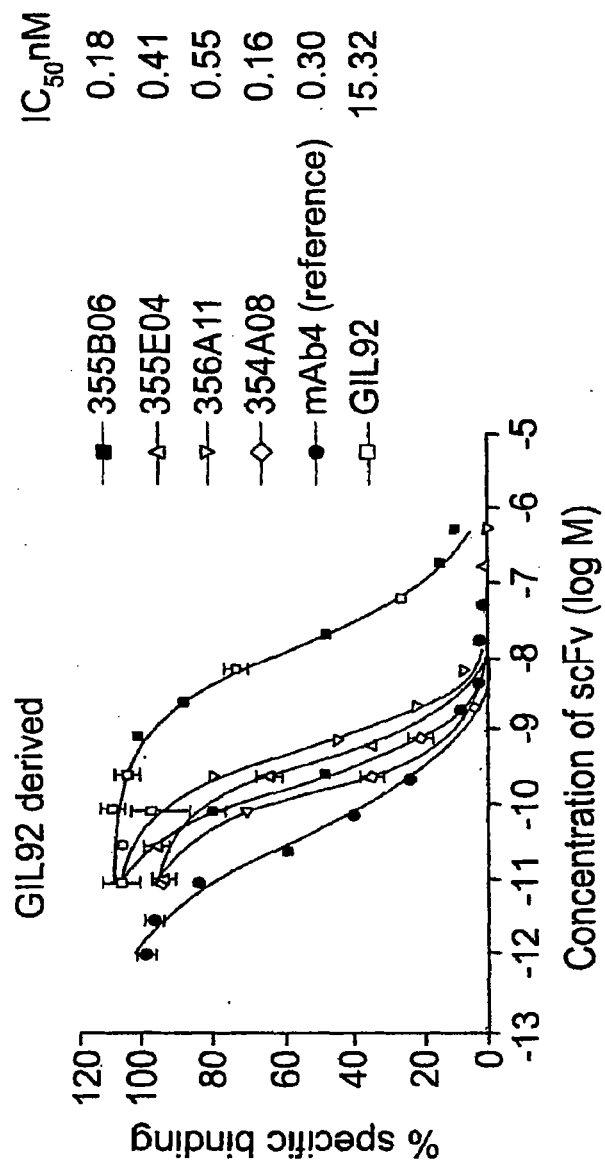


FIG. 2G

Germinated IgG

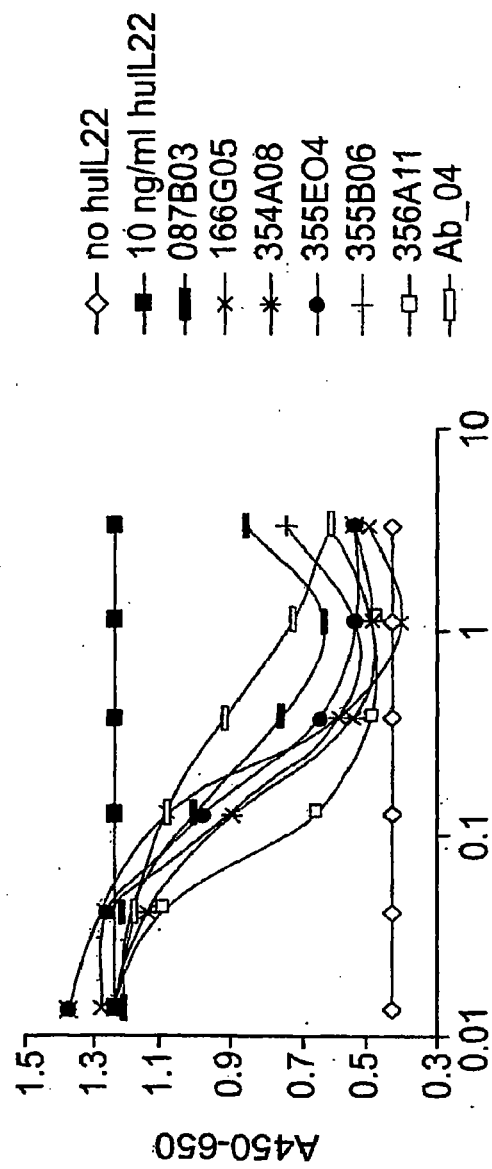


FIG. 3A

Non-germlined IgG

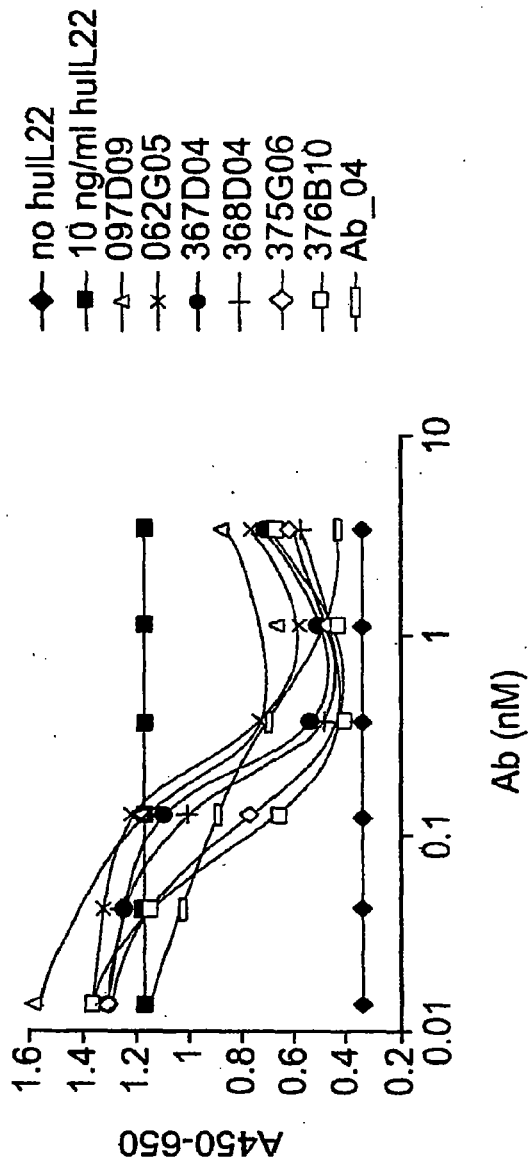


FIG. 3B

Germlined IgG

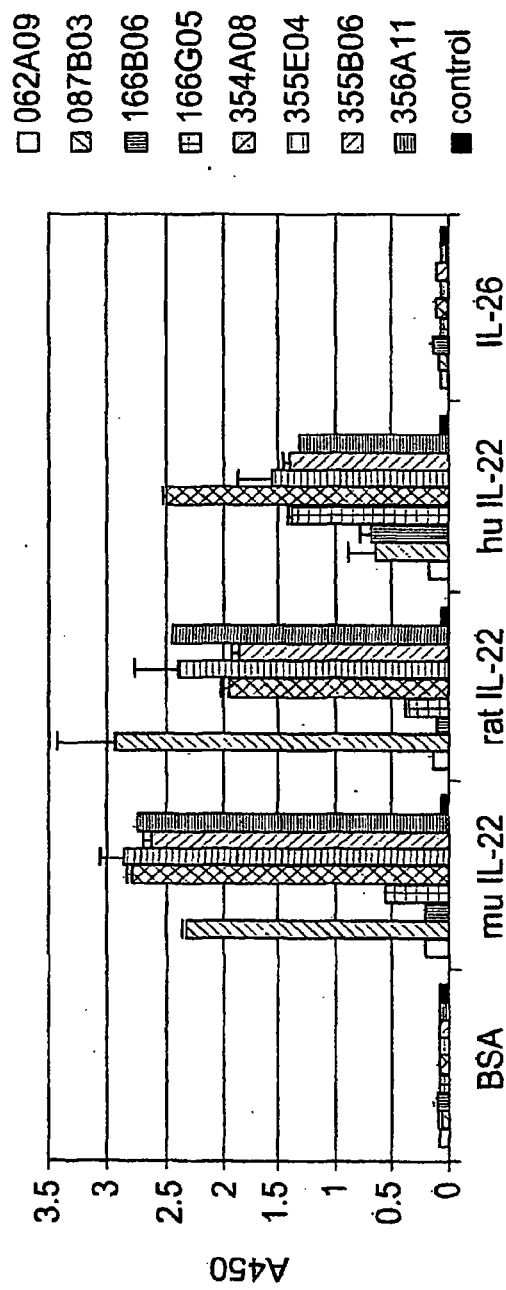


FIG. 4A

Non-Germinal IgG

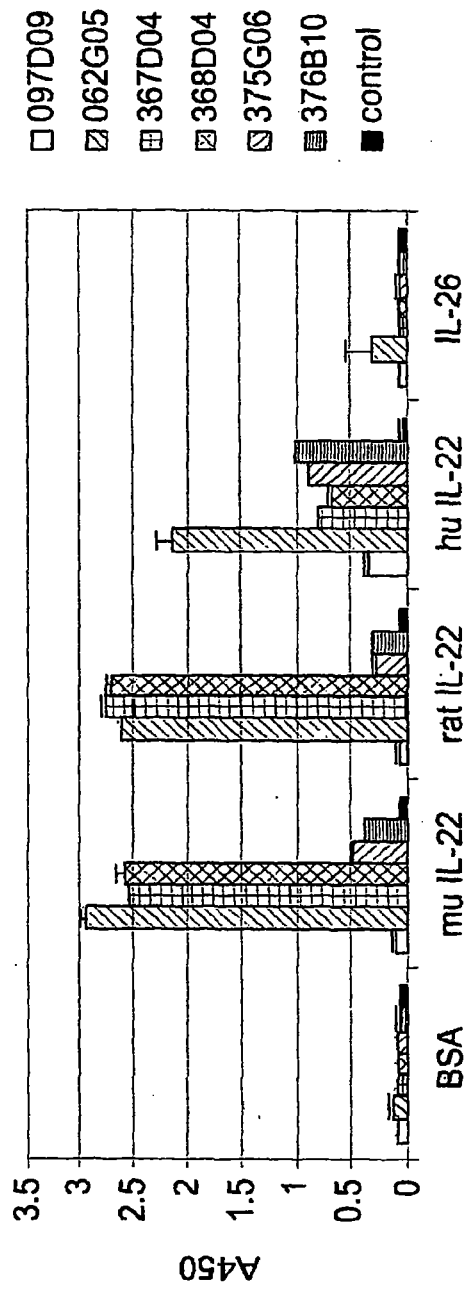


FIG. 4B

SEQ ID NO:1

1 MAALQKSVSS FLMGTLATSC LLLLALLVQG GAAAPISSHC RLDKSNFQQP
51 YITNRTFMLA KEASLADNNT DVRLIGEKLF HGVSMSERCY LMKQVLNFTL
101 EEVLFPQSDR FQPYMQEWPF LARLSNRLST CHIEGDDLHI QRVQKLKD
151 TVKKLGESGE IKAIGELDLL FMSLRNACI

SEQ ID NO:2

1 GAATTCGGCC AAAGAGGCCT ACAGGTTCTC CTTCCCCAGT CACCAGTTGC
51 TCGAGTTAGA ATTGTCTGCA ATGGCCGCCC TGCAGAAATC TGTGAGCTCT
101 TTCCTTATGG GGACCCTGGC CACCAGCTGC CTCCTTCTCT TGGCCCTCTT
151 GGTACAGGGA GGAGCAGCTG CGCCCATCAG CTCCCAGTGC AGGCTTGACA
201 AGTCCAACCT CCAGCAGCCC TATATCACCA ACCGCACCTT CATGCTGGCT
251 AAGGAGGCTA GCTTGGCTGA TAACAACACA GACGTTTCGT TCATTGGGGA
301 GAAACTGTTC CACGGAGTCA GTATGAGTGA GCGCTGCTAT CTGATGAAGC
351 AGGTGCTGAA CTTCAACCCTT GAAGAAGTGC TGTTCCTCA ATCTGATAGG
401 TTCCAGCCTT ATATGCAGGA GGTGGTGCCC TTCCTGGCCA GGCTCAGCAA
451 CAGGCTAAGC ACATGTCATA TTGAAGGTGA TGACCTGCAT ATCCAGAGGA
501 ATGTGCAAAA GCTGAAGGAC ACAGTGAAAA AGCTTGAGAG GAGTGGAGAG
551 ATCAAAGCAA TTGGAGAACT GGATTTGCTG TTTATGTCTC TGAGAAATGC
601 CTGCATTTGA CCAGAGCAAA GCTGAAAAAT GAATAACTAA CCCCTTTTCC
651 CTGCTAGAAA TAACAATTAG ATGCCCCAAA GCGATTTTTT TTAACCAAAA
701 GGAAGATGGG AAGCCAACT CCATCATGAT GGGTGGATTC CAAATGAACC
751 CCTGCGTTAG TTACAAAGGA AACCAATGCC ACTTTTGTTT ATAAGACCAG
801 AAGGTAGACT TTCTAAGCAT AGATATTTAT TGATAACATT TCATTGTAAC
851 TGGTGTTCTA TACACAGAAA ACAATTTATT TTTTAAATAA TTGTCTTTTT
901 CCATAAAAAA GATTACTTTC CATTCCTTTA GGGGAAAAAA CCCCTAAATA
951 GCTTCATGTT TCCATAATCA GTACTTTATA TTTATAAATG TATTTATTAT
1001 TATTATAAGA CTGCATTTTA TTTATATCAT TTTATTAATA TGGATTATT
1051 TATAGAAACA TCATTCGATA TTGCTACTTG AGTGTAAGGC TAATATTGAT
1101 ATTTATGACA ATAATTATAG AGCTATAACA TGTTTATTTG ACCTCAATAA
1151 ACACTTGGAT ATCCTAAAAA AAAAAAAAAA AAAGCGGCCG C

FIG. 5

SEQ ID NO:3

MAVLQKSMSESLMGTLAASCLLLIALWAEANALPVNTRCKLEVSNFQOPYI
VNRTEMLAKEASLADNNTDVRLIGEKLFGRVSAKDQCYLMKQVLNFTLEDVL
LPQSDRFQPYMQEVVPFLTKLSNQLSSCHISGDDQNIQKNVRLKETVKKLG
ESGEIKAIGELDLLFMSLRNACV

SEQ ID NO:4

ATGGCTGTCCTGCAGAAATCTATGAGTTTTTCCCTTATGGGGACTTTGGC
CGCCAGCTGCCTGCTTCTCATTGCCCTGTGGGGCCAGGAGGCAAATGCGC
TGCCCGTCAACACCCGGTGCAAGCTTGAGGTGTCCAACCTCCAGCAGCCG
TACATCGTCAACCGCACCTTTATGCTGGCCAAGGAGGCCAGCCTTGCAGA
TAACAACACAGACGTCCGGCTCATCGGGGAGAACTGTTCCGAGGAGTCA
GTGCTAAAGATCAGTGCTACCTGATGAAGCAGGTGCTCAACTTCACCCTG
GAAGACGTTCTGCTCCCCCAGTCAGACAGGTCCAGCCCTACATGCAGGA
GGTGGTACCTTTCCTGACCAAACCTCAGCAATCAGCTCAGCTCCTGTCACA
TCAGCGGTGACGACCAGAACATCCAGAAGAATGTCAGAAGGCTGAAGGAG
ACAGTGAAAAAGCTTGGAGAGAGTGGAGAGATCAAGGCGATTGGGGAACT
GGACCTGCTGTTTATGTCTCTGAGAAATGCTTGCGTCTGA

FIG. 6

GIL01

V_H (SEQ ID NO:5) with H1, H2, and H3 underlined (SEQ ID NO:8-10, respectively)

E V Q L V E S G G G L V T P G G S L R L S C A A S G F T F S
 D Y Y M S W I R Q A P G R G L E W V S A I S G S G S T Y Y
A D S V K G R I T I S R D N A K N S L Y L Q M S S L R S E D
T A V Y Y C A R G L W V W D P L D Y W G R G T L V T V S S

V_H (SEQ ID NO:14) with H1, H2, and H3 underlined (SEQ ID NO:17-19, respectively)

GAGTGCAGTTGGTGGACTCTGGGGGAGGCTTGCTCACCCCTGGAGGGTCCCTGAGACTCTCCTGTGTCAGCCCTTGATTACCTTCACTGACTACTACATGAGCTGGATCCGCCAGGCTCCAGG
 GAGGGGCTGGAGTGGTCTCAGCTATAGTGGTAGTGGTAGCAGACTACGAGACTCCGTGAGGGCCGATCACCATCTCCAGAGACAAACGCAAGAACTCACTGTA TCTGCAAAATGA
 GCAGCCTGAGATCTGAGGACACGGCCCTGATTACTGTGCGAGAGGGCTTGGGTTGGGATCCTTTCAGTACTACTGGGCGAGAGAACCCCTGGTCAACCGTCTCTCTCA

V_L (SEQ ID NO:6) with L1, L2, and L3 underlined (SEQ ID NO:11-13, respectively)

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

V_L (SEQ ID NO:15) with L1, L2, and L3 underlined (SEQ ID NO:20-22, respectively)

GACATCCAGATGACCCAGTCTCCTCCACCCCTGTCTGCATCTATTGGACAGAGTCACCATCACCTGCCGGGCCAGTGAGGGIATTTATCACTGGTGGCTGGTATCAGCAGAAGCCAGG
 GAAGCCCTAAACTCCTGATCTATAAGGCCCTAGTTAGCCAGTGGGGCCCCCATCAAGTTACGGGCGAGTGGATCTGGGACAGATTTTCACTCTCACCATCAGCAGCCTGCAGCCTGATG
 ATTTGCAACTTATTACTGCCCAACATATAGTAATTATCCGCTCACTTTCGGCGGAGGAGCCAGCTGGAGATCAACGT

FIG. 7

V_H (SEQ ID NO:23) with H1, H2, and H3 underlined (SEQ ID NO:26-28, respectively)

Q S T V

V_H (SEQ ID NO:32) with H1, H2, and H3 underlined (SEQ ID NO:35-37, respectively)

CAGGTGCAGCTGGTGGAGTCTGGAGCTGAGGTGAAGAAGCTGGGGCTCAGTGAAGGTCTCTGCAAGGCTTCTGGTTACACCTTTACCGAGTTATGGTATC
AGCTGGTGGCAGACAGGCCCTTGGACAAAGGCTTGAATGGATGGATTCAGCGCTTACACTGGTTACACAAACTATGCCACAGAGTTCACGGCCAGAGTC
ACCATACACACAGACACATCCACAGACACAGCCTACATGAACCTGAGGAGCCTGAGATCTGACGACACGGCCGCTGTATTACTGTGCCAGAGATCGTGGATAC
TATGATGCTTTTGATATCTGGGGCCAAAGGACCCCTGGTCACCGCTCTCTCTCA

v_L (SEQ ID NO:24) with L1, L2, and L3 underlined (SEQ ID NO:29-31, respectively)

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

V_L (SEQ ID NO:33) with L1, L2, and L3 underlined (SEQ ID NO:38-40, respectively)

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTATTGGAGACAGAGTCACCATCACCTGCGGGGCCAGTGAGGGTATTTATCATCTGGTTGGCC
TGGTATCAGCAGAGCCAGGGAAGCCCTAAACTCTGATCTATAAGCCCTCTAGTTTAGCCAGTGGGCCCATCAAGTTCAGCGGCACGTGATCTGGG
ACAGATTTCACTCTCAACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAACATATAGTAAATTATCCGCTCACTTTCGGCGGAGGGACC
AAGCTGGAGATCAACGT

FIG. 7(cont.)

GIL45

V_H (SEQ ID NO:41) with H1, H2, and H3 underlined (SEQ ID NO:44-46, respectively)

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

V_H (SEQ ID NO:50) with H1, H2, and H3 underlined (SEQ ID NO:53-55, respectively)

CAGATGCAGCTGGTGCAGTCTGGGGAGGCGGTGTCAGCCCTGGAGGTCCTCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAACATATGGCATGTACTGGGTCCGCCA
GGCTCCAGGCAAGGGCTGGAGTGGTGGACATATTTGGTATGATGAAGTAATGAAGAACTATGAGACTCCGTGAAGGCCCGGAATGACCGTCTCCAGAGACAATTCAGGAACA
CGTTGTATTTGCAATGAACAGCCTGAGAGCCGAGGACAGCGCTGTATTACTGTGCAGACAGACACATGATTAATCTGGGGCAAGGCCCTGGTCCACCGTCTCTCA

V_L (SEQ ID NO:42) with L1, L2, and L3 underlined (SEQ ID NO:47-49, respectively)

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

V_L (SEQ ID NO:51) with L1, L2, and L3 underlined (SEQ ID NO:56-58, respectively)

CAGTCTGTGCTGACTCAGCTGCCGTCTGGTCTGGTCTCTGGACAGTCGATACCATCTCCTGCACCTGGAACAGGAGTGACGTGGTGGTTATACTATGTCTCTCGGTACCA
ACAACACCCAGGCAAGCCCCAAACTCATGTATTTATGAGGCGAGTAAGCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCTCCCTGACAACTCT
CTGGGCTCCAGGCTGAGGAGGCGGTGATTATTACTGCAGCTCATATACAAACAGGAGCACTCGAGTTTTCGGCGGAGGACCAAGCTGACCGTCCCTAGGT

FIG. 7(cont.)

GIL60

V_H (SEQ ID NO:59) with H1, H2, and H3 underlined (SEQ ID NO:62-64, respectively)

E V Q L V E S G G G V V R P G G S L R L S C A A S G F T F D Y G M N
W V R Q A P G K G L E W V S G V N W N G G T R D Y A A S V K G R F T I
S R D N A K N S L Y L Q M N S L R A E D T A L Y Y C A R G W Y S G S F
Y Y F G Y W G R G T L V T V S S

V_H (SEQ ID NO:68) with H1, H2, and H3 underlined (SEQ ID NO:71-73, respectively)

GAGGTGACGTGTGGAGTCGGGGGAGGTGTGGTACGGGCTGGGGGTCCTGAGACTCTCTGTGCGAGCCTCTGGATTACCTTTACGATTATGGCATGAA
CTGGGTCCGCCAAGCTCCAGGAAGGGCTGGAGTGGGTCTCTGGTGTAAATTGGAATGGTGTACAGAGATTATGCAAGCTCCGTGAAGGGCCGATTCACCA
TCTCCAGAGACACGCCAAGAACTCCCTGTATCTGCAATGAACAGTCTGAGAGCCGAGGACACGGCCTGTATTACTGTGCGAGAGGATGGTATAGTGGGAGC
TTCTACTACTTTGGCTACTTGGGGCCGAGGAACCTGTGTCACCGTCTCCTCA

V_L (SEQ ID NO:60) with L1, L2, and L3 underlined (SEQ ID NO:65-67, respectively)

Q A V L T Q P S S V S G S P G Q S I T I S C T G A S G D V G A Y N F V
S W Y Q Q H P P G K T P K L I I Y D V N K R P S G V S N R F S G S K S G
N T A S L T I S G L Q A E D E S D Y Y C S S Y T S T F S V V F G G G T
K V T V L G

V_L (SEQ ID NO:69) with L1, L2, and L3 underlined (SEQ ID NO:74-76, respectively)

CAGGCTGTGCTGACTCAGCCGTCCTCCGTCTCTGGTCTCTGGACAGTCTCATACCATCTCTGCACTGGAGCCAGCGTGACGTTGGTCTTATTAACCTTGT
CTCCTGGTACCAACAACACCCAGGCAAAACCCCAACTCATATTATGATGTCAATAAGCGGCCCTCAGGGGTTTCTAATCGGTTCTCTGGCTCCAAGTCTG
GCAACAGGCTCTCCCTGACCATCTCTGGGCTCCAGGCGGAGGACGAGTCTGATTATTACTGCGCTCATATACAGCACCTTCTCTGTGGTATTGGCGGAGGG
ACCAAGGTCACCGTCTCTAGGT

FIG. 7(cont.)

GIL68

V_H (SEQ ID NO:77) with H1, H2, and H3 underlined (SEQ ID NO:80-82, respectively)

E V Q L V Q S G A E V K K P G A S V K V S C Q A S G Y T F S D Y Y I H W V R Q T P G
Q G F E W M G W V N P D T G G T R Y A O K F O G W V T M T R D M S N T T A Y M E L P
R L R D D D T A V Y Y C A R D L T G F D P F D I W G Q G T L V T V S S

V_H (SEQ ID NO:86) with H1, H2, and H3 underlined (SEQ ID NO:89-91, respectively)

GAGGTCCAGCTGGTGCAGTCTGGGCTGAGGTGAAGAGCCCTGGGGCTCAGTGAAGTCTCTCTCAGGCTTCTGGATACACCTTCAGCGATTACTATATTCACCTGGTGCGACAGACCCCTGGA
CAAGGTTTGAGTGGATGGGTCAACCTGACACTGGTGGCACAAGATACCGCAGAGTTTCAGGGCTGGTCAATGACCAGGACATGTCCAACACACACAGCTACATGGAGCTGCCC
AGGCTGAGAGACGACGACGGCCGTATATTACTGTGCGAGATCTAACGTGATTGATCTTTTGATATCTGGGGCCAGGGAACCTTGGTCAACCGTCTCTCA

V_L (SEQ ID NO:78) with L1, L2, and L3 underlined (SEQ ID NO:83-85, respectively)

Q S V L T Q P P S V S V A P G K T A T I T C G G N N F R N K R V H W Y Q Q R P G Q A
P V L V I Y D S D R P S G I P E R F S G S R S G N T A T L T I S R V E A G D E A D
F Y C Q V W D S S T D R P L F G G G T K L T V L G

V_L (SEQ ID NO:87) with L1, L2, and L3 underlined (SEQ ID NO:92-94, respectively)

CAGTCTGTGCTCAGCCACCCTCAGTGTCACTGGGCCCCAGGAAGACGGCCAGGATTACCTGTGGGGAACAACCTTCGAATAAAGAGTACACTGGTATCAGCAGAGGCCAGGCCAGG
CCCCGTCTCTGCTCATCTATTATGATTACAGACCGGCCCTCAGGGATCCCTCAGCGATTCTTGCTCCCGTCTGGGAACAGGGCCACCCCTGACCATCAGCAGGTCGAGGCGGGGATGAGC
CGACTTTACTGTCAAGTGTGGGATAGTAGTACTGATCGTCCGCTTTCGGCGGAGGACCAAGCTGACCCCTCCTAGGT

FIG. 7(cont.)

GIL92

V_H (SEQ ID NO:95) with H1, H2, and H3 underlined (SEQ ID NO:98-100, respectively)

Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T F T D Y Y
M H W V R Q A P G Q G L E W V G W I N P Y T G G A F Y A O K F R G
R V T M T R D T S I N T A Y M E L S R L G S D D T A V Y Y C A R E
P E K F D F W G G D N W G R G T M V T V S S

V_H (SEQ ID NO:104) with H1, H2, and H3 underlined (SEQ ID NO:107-109, respectively)

CAGGTCACGCTGGTCCAGTCTGGGGCTGAGGTGAAGACCTGGGGCTCAGTGAAGGCTCTCTGCAAGGCTCTGGATACACCTTCACCGACTACTA
TATGCACTGGGTCCGACAGGCCCTGGACAAGGCTTGAAGGCTGGATGATCAACCTTATCTGCTGGCCATCTATGCACAGAAGTTCCGGG
GCAGGTCAATGACAGGGACAGCTCCATCAACAGCTACATGAGCTAGCAGACTGGGATCTGACGACACGGCCGTGTTATTGTGCGAGA
GAACCTGAATAATTCGATTTTGGGGGGTGACAACTGGGGCCGGGACAAATGGTCACCGTCTCCTCA

V_L (SEQ ID NO:96) with L1, L2, and L3 underlined (SEQ ID NO:101-103, respectively)

Q A V L T Q P S S V S G A P G Q R V T I S C T G S S S N I G A G Y
G V H W Y Q Q L P G T A P K L L I Y G N S N R P S G V P D R F S G
S K S G T S A S L A I T G L Q A E D E A D Y Y C Q S Y D S S L S G
Y V F G T G T Q L T V L G

V_L (SEQ ID NO:105) with L1, L2, and L3 underlined (SEQ ID NO:110-112, respectively)

CAGGCTGTGCTGACTCAGCCGCTCCTCAGTGTCTGGGGCCCGAGGAGGCTCACCATCTCTGCACTGGGAGGAGCTCCAACATCGGGGACGGTTA
TGGTGACACTGGTACCAACAGTTCCAGGAACAGCCCCCAAACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTG
GCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCTCTATGACAGCAGCCCTGAGT
GGTTATGCTTCGGAACTGGGACCCAGCTCACCGTCTCCTAGGT

FIG. 7 (cont.)

097D09

V_H (SEQ ID NO:113) with H1, H2, and H3 underlined (SEQ ID NO:116-118, respectively)

E V Q L V E S G G G L V T P G G S L R L S C A A S G F T F S D Y Y M
S W V R Q A P G R G L E W V S A I S G S G G S T Y Y A D S V K G R I
T I S R D N A K N S L Y L Q M S S L R S E D T A V Y Y C A R G L W V
W D P L D Y W G R G T L V T V S S

V_H (SEQ ID NO:122) with H1, H2, and H3 underlined (SEQ ID NO:125-127, respectively)

G A G G T C A G C T G T G G A G T C G G G A G G C T T G G T C A C G C C T G G A G A C T C T C C T G T G C A G C C T C T G G A T T C A C T T C A G T A C T A C A T G
A G C T G G T C C G C A G G C C A G G A G G G C T G G A G T G G T C A G C T A T T A G G T A G T G T G T A G C A T A C T A C G C A G A C T C C G T G A A G G G C G G A T C
A C C A T C C A G A C A C C A A G A A C T C A C T G T A T C T G C A A T G A G C A G C C T G A G A T C T G A G G A C A C G G C G T G T A T T A C T G C G A G A G G C T T T G G G T T
T G G A T C C T C T T G A C T A C T G G G C A G A G G A A C C C T G T C A C C G T C T C C T C A

V_L (SEQ ID NO:114) with L1, L2, and L3 underlined (SEQ ID NO:119-121, respectively)

D I Q M T Q S P S T L S A S I G D R V T I T C R A S E G I Y H W L A
W Y Q Q K P G K A P K L L I Y K A S S L A S G A P S R F S G S G F G
T D F T L T I S S L Q P D D F A T Y Y C Q O Y S E F A W T F G G G T
K L E I K R

V_L (SEQ ID NO:123) with L1, L2, and L3 underlined (SEQ ID NO:128-130, respectively)

G A C A T C A G A T G A C C C A G T C C T T C C A C C C T G T G C A T C T A T T G G A C A C A G T C A C C A T C A C C T G C C G G G C C A G T C A G G G T A T T A T C A C I G T T G G C C
T G G T A T C A G C A G A G C C A G G A A G C C C T A A C T C T G A T C T A T A G G C C T C T A G T T A G C C A G T G G G C C C A T C A G G T T C A G C G C A G T G G A T T G G G
A C C G A T T C A C T C T C A C C A T C A G C A G C C T G C A G C C T G A T G A T T T G C A A C T A T T A C T G C C A C A T A C A G C A G T T C C C T G S A C C T T C G C G G A G G A C C
A A G C T G C A G A T C A A A C G T

FIG. 7(cont.)

062A09

V_H (SEQ ID NO:131) with H1, H2, and H3 underlined (SEQ ID NO:134-136, respectively)

Q V Q L V E S G A E V K K P G A S V K V S C K A S G Y T F T S Y G I
S W V R Q A P G Q G L E W M G W V S A Y T G N T N Y A O K F O G R V
T M T T D T S T S T A Y M E L R G L R S D D T A V Y Y C A R D R G Y
Y D A F D I W G Q G T L V T V S S

V_H (SEQ ID NO:84) with H1, H2, and H3 underlined (SEQ ID NO:143-145, respectively)

AGGTGCAGCTGGTGGAGTCTGGGGCTGAGGTGAAGAGCCCTGAGTGAGGCTCTCTGCAAGGCTTCTGGTTACACCTTTACCACTTANGSTATCA
GCTGGGTGGACAGCCCTGGACAGGGCTTGAGTGGATGGGATGGGCTTACACTGGTAAACAAACTAAGCACAGAGTTCCAGGGCAGAGTCA
CCATGACCACAGACATCCACGAGCACAGCCATCATGGAACCTGAGGGGCTGAGATCTGACGACACGGCCGCTGTATTACTGTGCGAGATCGTGGATACT
ATGATGCTTTTGATATCTGGGGCCAAAGGCACCCCTGGTCACCGTCTCTCA

L (SEQ ID NO:132) with L1, L2, and L3 underlined (SEQ ID NO:137-139, respectively)

I Q M T Q S P S T L S A S I G D R V T I T C R A S E G I Y H W L A W
Y Q Q K P G K A P K L L I Y K A S S L A S G A P S R F S G S G F G T
D F T L T I S S L Q P D D F A T Y Y C O O M G E Y N A T I G G G T K
L E I K R

L (SEQ ID NO:141) with L1, L2, and L3 underlined (SEQ ID NO:146-148, respectively)

ACATCCAGATGACCCAGTCTCTCCACCCCTGTCTGCATCTATTGGAGACAGAGTCACCATCACCTGCCGGCCAGTGAGGGTATTATCACTGGTTGGCCT
GGTATCAGCAGAACCCAGGAAGCCCTAACTCCCTGATCTATAGCCCTCTAGTTAGCCAGTGGGGCCCATCAAGTTTCAGCGGCAGTGGATTGGGA
CAGATTTCACCTCACCATCAGCAGCCTGCAGCCTGATTTTGCACCTATTACTGCCAACAAATGGGGGAGTACACGCCACCATCGCGGGAGSGACCA
AGCTGGAGATCAACCGT

FIG. 7(cont.)

062G05

V_H (SEQ ID NO:149) with H1, H2, and H3 underlined (SEQ ID NO:152-154, respectively)

Q V Q L V E S G A E V K K P G A S V K V S C K A S G Y T F T S Y G I S
W V R Q A P G Q G L E W M G W I S A Y T G N T N Y A O K F O G R V T M
T T D T S T S T A Y M E L R S L R S D D T A V Y Y C A R D R G Y Y D A
F D I W G Q G T L V T V S S

V_H (SEQ ID NO:158) with H1, H2, and H3 underlined (SEQ ID NO:161-163, respectively)

CAGGTGCAGCTGGTGGAGCTCGAGGTGAGTGAAGACCTGGGGCCCTCAGTGAAGGTCCTCGCAGGCTTCTGGTACACCTTTACCAGTTATGGTATCAGC
TGGGTGGCAGACAGGCCCTGGACAGGGCTTGAGTGGATGGATCAGGCTTACACTGGTAACAGAACTATGCACAGAGTTCAGGCGCAGAGTCACCATG
ACCACAGACACATCCACGACAGCCTACATGGAACTGAGAGGCTGAGATCTGACGACACGGCCGTATTACTGTGCGAGAGATCGTGGATACATGATGCT
TTGGATATCTGGGGCCAGGCACCTGGTCACCGTCTCCTCA

V_L (SEQ ID NO:150) with L1, L2, and L3 underlined (SEQ ID NO:155-157, respectively)

D I Q M T Q S P S T L S A S I G D R V T I T C R A S E G I Y H N L A W
Y Q Q K P G K A P K L L I Y K A S S L A S G A P S R F S G S G F G T D
F T L T I S S L Q P D D F A T Y Y C Q O M G E W K A A F G G G T K L E
I K R

V_L (SEQ ID NO:159) with L1, L2, and L3 underlined (SEQ ID NO:164-166, respectively)

GACATCCAGATGACCCAGTCTCTCCACCCCTGCTCCATCTATTGGAGACAGATCACCATCACCTGCCGGGCCAGTGAAGGTATTTATCACTGGTTGGCCTGG
TATCAGCAGAGCCAGGGAAGCCCTAACTCTGATCTATAGGCCCTTAGTTAGCCAGTGGGCCCCATCAAGGTTACAGCGCAGTGGATTGGGACAGAT
TTCATCTCACCATCAGCAGCCCTGACGCTGATGTTTGGCACTTATTACTGCCAACAAATGGGGAGTGGAGGGGCTTCGGCGGAGGCAAGCTGGAGATCAACGCT

FIG. 7(cont.)

087B03

V_H (SEQ ID NO:167) with H1, H2, and H3 underlined (SEQ ID NO:170-172, respectively)

E V Q L V E S G G G V V R P G G S L R L S C A A S G F T F D D Y G M N
W V R Q A P G K G L E W V S G V N W N G G T R D Y A A S V K G R F T I
S R D N A K N S L Y L Q M N S L R A E D T A L Y Y C A R G W Y S G A A
W N M G Y W G R G T L V T V S S

V_H (SEQ ID NO:176) with H1, H2, and H3 underlined (SEQ ID NO:179-181, respectively)

GAGGTGACGTGTTGAGTCCGGGGAGGTGTGGTACGGCCCTGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTGACGATTATGGCAIGAAC
TGGTCCGCCAAGCTCCAGGAAGGGCTGGAGTGGTCTCTGTGTAAATGGATGGTGTACAGAGATTATGCAGCTCCGTGAAGGCCGCGATTCCACCATC
TCCAGAGACAACGCCAAGACTCCCTGTATCTGCAATGAACAGTCTGAGCGCGAGACACGGCTTGATTACTGTGCGAGAGATTGGTATAGTGGGGCCGCG
TGGAACATGGGCTACTGGGCGGAGGAACCCCTGGTCAACGCTCTCTCA

V_L (SEQ ID NO:168) with L1, L2, and L3 underlined (SEQ ID NO:173-175, respectively)

Q A V L T Q P S S V S G S P G Q S I T I S C T G A S G D V G A Y N F V
S W Y Q Q H P G K T P K L I I Y D V N K R P S G V S N R F S G S K S S
N T A S L T I S G L Q A E D E S D Y Y C S S Y T S T F S V V F G G G T
K V T V L G

V_L (SEQ ID NO:177) with L1, L2, and L3 underlined (SEQ ID NO:182-184, respectively)

CAGGCTGTGCTGACTCAGCCGTCCTCGGTGTCTGGGTCTCTGACAGTCGATCACCATCTCTGCACTGGAGCCAGCGGTGACGTTGGTGCTATATACTTTGTC
TCCTGGTACCAACAACAGCCAGGCAACCCCAACTCATATTATGATGTCATAGCGGCCCTCAGGGTTCTAATCGCTTCTCTGGCTCCCAAGCTAGC
AACACGGCTCCCTGACCATCTCTGGGCTCCAGGCCGAGGACGAGTCTGATTATTACTGCAGCTCATATACACACCTCTCTGTTGGTATTGGCGGAGGGACC
AAGGTCACCGTCTCTAGGT

FIG. 7(cont.)

367D04

V_H (SEQ ID NO:185) with H1, H2, and H3 underlined (SEQ ID NO:188-190, respectively)

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

V_H (SEQ ID NO:194) with H1, H2, and H3 underlined (SEQ ID NO:197-199, respectively)

GAGGTGAGCTGGTGGAGTCCGGGGGAGGTGGGTACGGCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCCTTGGATTCACTTGCAGATTATGGCATGAACCTGGGT
CCGCCAAGCTCCAGGAAGGGCTGGAGTGGTCTCTGCTGTTAAATTGCAATGGTGGTACAGAGATTATGCAGCCCTCCGTGAGGGCCGATTACCATCTCCAGAGACA
ACGCCAAGAATCCCTGTATCTGCAATGAACAGTCTGAGAGCCGAGGACACGGCTTGTATTACTGTGGCAGAGGATGGTATAGTGGAGCCCGTGGTGGCTGGGCCAC
TGGGGCCGAGGAACCTGTGTCACCGTCTCCTCA

V_L (SEQ ID NO:186) with L1, L2, and L3 underlined (SEQ ID NO:191-193, respectively)

Q A V L T Q P S S V S G S P G Q S V T I S C T G A S G D V G A Y N F V S W
Y Q Q H P G K T P K L I I Y D V N K R P S G V S N R F S G S K S G N T A S
L T I S R L Q A E D E S D Y Y C S S Y T S R Y T T E F G G G T K V T V L G

V_L (SEQ ID NO:195) with L1, L2, and L3 underlined (SEQ ID NO:200-202, respectively)

CAGGCTGTGCTGACTCAGCGCTCCTCGGTGTGGTCTCCTGCACAGTCGGTCACTCTCCATCTCTGCAGTGGAGCCAGCGGTGAGCTTGGTGCTTATAAATTTGTCTCTG
GTACCAACAACACCCAGGAAACCCCAACTCATATTTATGATGTCAATAAGCGGCTCAGGGTTCTAATCGCTTCTCTGGCTCAAGTCTGGCAACACGGCT
CCCTGACCATCTCTAGGCTCCAGGCCGAGGACGAGTCTGATTATTACTGAGCTCATATACATCGAGGTACAGACCGAGTTTGGCGAGGGACCAAGTCAACCGTCCCTAGGT

FIG. 7(cont.)

368D04

V_H (SEQ ID NO:203) with H1, H2, and H3 underlined (SEQ ID NO:206-208, respectively)

E V Q L V E S G G G V V R P G G S L R L S C A A S G F T F D D Y G M N W
V R Q A P G K G L E W V S G V N W N G G T R D Y A A S V K G R F T I S R
D N A K N S L Y L Q M N S L R A E D T A L Y Y C A R G W Y S G A A W N M
G Y W G R G T L V T V S S

V_H (SEQ ID NO:212) with H1, H2, and H3 underlined (SEQ ID NO:215-217, respectively)

GAGGTGACGCTGGTGGAGTCCGGGGAGGTGGTACGGCTGGGGCTCCCTGAGACTCTCTGTCAGCCTTGATTCACCTTTGACGATTATGGCATGAAC TG
GGTCCGCCAAGCTCCAGGGAAGGGCTGGAGTGGGTCTCTGGTGTAAATGGATGGTGACAGAGATTATG CAGCCTCCGTGAAGGCGGATTCACCATCTCCA
GAGACACGCCAAGAACTCCCTGTATCTGCAATGAACAGTCTGAGAGCCGAGCACCGGCTTGTATTACTGTGCGAGAGGATGGTATAGTGGGCGCGGTGGAA C
ATGGGCTACTGGGCGGAGAACCCCTGGTCACCGTCTCTCA

V_L (SEQ ID NO:204) with L1, L2, and L3 underlined (SEQ ID NO:209-211, respectively)

Q A V L T Q P S S V S G S P G Q S I T I S C T G A S G D V G A Y N F V S
W Y Q Q H P G K T P K L I I Y D V N K R P S G V S N R F S G S K S G N T
A S L T I S G L Q A E D E S D Y Y C A S L V S D F S V V F G G G T K V T
V L G

V_L (SEQ ID NO:213) with L1, L2, and L3 underlined (SEQ ID NO:218-220, respectively)

CAGGCTGTGACTCAGCCGTCCTCGGTGTCTGGTCCCTGGACACTCGATCACCATCTCTGCACTGGAGCCAGCGGTGACGTTGGTGTATAACTTTGTCTC
CTGGTACCAACACCCAGGCAAAACCCCAACTCATAATTATGATGTCATAAAGCGGCTCAGGGGTTCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACA
CGGCTCCCTGACCACTCTGGGCTCCAGGCGGAGGAGTCTGATTTACTGGCTCCCTGCTCGGACTTCTGTTGGTATTGGCGGAGGACCAAGGTACCGTCTTAGGT

FIG. 7(cont.)

166B06

V_H (SEQ ID NO:221) with H1, H2, and H3 underlined (SEQ ID NO:224-226, respectively)

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

V_H (SEQ ID NO:230) with H1, H2, and H3 underlined (SEQ ID NO:233-235, respectively)

GAGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAGAAGCTGGGGCTCAGTGAAGTCTCCTGTACGGTCTCGGATACACCTTCACGGATTACTATATTCACCTG
GGTCCGACAGACCCCTGGACAAGGTTTGAGTGGATGGGATGGGTACCCCTGACACCTGGTGGCACAAGATACCGGCAGAGTTTCAGGGCTGGTCACAATGACCA
GGACATGTCCAAACACACAGCCTACATGGAGCTGCCAGCTGAGAGACGACACGCGCGTATATTACTGTCCGAGAGATCTAACTGGATTGATCCCTTTTGAT
ATCTGGGGCCAGGGAAACCTGGTCACCGTCTCTCA

V_L (SEQ ID NO:222) with L1, L2, and L3 underlined (SEQ ID NO:227-229, respectively)

Q S V L T Q P P S V S V A P G K T A T I T C G G N N F R N K R V H W Y Q
Q R P G Q A P V L V I Y Y D S D R P S G I P E R F S G S R S G N T A T L
T I S R V E A G D E A D F Y C Q V W D L F N D N G V F G G G T K L T V L
G

V_L (SEQ ID NO:231) with L1, L2, and L3 underlined (SEQ ID NO:236-238, respectively)

CAGTCTGTGCTGACTCAGCCACCTCAGTGTGAGTGGCCCGCAGGAACACCGCCACGATTACCTGTGGGGAAACAACCTTCGAAATAAAGATACACTGGTATCA
GCAGAGGCCAGGCCGCCCTGTCTGTGTCATCTATTATGACTCAGACCGGCCCTCAGGGATCCCTGAGCGATTCTGTGGTCCCGTCTGGGAACACGGCCACCC
TGACCATCAGAGGTGAGGCCGGGATGAGGCCGACTTTTACTGTGAGGTGGGATCTCTCAAGGACACGGGGTTCGGGGAGGACCAAGCTACCGTCTCTAGGT

FIG. 7(cont.)

166G05

V_H (SEQ ID NO:239) with H1, H2, and H3 underlined (SEQ ID NO:242-244, respectively)

E V Q L V Q S G A E V K K P G A S V K V S C Q A S G Y T F S D Y Y I H W V
R Q T P G Q G F E W M G W V N P D T G G T R Y A O K F Q G W V T M T R D M
S N T T A Y M E L P R L R D D D T A V Y Y C A R D L T G F D P F D I W G Q
G T L V T V S S

V_H (SEQ ID NO:248) with H1, H2, and H3 underlined (SEQ ID NO:251-253, respectively)

GAGGTGCAGCTGGTGCAGCTGGGGCTGAGTGAAGAGCCCTGGGGCCCTCAGTGAAGGCTCTCTGTCAGGCTTCTGGATACACCTTCAGCGATTACTATATCACTGGGT
GGCACAGACCCCTGGACACAGGTTTGGAGTGGATGGGTGACCTGACCTGACCTGGTGGCACAAGATACCGCAGAGATTTCAGGGCTGGGTACACATGACCAGGGACA
TGTCACACACACAGCTACATGGAGTGGCAGCTGCCAGGCTGAGAGACGACACGCGCGTATATTACTGTGCGAGAGATCTAACTGGATTTCATCTTTGATATCTGGGGC
CAGGACCCCTGGTCACCGTCTCTCA

V_L (SEQ ID NO:240) with L1, L2, and L3 underlined (SEQ ID NO:245-247, respectively)

Q S V L T Q P P S V S V A P G K T A T I T C G G N N F R N K R V H W Y Q Q
R P G Q A P V L V I Y Y D S D R P S G I P E R F S G S R S G N T A T L T I
S R V E A G D E A D F Y C Q V W D F L T D S G S F G G G T K L T V L G

V_L (SEQ ID NO:249) with L1, L2, and L3 underlined (SEQ ID NO:254-256, respectively)

CAGTCTGTGCTACTCAGCACCCCTCAGTGTGAGTGGCCCCAGAAAGACGGCCACAATTACCTGTGGGGGAACAACCTTCGAATAAAGAGTACACTGGTATCAGCA
GAGGCCAGCCAGCGCCCTGTCTGTGTCATCTATTATGATTACACACCGCCCTCAGGATCCCTGACGATTCTCTGGTCCCGCTCTGGGAACACGGCCACCCCTGACCA
TCAGCAGGCTCGAGCGGGGATGAGCCGACTTTTACTGTCAAGTGTGGGATTTCCTCAGCGACTCGGGGTCGTTCGGCGGAGGACCAAGCTGACCGTCCCTAGGT

FIG. 7(cont.)

375G06

V_H (SEQ ID NO:257) with H1, H2, and H3 underlined (SEQ ID NO:260-262, respectively)

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

V_H (SEQ ID NO:266) with H1, H2, and H3 underlined (SEQ ID NO:269-271, respectively)

GAGTGCAGCTGGTGGGGCTGAGGTGAAGAGCCTGGGGCCTCAGTGAAGTCTCTGTCAAGCTTCTGGATACACCTTCAGCGATTACTATATTCACTG
GGTGGCAGACACCCCTGGACAGGGTTTGAAGTGGATGGGTCAACCTGACACTGGTGGCACAAGATACGGGCAGAGTTTCAGGGTGGGTACACATGACCA
GGGACATGTCCAACACACACAGCCTACATGGAGCTGCCAGGCTGAGAGACGACGACGGCCGTATATTACTGTGCGAGAGATCTTAAGTGGATACGACTACTACGAC
CGTGGGGCCAGGGAACCCCTGGTCACCGTCTCTCTCA

V_L (SEQ ID NO:258) with L1, L2, and L3 underlined (SEQ ID NO:263-265, respectively)

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

V_L (SEQ ID NO:267) with L1, L2, and L3 underlined (SEQ ID NO:272-274, respectively)

CAGTCTGTGCTGACTCAGCCGCCCTCAATGTCACTGGCCCGCCAGGAAGACGGCCACCATTAACCTGTGGGGGAACAACACTTTCGAATAAAGAGTACACTGGTATCA
GCAGAGGCCAGGCCGCCCTGTCTGTGTCATCTATTATGATTACAGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCCGCTCTGGGAACACGGGCCACCC
TGACCATCAGCAGGTCGAGCGCGGATGAGGCCACTTTTACTGTCAAGTCTGGATTCTCTGGCCGACGAGCGGATGTGGCGGAGGACCAAGCTGACCGTCTAGGT

FIG. 7(cont.)

376B10

V_H (SEQ ID NO:275) with H1, H2, and H3 underlined (SEQ ID NO:278-280, respectively)

E V Q L V Q S G A E V K K P G A S V K V S C Q A S G Y T F S D Y Y I H
W V R Q T P G Q G F E W M G W V N P D T G G T R Y A Q K F O G W V T M
T R D M S N T T A Y M E L P G L R D D T A V Y Y C A R D L T G Y D Q
Y T A W G Q G T L V T V S S

V_H (SEQ ID NO:284) with H1, H2, and H3 underlined (SEQ ID NO:287-289, respectively)

G A G T G C A G C T G G T G C A G T C T G G G C T G A G T G A A G G T C C T G T C A G G C T T C T G G A T A C A C C T T C A G G A T T A C T A T T C A
C T G G T G C G A C A C C C C A G G A C A G G G T T G A G T G A T G G T A G C C C T G A C A C T G G T G G C A G A T A C G C G C A A G T T C A G G G C T G G G T C A C A A
T G A C C A G G G A C A T G T C C A C A C C A C A G C C T A C A T G G A G C T G C C C G G C T G A G A G A C G A C A C G C G C G T A T T A C T G T G C G A G A G A T C T A A C T G G G T A C G A C
C A G T A C A C G G C T G G G G C C A G G A A C C C T G G T C A C C C T C T C T C A

V_L (SEQ ID NO:276) with L1, L2, and L3 underlined (SEQ ID NO:281-283, respectively)

Q S V L T Q P P S V S V A P G K T A T I T C G G N N F R N K R V H W Y
Q Q R P G Q A P V L V I Y Y D S D R P S G I P E R F S G S R S G N T A
T L T I S R V E A G D E A D F Y C S T F D P F T D R P L F G G G T K L
T V L G

V_L (SEQ ID NO:285) with L1, L2, and L3 underlined (SEQ ID NO:290-292, respectively)

C A G T C T G T G A C T A G C C A C C C T C A G T G T C A G T G C C C C A G A A G A C G G C C A G A T T A C C T G T G G G G A A C A A C T T C G A A T A A A G A G T A C A C T G G T A
T C A G C A G G C C A G G C C C T G T C C T G G T C A T T A T A T G A T T C A G A C C G G C C C T C A G G A T C C C T G A G C G A T T C T C T G G C T C C C G C T C T G G A C A C A G G
C C A C C C T G A C C A T C A G C A G G G T C G A G G C C G G G A T G A G C C G A C T T T T A C T G T A G C A C C T T G A C C C C T T C A C T G A T C G T C C G C T G T T C G G C G G A G G G A C C A A G
C T G A C C C T C C T A G G T

FIG. 7(cont.)

354A08

V_H (SEQ ID NO:293) with H1, H2, and H3 underlined (SEQ ID NO:296-298, respectively)

QVQLVQSGAEKKPGASVKVSKASGYTFDYYMHWRQAPGQGLEWVGMINPYTGGLFYAOKERGRVTMRDTSINTAYMELSRGLSDDTAVYYCAREPEREGGSTG
QYWGRGTWTVSS

V_H (SEQ ID NO:302) with H1, H2, and H3 underlined (SEQ ID NO:305-307, respectively)

CAGTCCAGTTGGTCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGTCTCCTGCAGGCTTCTGGATACACCTTCACCGACTACTATATGCACATG
GGTCCGACAGGCCCCCTGGACAGGGCTTGAGTGGGTGGATGGATCAACCTTATATCTGGTGGCGCATCTATGCACAGAGTTTCGGGCGCAGGGTCACAATGACCA
GGGACACGTTCCATCAACACAGCCTACATGGAGCTAAGCAGACTGGGATCTGACGACAGCGCCGTGTATTATTGTGGGAGAGAACCTGANAAGATTCGGGCACTCCACG
GGGCAGGCTCTGGGGCGGGGACAAATGGTCACCGTCTCGAGT

V_L (SEQ ID NO:294) with L1, L2, and L3 underlined (SEQ ID NO:299-301, respectively)

QAVLTQPSVSGAPRQRVTISCTGSSSNIGAGYGVHWYQQLPGTAPKLLIYGNINRPSGVDPDRFGSKSGTSASLSAITGLQAEDEADYYCVHWDKEOSGVYFGTGTQLTVLSA

V_L (SEQ ID NO:303) with L1, L2, and L3 underlined (SEQ ID NO:308-310, respectively)

CAGGCTGTGCTGACTCAGCGCTCCTCAGTGTCTGGGGCCCCAAGGCAGAGGGTCACCATCTCTGCACTGGGAGCAGCTCCAACATCGGGGCGAGGTTATGGTGTACA
CTGGTACCAACAGCTTCCAGGACAGCCCCCAACTCCTCATCTATGGTAACAGCAATCGGCGCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCT
CAGCCTCCCTGGCCATCACTGGCTCCAGGCTCAGGATGAGGCTGATTATTACTGCTACCACTGGGCAAGGACAGAGTGGTTATGCTTTCGGAACCTGGGACCCAG
CTCACCGTTTAAAGTGGC

FIG. 7(cont.)

355806

V_H (SEQ ID NO:311) with H1, H2, and H3 underlined (SEQ ID NO:314-316, respectively)

EVQLVQSGAEVKKPGASVKVSQASGYTFTDYMHVVRQAPGGLEWVGWINPYTGSAFYAOKERGRATMTRNTSINTAYNELSRLGSDDTAVYYCAREPERKEGES
SGQLNGRGTMVTISS

V_H (SEQ ID NO:320) with H1, H2, and H3 underlined (SEQ ID NO:323-325, respectively)

GAAGTGCAGCTGGTGCAGTCTGGGGCTGAGGTCAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGTCAGAGTCTTCTGGATACACCTTCACCGACTACTATATGCACT
GGTGGCAGACAGCCCCCTGGACAGGGCTTGACTGGGTGGGTGGATCAACCTTATACTGGTAGCGCATTCATGACAGAGTTTCGGGGCAGGGCCACAAATGAC
CAGGAACAGTCCATCAACACAGCCTACATGAGCTGAGCTGGGATCTGACGACACGGCCGTGTATTATTGTGCGAGAGAACCTTGAAAAATTCGGGGAGTCC
AGCGGCCAGTTGTGGGGCCGGGGACAATGGTCACCACTCGAGT

V_L (SEQ ID NO:312) with L1, L2, and L3 underlined (SEQ ID NO:317-319, respectively)

QAVLTQPSVSGAPGQRTTISCTGSSSNIGPGVHWYQQLPGTAPKLLIYGDSNRPSGVPDRFSGSKSGTSASIAITGLQAEDEADYYCOSYDSGLSGYVFGTGTQTLVLSA

V_L (SEQ ID NO:321) with L1, L2, and L3 underlined (SEQ ID NO:326-328, respectively)

CAGGCTGTGCTGACTCAGCGTCCCTCAGTGTCTGGGGCCCGAGGGCAGAGGGTCAACCATCTCCTGACTGGGAGCAGCTCCACATCGGGCAGGTTATGGTGTAC
ACTGGTACCAACAGCTTCCAGGAACAGCCCCCAACTCTCATCTATGGTGACAGCAATCGGCCCTCAGGGTCCCTGACCGATTCTCTGGCTCCAAAGTCTGGCAC
CTCAGCCTCCCTGGCGATCAGTGGGTCCAGGCCGAGGATGAGGCTGATTATTACTGCCAGTCCCTATGACAGCGGCCCTGAGTGGTTATGICTTCGGAACTGGGACC
CAGCTCACCGTTTAAAGTGG

FIG. 7(cont.)

355E04

V_H (SEQ ID NO:329) with H1, H2, and H3 underlined (SEQ ID NO:332-334, respectively)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTHYYMHWVRQAPGQGLEWGMINPVTGGAFYAKOEGRVMTFRDTSINTAYMELSRIGSDDTAVVYCAREPEKEFDSPN
AEIWRGRTWVTISS

V_H (SEQ ID NO:338) with H1, H2, and H3 underlined (SEQ ID NO:341-343, respectively)

CAGGTCAGCTGGTGCAGTCTGGGCTGAGGTGAAGCCCTGGGGCTCAGTGAAGTCTCCTCGAAGGCTTCTGGATACACCTTCACCCACTACTATATGCACITG
GGTGCACAGGCCCTGACAAAGGCTTGAGTGGTGGGATGGATCAACCTTATCTGTGGCCGATTCATGCACAGAGTTTCAGGCAGGGTCAACATGACCA
GGGACAGTCCATCAACACAGCCTACATGAGCTGAGCTGAGCACTGGGATCTGACGACACGGCCGTGTATTATTGTGCCGAGAGACCTGAAAAATTCCACTCCCGGAAAC
GCCGAGATCTGGGGCCGGGACAATGGTCACCATCTCGAGT

V_L (SEQ ID NO:330) with L1, L2, and L3 underlined (SEQ ID NO:335-337, respectively)

QAVLTQPSVSVPQQRVTISCTGSSNIGAGYGVHWYQLPGTAPKLLIYGNRNREGVPDRFSGSKGTSASLAITGLQAEDEADYYCOSYDSSLSGYVFGTGTQLTVLSA

V_L (SEQ ID NO:339) with L1, L2, and L3 underlined (SEQ ID NO:344-346, respectively)

CAGGCTGTGCTGACTCAGCCGTCCTCAGTGTCTGGGGCCCCAGGCAGAGGGTCACCATCTCCTGCAGCTGGCAGCAGCTCCACATCGGGCAGGGTATGGTGTACA
CTGGTACCAACAGCTTCCAGGAACAGCCCCCAACTCTCATCTATGTGTACAGCAATCGGCCCCCAGGGGTCCCTGACCGATTCTCTGGCTCCCAAGTCTGGCACCT
CAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGCTGATTATTACTGCCAGTCTATGACAGCAGCCCTGAGTGGTTATGTCTTCGGAACCCGGGACCCAG
CTCACCGTTTTAAGTGGC

FIG. 7(cont.)

356A11

V_H (SEQ ID NO:347) with H1, H2, and H3 underlined (SEQ ID NO:350-352, respectively)

QVQLVQSGAEVKKPGASVKVSKASGYTFETNYXMHVWRQAPGQGLEWVGMINPVTGSAFYAOKFRGRVWTWTRDTSINTAYMELSRGLGSDDTAVVYICAREPE
KEDSDSDYNGRGTMVTVSG

V_H (SEQ ID NO:356) with H1, H2, and H3 underlined (SEQ ID NO:359-361, respectively)

CAGGTTCAGCTGGTGCACTCTGGGGCTGAGGTGAAGAGCCCTGGGGCTCAGTGAAGGTCTCCTGCAAGGCTCTGGATACACCTTCACCAACTACTATAT
GCACTGGGTGGACACAGCCCCCTGGACAGGGCTTGAGTGGGTGGATGGATCAACCTWTATCTGCTAGCGCATTCATGACACAGAGTTTCGGGGCAGGG
TTACANTGACCAAGGGACAGCTCCATCAACACAGCCTACATGGAGCTGACAGCTGGGATCTGACACACGGCCGTGTATTATTGTGGGAGAGAACCTGAA
AAATTCGACTCCGACGACTCCGACCTCTGGGGCCGGGCAATGGTCACCGTCTCGGGT

V_L (SEQ ID NO:348) with L1, L2, and L3 underlined (SEQ ID NO:353-355, respectively)

QAVLTPPSVSGAFGRVTISCTGSSSNIGAGYGVHWYQQLPETA PKLIITVGDSSRRESGVPRFSGSKSGTSASIALITGLQAEDEADYQCOSYDNSLSGVFTGTQLTVLSA

V_L (SEQ ID NO:357) with L1, L2, and L3 underlined (SEQ ID NO:362-364, respectively)

CAGGCTGTGCTACTCAGCGCGCCCTCAGTGTCTGGGGCCCCAGGGGCAGAGGGTCACCATCTCCTGCACCTGGGAGCAGCTCCCAACATCGGGGCAGGTTATGG
TGTA~~CACTGGT~~ACCAACAGCTTCCAGGACACAGCCCCCAACTCATCTATGGTGACAGAGTCGGCCCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCA
AGTCTGGACCTCAGCCTCCCTGGCCATCACTGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCTCTATGACACACAGCCTGAGCGGTTATGTC
TTCGGAACTGGGACCCAGCTCACCGTTTAAAGTGCG

FIG. 7(cont.)

GIL01

V_H (SEQ ID NO:365) with H1, H2, and H3 underlined (SEQ ID NO:368-370, respectively)

Q V Q L V E S G G G L V K P G G S L R L S C A A S G F T F S D Y Y M S W I R Q
A P G K G L E W V S A I S G S G G S T Y Y A D S V K G R I T I S R D N A K N S
L Y L Q M N S L R A E D T A V Y Y C A R G L W V W D P L D Y W G R G T L V T V
S S

V_H (SEQ ID NO:374) with H1, H2, and H3 underlined (SEQ ID NO:377-379, respectively)

CAAGTCAGCTGGTGGAGTCTGGGGAGGCTTGGTCAAGCCGAGGTCCTCAGACTCTCCTGTCAGGCTCTGGATTCACTTCAGTACTACTACTAGAGTGGATCCGCCA
GGCTCCAGGGAGGGGCTGAGTGGTCTCAGCTATTAGTGTAGTGGTGTAGCACATACAGCAGACTCCGTGAAGGGCGGATCACCATTCTCCAGAGACAAAGCCCAAGAACT
CACTGTATCTGCAATGAACAGCCTGAGAGCTGAGGACACGGCCGTGTATTACTCTGCGAGAGGCTTTGGGTTGGGATCCTCTTGACTACTGGGCGAGAGGAACCTGGTCACCGTCTCTTCA

V_L (SEQ ID NO:366) with L1, L2, and L3 underlined (SEQ ID NO:371-373, respectively)

D I Q M T Q S P S T L S A S V G D R V T I T C R A S E G I Y H W L A W Y Q Q K
P G K A P K L L I Y K A S S L A S G V P S R F S G S G S G T E F T L T I S S L
Q P D D F A T Y Y C Q O Y S N Y P L T F G G G T K V E I K R

V_L (SEQ ID NO:375) with L1, L2, and L3 underlined (SEQ ID NO:380-382, respectively)

GACATCCAGATCACCCAGTCTCCTCCACCCTGCTGCAATCTGTTGGAGACAGAGTCACCATCACTGCCGGGCCAGTCAGGGTATTTATCACTGGTGGCTGGTATCAGCAGAA
GCCAGGGAAAGCCCTAACTCCCTGATCTATAGGCTCTAGTTAGCCAGTGGGTCCCATCAGGTTCAAGGTTCAAGGCGAGTGGATCTGGGACAGAGTTCACCTCACCATCAGCAGCC
TGCAGCCTGATGATTTTGCACCTTATTACTGCCACAAATATAGTAATATTCGCTCAGTTTCGGCGGAGGACCAGGTGGAGATCAACGCT

FIG. 8

GILL16

V_H (SEQ ID NO:383) with H1, H2, and H3 underlined (SEQ ID NO:386-388, respectively)

Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T F T S Y G I S W V
R Q A P G Q G L E W M G W I S A Y T G N T N Y A O K F O G R V T M T T D T
S T S T A Y M E L R S L R S D D T A V Y Y C A R D R G Y Y D A F D I W G Q
G T L V T V S S

V_H (SEQ ID NO:392) with H1, H2, and H3 underlined (SEQ ID NO:395-397, respectively)

CAGTGCAGCTGGTGCAGTCTGGAGCTGAGTGAAGAGCTGGGGCCTCAGTGAAGTCTCTGCAAGGCTTCTGGTTACACCTTTACCAGTATGGTATCAGCTGGGT
GCACAGGCCCCGTGCACAAGGCTTGAAGTGGATGGATCAGGCTTACACTGCTAACAACAACACTATGCACAGAAGTTCACAGGCAGAGTCACCATGACCCACAGACA
CATCCACGAGCACAGCCTACATGGAACTGAGGAGCCTGAGATCTCAGCACAGCGGCTGTATTACTGTGGGAGAGATCGTGGATACATATGATGCTTTTGATATCTGGGGC
CAAGGCACCCCTGGTCACCGTCTCTCTCA

V_L (SEQ ID NO:384) with L1, L2, and L3 underlined (SEQ ID NO:389-391, respectively)

D I Q M T Q S P S T L S A S V G D R V T I T C R A S E G I Y H W L A W Y Q
Q K P G K A P K L L I Y K A S S L A S G V P S R F S G S G T E F T L T
I S S L Q P D D F A T Y Y C O O Y S N Y P L T F G G G T K V E I K R

V_L (SEQ ID NO:393) with L1, L2, and L3 underlined (SEQ ID NO:398-400, respectively)

GACATCCAGATGACCCAGTCTCCTTCACCCCTCTCTGCATCTGTGGAGACAGATCACCATCACCTCCCGGCCAGTGGGTATTTATCACTGGTGGCCTGGTATCA
GCAGAGCCAGGGAAAGCCCTAACTCCTGATCTATAGCCCTTACTTTAGCCAGTGGGTCCCATCAAGTTACGCCGAGTGGATCTGGACACAGATTCATCTCA
CCATCAGAGCCCTGCAGCCTGATGATTTGCACTTATTAATCTGCCAACAATATAGTAATTATCCGCTACCTTTCCGGCGAGGCCAAGGTCGAGATCAAAACGT

FIG. 8(cont.)

GIL45

V_H (SEQ ID NO:401) with H1, H2, and H3 underlined (SEQ ID NO:404-406, respectively)

Q M Q L V E S G G G V V Q P G R S L R L S C A A S G F T F S N Y G M
Y W V R Q A P G K G L E W V A H I W Y D G S N E K Y A D S V K G R M
T V S R D N S K N T L L Y L Q M N S L R A E D T A V Y Y C A T E O H W
I T A F D I W G K G T L V T V S S

V_H (SEQ ID NO:410) with H1, H2, and H3 underlined (SEQ ID NO:413-415, respectively)

CAGATCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCCTGGGAGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAAGGCAT
GTACTGGGTCCCGCAGGCTCCAGGCAAGGGCTGGAGTGGGTGGACATATTTGGTATGATGGAGTAATGAAGTATGACACTCCGTGAAGGGCGAA
TGACCGTCTCCAGAGACAATCCAGACACGTTGTATTGGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGGGACAGAGCAACAC
TGGATTACTGCTTTTGATATCTGGGGCAAGGAACCCCTGGTCACCGTCTCTCTCA

V_L (SEQ ID NO:402) with L1, L2, and L3 underlined (SEQ ID NO:407-409, respectively)

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

V_L (SEQ ID NO:411) with L1, L2, and L3 underlined (SEQ ID NO:416-418, respectively)

CAGTGTGCCCTGACTCAGCCTGCCCTCCGTGTCTGGTCTCCTGGACAGTCGATCACCATCTCCTGACTGGAACACAGAGTGGTGGTTATAACTA
TGCTCTCCTGGTACCAACACACCCAGGCAAGCCCCAACTCATGATTATGAGGGCAGTAAGGGCCCTCAGGGGTTCTTAATCGCTTCTCTGGCTCCA
AGTCTGGCAACACGGCCTCCCTGACAATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTACTACTGCACTCATATACACAGGAGGACTCGAGTTTC
GGCGAGGGGACCAAGCTGACCGTCTCTAGGT

FIG. 8(cont.)

GIL60

V_H (SEQ ID NO:419) with H1, H2, and H3 underlined (SEQ ID NO:422-424, respectively)

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

V_H (SEQ ID NO:428) with H1, H2, and H3 underlined (SEQ ID NO:431-433, respectively)

GAGGTGACGTGTGGAGAGCGGGGAGGTGGTACGGCCCTGGGGGTCCTGACACTCTCTGTGAGCCTCTGGATTACCTTTGACGATTATGGCATGAACCTGGTC
CGCCAAAGCTCCAGGAAGGGCTGGAGTGGTCTCTGTGTAAATGGAAATGGTACCAAGATTATGACGCTCCGTGAAGGCCGATTCACCATCTCCAGAGACAAC
GCCAAGAACTCCCTGTATCTGCAATGAACAGTCTGAGAGCCGAGCACAGGCCCTTGTATCACTGTGCGAGAGGATGGTATAGTGGAGCTTCTACTACTTTGGCTACTGG
GGCCGAGGAACCTGGTCACGCTCTCTCA

V_L (SEQ ID NO:420) with L1, L2, and L3 underlined (SEQ ID NO:425-427, respectively)

Q A A L T Q P A S V S G S P G Q S I T I S C T G A S G D V G A Y N F V S W
Y Q Q H P G K A P K L I I Y D V N K R P S G V S N R F S G S K S G N T A S
L T I S G L Q A E D E A D Y Y C S S Y T S T F S V Y F G G G T K L T V L G

V_L (SEQ ID NO:429) with L1, L2, and L3 underlined (SEQ ID NO:434-436, respectively)

CAGGCTGGCGTACTACCGCGCCCTCGGTGTCTGGGTCTCCTGGACAGTCATCACCATCTCTGCACTGGAGCCAGCGGTGCTTATATACTTTGCTCTCTGG
TACCAACACACCCAGGCAAGCCCCCAACTCATAATTTATGATCTCATAGCCGCCCTCAGGGTTTCTAATCGCTTCTCTGGCTCCAGCTCTGGCAACACCGCCTCC
CTGACCACTCTCTGGGCTCCAGGCCGAGGACGAGGCTGATTATTACTGCAGCTCATATACAGCACTTCTCTGTGGTATTGGCGGAGGGACCAAGCTGACCGTCTCTAGGT

FIG. 8(cont.)

GLL68

V_H (SEQ ID NO:437) with H1, H2, and H3 underlined (SEQ ID NO:440-442, respectively)

Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T F S D Y Y I H W V R Q
A P G Q G L E W M G W V N P D T G G T R Y A O K F O G R V T M T R D M S I S T
A Y M E L S R L R S D D T A V Y Y C A R D L T G F D P F D I W G Q G T L V T V
S S

V_H (SEQ ID NO:446) with H1, H2, and H3 underlined (SEQ ID NO:449-451, respectively)

CAGGTCCAGCTGGTGCAGCTGGGGCTGAGGTGAACAAGCCTGGGGCTCACTGAAGTCTCTTAAGCTTCTGGATACACCTTCAGCGATTACTATATTCACTGGGTGGGACA
GGCCCTGGACAAGGTTGGAGTGGATGGGTCAACCTGACACTGGTGGCACAGATACCGCAGAGTTTCAGGGCGGGTCACAAATGACCAGGACATGTCCATCTCCA
CAGCTACATGGAGCTGTCCAGCTGAGAGCGACACAGCCGCTATATTACTGTGGAGAGTCTACTGATTGCTTTGATATCTGGGGCCAGGACCCCTGGTCACCGTCTCTCA

V_L (SEQ ID NO:438) with L1, L2, and L3 underlined (SEQ ID NO:443-445, respectively)

S S V L T Q P P S V S V A P G K T A R I T C G G N N E R N K R V H W Y Q Q K P
G Q A P V L V I Y Y D S D R P S G I P E R F S G S R S G N T A T L T I S R V E
A G D E A D Y Y C Q V W D S S T D R P L F G G G T K L T V L G

V_L (SEQ ID NO:447) with L1, L2, and L3 underlined (SEQ ID NO:452-454, respectively)

TCGTCTGTCTGCTACCTACCCACCTCAGTGTCTAGTGGCCCGGAGAACAGCGCCCGCATTAACCTGTGGGGAACAACACTTTCGAAATATAAAGATACACTGGTATCAGCAGAGCC
AGGCCAGGCCCTGTCTGGTCACTATTATGATTACAGACGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCGCTCGGGACACGCGCCCTGACCATCAGCAGGTCG
AGGCCGGGATGAGGCCGACTATTACTGTCAAGGTGTGGGATAGTACTGATCGTCCGCTGTTCGGCGGAGGACCAAGCTGACCCGCTCTAGGT

FIG. 8(cont.)

GIL92

V_H (SEQ ID NO:455) with H1, H2, and H3 underlined (SEQ ID NO:458-460, respectively)

Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T F T D Y Y M H W V R
Q A P G Q G L E W V G W I N P Y T G G A F Y A O K F R G R V T M T R D T S I
S T A Y M E L S R L R S D D T A V Y Y C A R E P E K F D F W G G D N W G R G
T L V T V S S

V_H (SEQ ID NO:464) with H1, H2, and H3 underlined (SEQ ID NO:467-469, respectively)

CAGGTGCAGCTGGTGCAGTCTGGGCTGAGTGAAGCCCTGGGCTCAGTGAAGTCTCTGCAAGCTTCTGGATACACCTTACCGACTACTATATGCACCTGGGTGCG
ACAGGCCCTGGACAGGGCTTGAGTGGTGGGATGATCAACCTTATCTGTTGGGATTCATGACAGAGTTTCGGGCGAGGTTCACATGACCGGACACGTCCA
TCAGCACGCCCTACATGGAGCTGACGAGACTGAGATCTGACGACAGCGCGTGTATTATGTGCGAGAGACCTGAAAAATTCGATTTTTGGGGGGGTGACAACTGGGGCCCGG
GGGACATTGGTCACCGTCTCTCTCA

V_L (SEQ ID NO:456) with L1, L2, and L3 underlined (SEQ ID NO:461-463, respectively)

Q A V L T Q P P S V S G A P G Q R V T I S C T G S S S N I G A G Y G V H W Y
Q Q L P G T A P K L L I Y G N S N R P S G V P D R F S G S K S G T S A S L A
I T G L Q A E D E A D Y Y C Q S Y D S S L S G Y V F G G G T Q L T V L G

V_L (SEQ ID NO:465) with L1, L2, and L3 underlined (SEQ ID NO:470-472, respectively)

CAGGTGTGCTGACTCAGCCGCGTCAGTGTCTGGGCCCCAGGGCAGAGGTCCATCTCTGCACTGGGAGCAGCTCCACATCGGGGCGAGTTATGGTGTACACTGGTA
CCAACAGCTTCCAGGAACAGCCCCCAACCTCCTCATCTATGTTAAGCAATGGGCCCTCAGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCAGCTCAGCCTCCCTGG
CCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCTCTATGACAGCAGCCCTGAGTGGTTATGTCTCGAGGTGGGACCCAGCTCACCGTCCCTAGGT

FIG. 8(cont.)

062A09

V_H (SEQ ID NO:473) with H1, H2, and H3 underlined (SEQ ID NO:476-478, respectively)

Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T F T S Y G I S W
V R Q A P G Q G L E W M G W V S A Y T G N T N Y A O K F O G R V T M T T
D T S T S T A Y M E L R S L R S D D T A V Y Y C A R D R G Y Y D A F D I
W G Q G T L V T V S S

V_H (SEQ ID NO:482) with H1, H2, and H3 underlined (SEQ ID NO:485-487, respectively)

CAGTGCAGCTGGTGCAGCTGGAGCTGAGTGAAGCTGGGGCTCAGTGAAGTCTCTCTGCAAGCTTCTGGTTACACCTTTACCACTATGTTATCAGCTG
GGTCCGACAGGCCCTGGACAGGGCTTGAGTGGATGGGTGAGCTTACCTGGTACACAACTATGCACAGAGTTCAGGGCAGAGTCACCATGACCA
CAGACATCCACGAGCACAGCTACATGGAACCTGAGAGCTGAGATCTGACGACAGGGCGGTATTACTGTGGAGAGATCGTGATATGATGCTTTTGAT
ATCTGGGGCCAGGCACCCTGGTCAACCGTCTCTCTCA

V_L (SEQ ID NO:474) with L1, L2, and L3 underlined (SEQ ID NO:479-481, respectively)

D I Q M T Q S P S T L S A S V G D R V T I T C R A S E G I Y H W L A W Y
Q Q K P G K A P K L L I Y K A S S L A S G V P S R F S G S G T E F T
L T I S S L Q P D D F A T Y Y C Q O M G E Y N A T F G G G T K V E I K R

V_L (SEQ ID NO:483) with L1, L2, and L3 underlined (SEQ ID NO:488-490, respectively)

GACATCCAGATGACCCAGTCTCTCCACCCCTGCTGCATCTGTTGGAGACAGAGTCACCATCACCTGCGGGCCAGTGAGGGTATTTATCACTGGTTGCCCTGGTA
TCAGCAGAGCCAGGGAAGCCCTAACTCCTGATCTATAGGCTCTACTTTAGCCAGTGGGTCCCATCAAGTTACGGGCAGTGGATCTGGGACAGAGTTCA
CTCTCACCATCAGCAGCTGCAGCCTGATGATTTTCCAACTATTACTGCCAACAATGGGCGAGTACAAGCCACCTTCGGCGAGGACCAAGGTGGAGATCAACGT

FIG. 8(cont.)

087B03

V_H (SEQ ID NO:491) with H1, H2, and H3 underlined (SEQ ID NO:494-496, respectively)

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

V_H (SEQ ID NO:500) with H1, H2, and H3 underlined (SEQ ID NO:503-505, respectively)

GAGGTGCAGCTGGTGGAGAGCGGGGAGGTGGTACGGCCCTGGGGTCCCTGAGACTCTCCTGTGCAGCTCTGGATTACCTTTGACGATTATGGCATGAACCTGGGTC
CGCCAAGCTCCAGGGAGGGCTGGAGTGGTCTCTGGTGTATTTGGAATGGTGGTACCAAGAGATTATGACAGCTCCGTGAGGGCCGATTACCATCTCCAGAGACAAC
GCCAAGAACTCCCTGTATCTGCAATGACAGTCTGAGAGCGGAGACACGGCCTTGTATCCTGTGCGAGAGATGGTATAGTGGGGCCGCGTGGAAACATGGGCTACTGG
GGCCGAGGAACCCCTGGTCACCGTCTCTCA

V_L (SEQ ID NO:492) with L1, L2, and L3 underlined (SEQ ID NO:497-499, respectively)

Q A A L T Q P A S V S G S P G Q S I T I S C T G A S G D V G A Y N F V S W
Y Q Q H P G K A P K L I I Y D V N K R P S G V S N R F S G S K S G N T A S
L T I S G L Q A E D E A D Y Y C S S Y T S T F S V V F G G G T K L T V L G

V_L (SEQ ID NO:501) with L1, L2, and L3 underlined (SEQ ID NO:506-508, respectively)

CAGGTGGCTGACTCAGCGGCTCCGTGTCTGGGTCTCCTGGACACTCGATCACCATCTCCTGCACCTGAGCCACGGGTGACGTGGTGGCTTATTAACCTTGTCTCTGG
TACCAACAACACCCAGGCAAGCCCCCAACTATAATTATGATGTCAATAAGCGGCCCTCAGGGGTTTCTAATCCCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCC
CTGACCATCTCTGGGCTCCAGGGCGAGGAGGAGGCTGATTATTACTCAGCTCATATACAGACCTTCTCTGTGGTATTTGGGGAGGAGCCAAAGCTGACCGTCTCTAGGT

FIG. 8(cont.)

166B06

V_H (SEQ ID NO:509) with H1, H2, and H3 underlined (SEQ ID NO:512-514, respectively)

Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T F S D Y Y I H W V
R Q A P G Q G L E W M G W V N P D T G G T R Y A O K F O G R V T M T R D M
S I S T A Y M E L S R L R S D D T A V Y Y C A R D L T G F D P F D I W G Q
G T L V T V S S

V_H (SEQ ID NO:518) with H1, H2, and H3 underlined (SEQ ID NO:521-523, respectively)

CAGGTCAGCTGGTGCACTCTGGGCTGAGGTGAGAGCCCTGGGGCTCAGTGAAGGCTCTCTGAAGGCTCTGGATACACCTTCAGCGATTACTATATTCACCTGGGT
GCCACAGGCCCTGGACAGGGTTGGAGTGGATGGGTCAACCTGACACTGGTGGCACAAGATACGCCGAGAGTTTCAGGGCCGGGTCAATGACAGGGGACA
TGTCATCTCCACAGCCTACATGGAGCTGTCCAGGCTGAGAGCCGACACCGCCGTATATTACTGTGGCAGAGTCTAACTGGATTTCCTTTTGATATCTGGGGC
CAGGGAACCTTGGTCACCGTCTCCTCA

V_L (SEQ ID NO:510) with L1, L2, and L3 underlined (SEQ ID NO:515-517, respectively)

S S V L T Q P P S V S V A P G K T A R I T C G G N N F R N K V H W Y Q Q K
P G Q A P V L V I Y Y D S D R P S G I P E R F S G S R S G N T A T L T I S
R V E A G D E A D Y Y C Q V W D L F N D N G V F G G G T K L T V L G

V_L (SEQ ID NO:519) with L1, L2, and L3 underlined (SEQ ID NO:524-526, respectively)

TCGTCGTGCTCACTCAGCCACCTCAGTGTGAGTGGCCCCAGGAAGACGGCCCGCATACCTGTGGGGGAACAACCTTCGAAATAAAGAGTACACTGGTATCAGCA
GAAGCCAGGCCAGGCCCTGTCTGGTCACTATATGATTCAACCGCCCTCAGGGATCCCTGAGCGATTCTCTGGTCCCGTCTGGGAACACGGCCACCCCTGACCA
TCAGAGGTCGAGGCCGGGATGAGGCCGACTATTACTGTGAGGTGTGGGATCTCTTCACGACACGGCGGTTCGGCGGAGGGACCAAGCTGACCGTCCCTAGGT

FIG. 8(cont.)

166G05

V_H (SEQ ID NO:527) with H1, H2, and H3 underlined (SEQ ID NO:530-532, respectively)

Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T F S D Y Y I H W V R
Q A P G Q G L E W M G W V N P D T G G T R Y A O K F Q G R V T M T R D M S I
S T A Y M E L S R L R S D D T A V Y Y C A R D L T G F D P F D I W G Q G T L
V T V S S

V_H (SEQ ID NO:536) with H1, H2, and H3 underlined (SEQ ID NO:539-541, respectively)

CAGGTCAGCTGGTGCAGTCTGGGCTGAGGTGAAGAGCCCTGGGGCCCTCAGTGAAGGCTCTGTGAAGGCTTCGGATACACCTTCAGCGATTACTATATCACTGGGTGCG
ACAGGCCCTGGACAAGGTTGGAGTGGATGGGTCAACCTGACACTGGTGGCAAGATACCGCGCAGAGTTTCAGGGCCGGGTCAATACACCGGACATGTCCA
TCTCCACAGCCTACATGGAGCTGTCCAGGCTGAGAGCGACGACACGGCCGTATATTACTGTGCGAGAGATCTACGGATTTCGATCCTTTTGATATCTGGGGCCACGGGAACC
CTGGTCACCGTCTCCTCA

V_L (SEQ ID NO:528) with L1, L2, and L3 underlined (SEQ ID NO:533-535, respectively)

S S V L T Q P P S V S V A P G K T A R I T C G G N N F R N K R V H W Y Q Q K
P G Q A P V L V I Y Y D S D R P S G I P E R F S G S R S G N T A T L T I S R
V E A G D E A D Y Y C Q V W D F L T D S G S F G G G T K L T V L G

V_L (SEQ ID NO:537) with L1, L2, and L3 underlined (SEQ ID NO:542-544, respectively)

TCGTCTGTGCTGACTCAGCCACCTCAGTGTGAGTGGGCCCCAGGAAGACGGCCCGCATACCTGTGGGGGGAACAACATTCGAAATAAAGAGTACACTGGGTATCAGCAGAA
GCCAGGCCAGGCCCTGTCTGTGTCATCTATTATGATTCAGACCGGCCCTCAGGATCCCTGAGCGATTCTTGCTCCCGCTCTGGGACACGGCCACCCCTGACCATCAGCA
GGGTGAGGCCGGGATGAGGCCGACTATTACTGTGAGGTGGGATTTCCTACCGACTCGGGGTGCTTCGGCGGAGGACCAAGCTGACCGTCTCTAGGT.

FIG. 8(cont.)

354A08

V_H (SEQ ID NO:545) with H1, H2, and H3 underlined (SEQ ID NO:548-550, respectively)

Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T F T D Y Y M H W V R
Q A P G Q G L E W V G W I N P Y T G G A F Y A O K F R G R V T M T R D T S I
S T A Y M E L S R L R S D D T A V Y Y C A R E P E R F G D S T G Q V W G R G
T L V T V S S

V_H (SEQ ID NO:554) with H1, H2, and H3 underlined (SEQ ID NO:557-559, respectively)

CAGGTGCAGCTGGTCCAGTCTGGGCTGAGTGAAGACCTGGGGCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCGACTACTATATGCACTGGGTGCG
ACAGGCCCTGGACAAGGCTTGAGTGGGTGGATGATCAACCTTATCTGTTGGCGCATCTATGCCACAGAAGTTTCGGGGCAGGGTCAATGACCAGGGACACGTCCA
TCAGCACAGCCTACATGGAGCTGAGCAGACTGAGATCTGACGACGCGCGTGTATTATTGTGCCAGAGACCTGAAAGATTGGGCGACTCCACGGGGCAGGTCTGGGCGCGG
GGGACATTGGTCACCGTCTCCTCA

V_L (SEQ ID NO:546) with L1, L2, and L3 underlined (SEQ ID NO:551-553, respectively)

Q A V L T Q P P S V S G A P G Q R V T I S C T G S S S N I G A G Y G V H W Y
Q Q L P G T A P K L L I Y G N S N R P S G V P D R F S G S K S G T S A S L A
I T G L Q A E D E A D Y Y C Y H W D K E O S G Y V F G G G T Q L T V L G

V_L (SEQ ID NO:555) with L1, L2, and L3 underlined (SEQ ID NO:560-562, respectively)

CAGGCTGTGACTCAGCGCGCTCAGTGTCTGGGCCCCAGGGCAGAGGTACCATCTCCTGCACTGGGAGCAGCTCCACATCGGGCAGGTATGGTGTACACTGGTA
CCACAGCTTCCAGGAACAGCCCCCAAACTCCTCATCTATGGTACAGCAATCGCCCCCTCAGGGTCCCTGACCGATTCTTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGG
CCATCACTGGGCTCCAGGCTGAGGCTGATTATTACTGCTACCACCTGGGACAGAGTGGTATTGTCTTCGGAGGTGGGACCCAGCTCACCGTCTCTAGGT

FIG. 8(cont.)

355B06

V_H (SEQ ID NO:563) with H1, H2, and H3 underlined (SEQ ID NO:566-568, respectively)

Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T F T D Y Y M H W V
R Q A P G Q G L E W V G W I N P Y T G S A F Y A O K F R G R V T M T R D T
S I S T A Y M E L S R L R S D D T A V Y Y C A R E P E K F G E S S G O L W
G R G T L V T V S S

V_H (SEQ ID NO:572) with H1, H2, and H3 underlined (SEQ ID NO:575-577, respectively)

CAGGTGCAGCTGGGTGCACTGGGGCTGAGGTGACAGAGCTCTCTGCAAGGCTTCTGGATACCTTCACCEACTACTATATGCACCTGGGTG
CGACAGGCCCTGGACAGGGCTTCACTGGGTGGATGATCAACCTTATCTGGTAGCGCTTCTATGACACAGAGTTTCGGGGCAGGTTCACATGACACGGACACG
TCCATCAGCACAGCCATACATGAGCTGAGCAGACTCAGATCTGACGACACGGCGGTGTATTATTGTCGACAGAACCTGAAATAATTCGGCGAGTCCAGCGGCCCAGTTGTGG
GGCCGGGGACATTGGTCACCGTCTCTCA

V_L (SEQ ID NO:564) with L1, L2, and L3 underlined (SEQ ID NO:569-571, respectively)

Q A V L T Q P P S V S G A P G Q R V T I S C T G S S S N I G A G Y G V H W
Y Q Q L P G T A P K L L I Y G D S N R P S G V P D R F S G S K S G T S A S
L A I T G L Q A E D E A D Y Y C Q S Y D S G L S G Y V F G G G T Q L T V L
G

V_L (SEQ ID NO:573) with L1, L2, and L3 underlined (SEQ ID NO:578-580, respectively)

CAGGTGTGCTGACTAGCCCGCTGAGTGTCTGGGGCCCGAGGGCAGAGGTACCATCTCTGCACTGGGAGCAGCTCCACACATCGGGGCAGGTTATGGTGTACACTGG
TACCAACAGCTTCCAGGAACAGCCCCAACTCCTCATCTATGTTGACAGCAATCGGCCCTCAGGGTCCCTGACCGATTCTGTGGCTCCAAGTCTGGCAGCTCAGCCTCC
CTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCTCTATGACAGGGCCTGAGTGGTTATGCTTCGGAGGTGGGACCCAGCTCACCCTCCTAGGT

FIG. 8(cont.)

355E04

V_H (SEQ ID NO:581) with H1, H2, and H3 underlined (SEQ ID NO:584-586, respectively)

Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T F T H Y Y
M H W V R Q A P G Q G L E W V G W I N P Y T G G A F Y A O K F O G
R V T M T R D T S I S T A Y M E L S R L R S D D T A V Y Y C A R E
P E K F D S P N A E I W G R G T L V T V S S

V_H (SEQ ID NO:590) with H1, H2, and H3 underlined (SEQ ID NO:593-595, respectively)

C A G G T G C A G C T G G T G C A G T C T G G G C T G A G G T G A G G C T C C T G C A A G C T T C T G G A T A C A C C T T C A C C C A C T A C T A T
A T G C A C T G G G T G C G A C A G C C C T G G A C A G G C T T G A G T G G G A T G G A T C A C C C T T A C T A C T G T G G C G C A T T C T A T G C A C A G A G T T C A G G G C
A G G G T C A C A T G A C C A G G G A C A C G T C C A T C A G C A C A G C C T A C A T G G A G C T G A G A C T G A G A T C T G A C G A C A C G G C C G T C T A T T A T T G T G C G A G A G A A
C C T G A A A A A T T C G A C T C G C C G A A C G C C G A G A T C T G G G C C G G G G A C A T T G G T C A C C G T C T C C T C A

V_L (SEQ ID NO:582) with L1, L2, and L3 underlined (SEQ ID NO:587-589, respectively)

Q A V L T Q P P S V S G A P G Q R V T I S C T G S S S N I G A G Y
G V H W Y Q Q L P G T A P K L L I Y G N S N R P S S G V P D R F S G
S K S G T S A S L A I T G L Q A E D E A D Y Y C Q S Y D S S L S G
Y V F G G G T Q L T V L G

V_L (SEQ ID NO:591) with L1, L2, and L3 underlined (SEQ ID NO:596-598, respectively)

C A G G C T G C T G A C T C A G C C G C G T C A G T G T C T G G G G C C C A G G C A G A G G T C A C C A T C T C T G C A C T G G G A G C A G C T C C A C A C A T C G G G G C A G G T T A T
G G T G T A C A C T G G T A C C A C A G T T C C A G G A C A G C C C C A A C T C T C A T T A T G T A C A G A C A T C G G C C C T C A G G G T C C C T G A C C G A T T C T C T G G C
T C C A A G T C G G C A C C T C A G C C T C C C T G G C C A T C A C T G G G C T C C A G G T G A G G T G A T T A T T A C T G C C A G T C C T A T G A C A G C A G C C T G A G T G G T
T A T G T C T T C G G A G G T G G G A C C C A G C T C A C C G T C T C T A G G T

FIG. 8(cont.)

356A11

V_H (SEQ ID NO:599) with H1, H2, and H3 underlined (SEQ ID NO:602-604, respectively)

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

V_H (SEQ ID NO:608) with H1, H2, and H3 underlined (SEQ ID NO:611-613, respectively)

CAGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAGAAGCCCTGGGGCTCAGTAAGGCTCTCGAAGGCTTCGGATACACCTTCACCACTACTATATGCACCTGG
GTGCGACAGGCCCTGGACAAGGCTTGAGTGGGTGGGATGGATCAACCCCTTATCTGAGCGCATTCATGCCACAGAAGTTTCGGGGCAGGGTCACAATGACCAGG
GACACGTCCATCAGCACAGCCTACATGAGCTGAGCTGAGCAGACTGAGATCTGACGACACGGCCGTGTATTATTGTGCGAGAGAACCTGAAATTCGACTCCGACGACTCC
GACGCTGGGGCCGGGACATTGGTCACCGCTCTCTCA

V_L (SEQ ID NO:600) with L1, L2, and L3 underlined (SEQ ID NO:605-607, respectively)

Q A V L T Q P P S V S G A P G Q R V T I S C T G S S S N I G A G Y G V H
W Y Q Q L P G T A P K L L I Y G D S N R P S G V P D R F S G S K S G T S
A S L A I T G L Q A E D E A D Y Y C Q S Y D N S L S G Y V F G G G T Q L
T V L G

V_L (SEQ ID NO:609) with L1, L2, and L3 underlined (SEQ ID NO:614-616, respectively)

CAGGCTGTGCTGACTCAGCCGCCGCTCAGTGTCTGGGGCCCCAGGGCCAGGGTCACCATCTCTGCACTGGGAGCAGCTCCAAATCGGGGACGGTTATGGTGACAC
TGGTACCAACAGCTTCCAGGAACAGCCCCCAACTCTCATCTATGTGACAGCAATCGGCCCTCAGGGTCCCTGACCGATTCTCTGGCTCCAAAGTCTGGCACCTCA
GCCTCCCTGGCCATCCTGGCTCCAGGCTCAGGATGAGGCTGATTATTACCTCAGCTCATGACACACCCCTGAGGCTTATGCTTCGGAGTGGGACCCAGCTCACCGTCTCTAGGT

FIG. 8(cont.)

368D04

V_H (SEQ ID NO:617) with H1, H2, and H3 underlined (SEQ ID NO:620-622, respectively)

EVOLVESGGG VVRPGGSLRL SCAASGTFD DYGMNWVRQA PGKGLEWVSG

VNWNGGTRDY AASVKGRFTI SRDNAKNSLY LQMSLRAED TALLYHCARGW

YSGAANNMCGY WGRGTLTVTS S

V_H (SEQ ID NO:626) with H1, H2, and H3 underlined (SEQ ID NO:629-631, respectively)

GAGGTGCAGCTGTTGGAGAGCGCGGAGCGGTGGTGAGACACAGCGGCAGCCTGAGCTGAGTCCGCGCCACCTTCGACCTACGGCATGAA
CTGGGTGAGGCAGGCCCCAGGCARGGCCTGGAGTGGTGTCCGCGTGAACCGGSCACCCAGAGACTACGCCCTCTGTGAAGGECAGATTACCCA
TCAGCCGGGACAAACCCAAAGACAGCCTGTACCTGCAGATGAACAGCCTGAGAGCCGAGCACCCGCCCTGTACACTGGGCCACAGAGGCTGGTACAGCGGAGGC
GCCTGGAACATGGCTACTGGGGCAGAGGCACCCCTGGTGACCGTGTCCAGC

V_L (SEQ ID NO:618) with L1, L2, and L3 underlined (SEQ ID NO:623-625, respectively)

QAALTQPASV SCSPGQSITI SCTGASGDVG AYNFVSWYQQ HPGKAPKLII

YDYNKRPSGV SNRFGSKSG NTASLTISGL QAEDADYYC ASLVSESVY

FGGGTKLTVL

V_L (SEQ ID NO:627) with L1, L2, and L3 underlined (SEQ ID NO:632-634, respectively)

CAGGCCGCCCTGACCCAGCGCCAGCGGTGTTGGCAGCCAGGCAGAGCATCACATCAGTGCACCGGCGAGCGGCGATGNGGGCGCTACAACCTTCGT
GTCTGTGTATCAGCAGCACCCCGGCAAGGCCCAAGCTGATCATCTACACGTGAACAAGAGACCCAGCGGCGGTGTCCAACAGATTACGGGCAGCAAGAGCG
GCAACACCGCCAGCCTGACCATCAGCGGACTGCAGGCGGAGGACGAGCGGACTACTACTGGCCAGGCTGGTGTCCGACTTCAGCGTGGTGTTCGGCGGAGGC
ACCAAGCTGACCGTGCTG

FIG. 8(cont.)

GIL01

SEQ ID NO:7

E V Q L V E S S G G G Q A G L V T P G G L G S L W R L R L S C A A S G F T F
S D Y Y M S W I R R C A G G Q A P I S R R D N A E G L N S A S G F T F
Y Y A D S V K Y Y G S G R R C A R G G I T R G L W V S A L Y W G R Q M S S L V T R
S E D T A V G G G Y Y G S G R R C A R G G I T R G L W V S A L Y W G R Q M S S L V T R
V S S I G G D L L I S S L Q P D D F A T Y Y C P S R F S Q W Y S P S L V T L
S A S I G D L L I S S L Q P D D F A T Y Y C P S R F S Q W Y S P S L V T L
G K A P K L L I S S L Q P D D F A T Y Y C P S R F S Q W Y S P S L V T L
D F T L T I S S L Q P D D F A T Y Y C P S R F S Q W Y S P S L V T L
G G G T K L L E I K R A A A

SEQ ID NO:16

GAAGTCAGCTGGTGGAGTCTGGGGAGGCTTGGTCACGCCCTGGAGGGT
CCCTGAGACTCTCCTGTGCAGCCTCTGGATTACACCTTCAGTACTACTA
CATGAGCTGGATCCGCCAGGCTCCAGGGAGGGGCTGGAGTGGGTCTCA
GCTATTAGTGGTAGTGGTAGCACATACCTACCGAGACTCCGTGAAGG
GCCGGATCACCATCTCCAGAGACACGCCAAGAACTCACTGTATCTGCA
AATGAGCAGCCTGAGATCTGAGGACACGCCCTGTATTACTGTCCGAGA
GGGCTTTGGGTTTGGGATCCTCTTGACTACTTGGGGCAGAGGAACCTGG
TCACCGTCTCTTCAGGTGGAGGCGGTTTCAGGCGGAGGTGGCAGCGCGG
TGGCGGATCGGACATCCAGATGACCCAGTCTCCTTCCACCTGTCTGCA
TCTATTGGAGACAGAGTCACCATCACCTGCCGGCCAGTGAGGGTATT
ATCACTGGTTGGCTGGTATCAGCAGAAGCCAGGAAAGCCCTAAACT
CCTGATCTATAAGGCTCTAGTTAGCCAGTGGGGCCCCATCAAGGTTTC
AGCGCAGTGGATCTGGGACAGATTTCACCTCTCACCATCAGCAGCCTGC
AGCCTGATGATTTTGCAACTTAT TACTGCCAACAATATAGTAATTAICC
GCTCACTTTTCGGCGGAGGGACCAAGCTGGAGATCAAAACGTGCGGCCGCA

FIG. 9

GIL16

SEQ ID NO:25

Q V Q L V E S S G A E V K K P G A S V K V S W I S W V R R C Y Y G G G L T S E S T S D A S S W T S A Y M E L R S L T N T F
T S Y G I S W V R R C Y Y G G G L T S E S T S D A S S W T S A Y M E L R S L T N T F
N Y A Q K F Q G Y Y G G G L T S E S T S D A S S W T S A Y M E L R S L T N T F
S D D T A V Y Y G G G L T S E S T S D A S S W T S A Y M E L R S L T N T F
V S S G G G G S G G G I T C R A S S L A S G A P S R F S S Y P L T F
S A S I G D R V T I Y K Q P D D F A T Y Y C Q Q S G S Q K T F
G K A P K L L I S S L Q P D D F A T Y Y C Q Q S G S Q K T F
D F T L T I S S L Q P D D F A T Y Y C Q Q S G S Q K T F
G G G T K L E I K R A A A

SEQ ID NO:34

CAGGTGCAGCTGGTGAGTCTGGAGCTGAGGTGAAGAAGCCTGGGCGCTC
AGTGAAGTCTCCTGCAAGGCTTCTGGTTACACCTTACCAAGTTATGGTA
TCAGCTGGGTGCGACAGGCCCTGGACAAGGCTTGAGTGGATGGGATGG
ATCAGCGCTTACACTGGTAACACAACTATGCACAGAAGTCCAGGGCAG
AGTCACCATGACACAGACACATCCACGACACAGCCTACATGGAAGTGA
GGAGCCTGAGATCTGACGACAGGCCGCTGTATTACTGTGCGAGAGATCGT
GGATACTATGATGCTTTTGATATCTGGGGCCAAAGCACCCCTGGTCAACCGT
CTCCTCAGGTGGAGCGGTTACAGCGGAGGTGGCAGCGGCGGTGGCGGAT
CGGACATCCAGATGACCCAGTCTCCTTCCACCTGTCTGCATCTATTGGA
GACAGATCACCATCACCCTGCGGGCCAGTGAGGTTATTCACATGGTT
GGCCTGGTATCAGCAGAACCCAGGGAAGCCCTAACTCCTGATCTATA
AGGCCTCTAGTTAGCCAGTGGGGCCCCCATCAAGTTACGCGGCAGTGGA
TCTGGGACAGATTTTCACTCTCACCATCAGCAGCCTGACGCTGATGATTT
TGCAACTTATTACTGCCAACAATATAGTAATTATCCGCTCACTTTCGGCG
GAGGGACCAAGCTGGAGATCAACGTTGGGCGCGCA

FIG. 9(cont.)

GIL45

SEQ ID NO:43

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

SEQ ID NO:52

CAGATGCAGCTGGTGCAGTCTGGGGAGGCGGTGGTCCAGCCTGGGAGGT
CCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTCACTTCACTATGG
CATGTACTGGGTCCGCCAGGCTCCAGGCAAGGGCTGGAGTGGGTGGCA
CATATTTGGTATGATGGAAGTAATGAAAAGTATGCAGACTCCGTGAAGG
GCCGAATGACCGTCTCCAGAGACAATCCAGGAACACGTTGTATTGCA
AATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGACA
GAGCAACACTGGATTACTGCTTTTGATATCTGGGGCAAGGACCCCTGG
TCACCGTCTCCTCAGGTGGAGCGGTTTCAAGCGCAGGTGGCAGCGCGG
TGGCGGATCGCAGTCTGTGCTGACTCAGCCTGCCCTCCGTGTCTGGGTCT
CCTGGACAGTCGATCACCATCTCCTGCCTGGAACACGAGTGCCTTG
GTGGTTATACTATGTCCTCTGTTACCAACAACACCCAGGCAAGCCCC
CAAACTCATGATTTATGAGGGCAGTAAGCGGCCCTCAGGGGTTCCTAAT
CGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACAATCTCTG
GGCTCCAGGCTGAGGACGAGGCTGATTATTACTGCAGCTCATATACAA
CAGGAGCACTCGAGTTTTCGGCGGAGGGACCAAGCTGACCGTCCCTAGGT
GCGGCCGCA

FIG. 9(cont.)

GIL60

SEQ ID NO:61

E V Q L V E S G G G V V R P G G S L R L S C A A S G F T F D
D Y G M N W V R Q A P G K G L E W V S G V N G A A S G G T R D Y
A A S V K G A R G G G S G G S Y S L Y L Q M N S L R A E D
T A L Y Y C A R G G G S G G S F Y F G Y W G R Q P S V S
S G G G S G G T G A S G D V G A Y N F V S S V S G S
P G Q S I T I S C T G A S G D V G A Y N F V S S V S G S
K T P K L I I Y D V N K R P S G V S N R F S S G S N T A
S L T I S G L Q A E D E S D Y Y C S S T S F V G G
G T K V T V L G A A

SEQ ID NO:70

GAGGTGAGCTGGTGGAGTCCGGGGGAGGTGTGTACGGCTTGGGGGGT
CCCTGAGACTCTCTGTGCAGCCTCTGGATTACACCTTTGACGATTATGG
CATGAAC TGGTCCGCCAAGCTCCAGGGAAGGGCTGGAGTGGTCTCT
GGTGTATATGGGAATGGTGGTACCAGAGATTATGCAGCCTCCCGTGAAGG
GCCGATTCAACCATCTCCAGAGACAACGCCAAGAACTCCCTGTATCTGCA
AATGAACAGTCTGAGAGCCGAGGACACGGCCTTGTTACTGTGCGAGA
GGATGGTATAGTGGAGCTTCTACTACTTTGGCTACTGGGGCCGAGGAA
CCCTGGTCAACGCTCGAGTGGAGGGCGGTTTCCAGCGGAGGTGGCTC
TGGCGGTGGCGGAAGTGCACAGGCTGTGTGCTACTAGCCGTCCTCCGTG
TCTGGGTCTCTGGACAGTCGATCACCATCTCTCTGCTGCTGAGCCAGCG
GTGACGTGGTGGCTTATACTTTGTCTCTCTGGTACCAACACACCCAGG
CAAAACCCCAACTCATAATTTATGATGTCAATAAGCGGCCCTCAGGG
GTTTCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCTCCCTGA
CCATCTCTGGGTCCAGGCCGAGGACGAGTCTGATTATTACTGCAGCTC
ATATACAAGCACCTTCTCTGTGGTATTTGGCGGAGGGACCAAGTCAAC
GTCCTAGGTGGGGC

FIG. 9(cont.)

GIL68

SEQ ID NO:79

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

SEQ ID NO:88

GAAGTCAGCTGGTGCAGTCTGGGGCTGAGTGAAGACCTGGGGCTC
AGTGAAGTCTCCTGTGAGGCTTCTGGATACACCTTCAGCGATTACTATA
TTCACCTGGTGGACAGACCCCTGGACAAGGTTTGAGTGGATGGGATGG
GTCAACCTTGACACTGGTGGCACAGATACGGCGAGAAGTTTCAGGGCTG
GGTCACCATGACCAGGGACATGTCCAACACACAGCCTACATGGAGCTGC
CCAGGCTGAGAGACGACACAGCGCGTATATTACTGTGCGAGAGATCTA
ACTGGATTGATCCTTTTGATATCTGGGGCCAGGAAACCTGGTCACCGT
CTCGAGTGGAGGGCGGTTTCAGGGGAGGTGGCTCTGGCGGTGGCGGAA
GTGCACAGTCTGTGCTGACTCAGCCACCTCAGTGTAGTGGCCCCAGGA
AAGACGGCCACGATTACCTGTGGGGAAACAACCTTCGAAATAAAGAGT
ACACTGGTATCAGCAGAGGCCAGGCCAGCCCTGTCTGTCATCTATT
ATGATTACAGCCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCCGC
TCTGGGAACACGGCCACCTGACCATCAGCAGGTCGAGGCCGGGATGA
GGCCGACTTTTACTGTGAGGTGGGATAGTAGTACTGATCGTCCGCTGT
TCGGCGGAGGGACCAAGCTGACCGTCTTAGTGGGGCGCA

FIG. 9(cont.)

GIL92

SEQ ID NO:97

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

SEQ ID NO:106

CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCTGGGGCTC
AGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACGACTACTATA
TGCACCTGGTCCGACAGGCCCTGGACAAGGCTTGAAGTGGTGGATGG
ATCAACCTTATCTGTTGGGCAATCTATGACACAGAAGTTTCGGGGCAG
GGTACCATGACCAGGACACGTCCATCAACACAGCCTACATGGAGCTGA
GCAGACTGGGATCTGACGACACGCGCTGATATTTGCGAGAGAACCT
GAATAATCGATTTTGGGGGGTGACACTGGGGCGGGGACATGGT
CACCGTCTCGAGTGGAGGGGGTTCAGGGGAGGTGGCTCTGGCGGTG
GCGGAAGTGCACAGGCTGTGCTGACTCAGCGTCTCTCAGTCTCTGGGCC
CCAGGGCAGAGGTCACCATCTCCTGCACTGGAGCAGCTCCAACTCGG
GGCAGGTTATGGTTACACTGGTACCAACAGCTTCCAGGAACAGCCCCA
AACTCTCATCTATGGTAACAGCAATCGGCCCTCAGGGTCCCTGACCGA
TTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCT
CCAGGCTGAGGATGAGGCTGATTTATCTGCTGCTGCTGCTGCTGCTGCT
TGAGTGGTTATGCTTTCGGAACCTGGGACCCAGCTCACCGTTTAAAGTGG
GCCGCA

FIG. 9(cont.)

097D09

SEQ ID NO:115

EVQLVESGGGLVTPGSSRLRLSCAASGFTFSDIYMSWVRQAPGRGLEWVSAIS
GSGGSTYYADSVKGRITISRDNAKNSLYLQMSSLRSEDTAVYYCARGLWVWD
PLDYWGRGTLVTSSGGSGGGGGGGSDIQMTQSPSTLSASIGDRVTIT
CRASEGIYHWLAWYQOKPGKAPKLLIYKASSLASGAPSRFSSGSGFGTDFTLT
ISSLPDDFATYYCQOYSEFAWTFGGGTKLEIKRAAAH

SEQ ID NO:124

GAGGTGCAGCTGGTGAGTCTGGGGGAGGCTTGGTCACGCCTGGAGGGT
CCCTGAGACTCTCCTGTGTCAGCCTCTGGATTCACCTTCAGTGACTACTA
CATGAGCTGGTCCGCCAGGCTCCAGGGAGGGGCTTGGAGTGGGTCTCA
GCTATTAGTGGTAGTGGTGGTAGCACATACTACGCAGACTCCCGTGAAGG
GCCGGATCACCATCTCCAGAGACAAAGCCCAAGAACTCACTGTATCTGCA
AATGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA
GGGCTTTGGGTTTGGGATCCTCTTGACTACTTGGGCAGAGGAACCCCTGG
TCACCGTCTCTTCAGGTGGGGCGGTTCAGCGCGAGGTGGCAGCGCGCG
TGGCGGATCGGACATCCAGATGACCCAGTCCCCCTTCCACCCCTGTCTGCA
TCTATTGGAGACAGAGTACCATCACCTGCCGGCCAGTGAGGGTATTI
ATCACTGGTTGGCCTGGTATCAGCAGAAGCCAGGAAAGCCCCCTAAACT
CCTGATCTATAAGGCCCTCTAGTTAGCCAGTGGGGCCCATCAAGGTTT
AGCGGCAGTGGATTGGGACAGATTTCACTCTCACCATCAGCAGCCCTGC
AGCCTGATGATTTTGCAACTTATTACTGCCCAACAATACAGCGAGTTCGC
CTGGACCTTCGGCGGAGGGACCAAGCTGGAGATCAAAACGTGCGGCGCGCA
CAT

FIG. 9(cont.)

062A09

SEQ ID NO:133

QVQLVESGAEVKKPGASVKVSKASGYTFTSYGISWVRQAPGQGLEWMGV
SAYTGNNTYAOKFQGRVTMTTDTSTAYMELRGLRSDDTAVYYCARDRGY
YDAYDIWGQGLVTVSSGGGGSGGGGGGGSDIQMTQSPSTLSASIGDRV
TITCRASEGIYHMLAWYQQKPKAPKLLIYKASSIASGAPSRFSGSGFGTD
FTLTISLQPDFFATYYCQOMGEYNATIGGGTKLEIKRAAAH

SEQ ID NO:142

CAGGTGCAGCTGGTGGAGTCTGGGGCTGAGGTGAAGAACCCCTGGGGCCTC
AGTGAAGGTCTCCTGCAAGCTTCTGGTTACACCTTTACCAGTTATGGTA
TCAGCTGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGGATGG
GTCAGCGCTTACACTGGTAACACAACTATGCACAGAAAGTTCCAGGGCAG
AGTCACCATGACCACAGACACATCCACGAGCACAGCCTACATGGAACCTGA
GGGGCTGAGATCTGACGACACGGCCGTGTATTACTGTGGAGAGATCGT
GGATACTATGATGCTTATGATATCTGGGGCCCAAGCACCCCTGGTCACCGT
CTCCTCAGGTGAGGGGTTTCAGCGGAGGTGGCAGCGGGGTGGCGGAT
CGGACATCCAGATGACCCAGTCTCCTTCCACCCCTGTCTGCATCTATTGGA
GACAGAGTCACCATCACCTGCCGGCCAGTGAGGGTATTTTATCACTGGTT
GGCCTGGTATCAGCAGAAGCCAGGAAAGCCCTAAACTCCTGATCTATA
AGGCCTCTAGTTTAGCCAGTGGGGCCCCCATCAAGTTACGGCGGAGTGA
TTTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTT
TGCAACTTATTACTGCCAACAAATGGGCGAGTACAGCCACCATCGGCG
GAGGACCAAGCTGGAGATCAACGTTGGGGGGCCGACAT

FIG. 9(cont.)

062G05

SEQ ID NO:151

QVQLVESGAEVKKPGASVKVSKASGYTFTSYGISWVRQAPGQGLEWMGWI
SAYTGNTNYAOKFOGRVTMTTDSTSTAYMELRSLRSDDTAVYYCARDRGY
YDAFDIWGQGTLVTVSSGGSGSGGGGGSDIQMTQSPSTLSASIGDRV
TITCRASEGIYHWLAWYQQKPGKAPKLLIYKASSLASGAPSRFSGSGFGTD
FTLTISSLQPDDFATYYCOOMGEWKAAFGGGTKLEIKRAAAH

SEQ ID NO:160

CAGGTGCAGCTGGTGGAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTTACCAAGTTATGGTA
TCAGCTGGGTCCGACAGGCCCCCTGGACAAGGCTTGAGTGGATGGGATGG
ATCAGCGCTTACACTGGTAACACAAACTATGCACAGAAAGTCCAGGGCAG
AGTCACCATGACCCACAGACACATCCACGAGCACAGCCTACATGGAACTGA
GGAGCCTGAGATCTGACGACACGGCCGTGTATTACTGTGCGAGAGATCGT
GGATACTATGATGCTTTCGATATCTGGGGCCAAAGGCACCCCTGGTCACCGT
CTCCTCAGGTGGGGCGGTTCAGCGGAGGTGGCAGCGCGGTTGGCGGAT
CGGACATCCAGATGACCCAGTCTCCTTCCACCCCTGTCTGCATCTATTGGA
GACAGAGTCACCATCACCTGCCGGCCAGTGAGGGTATTTATCACTGGTT
GGCCTGGTATCAGCAGAAGCCAGGGAAAGCCCCCTAAACTCCTGATCTATA
AGGCCCTCTAGTTAGCCAGTGGGGCCCCCATCAAGGTTCAGCGGCAGTGGA
TTTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTT
TGCAACTTATTTACTGCCCAACAAATGGGGGAGTGGAGGGCGCCTTCGGCGG
GAGGGACCAAGCTGGAGATCAAAACGTCCGGGGCCGCACAT

FIG. 9(cont.)

087B03

SEQ ID NO:169

EVQLVESGGGVVRPGGSLRLSCAASGFTFDDYGMNWVRQAPCKGLEWVSGV
NWNGGTRDYAASVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCARGWYS
GAWNMGYNRGTLVTVSSGGGGGGGGGGSAQAVALTPSSVSGSPGQ
SITISCTGASGDVGAYNFVSWYQQHPGKTPKLIYDVNKRPSGVSNRFSGS
KSSNTASLTISGLQAEDESYYCSSYTSTFSVVFGGGKVTIVLGAHAH

SEQ ID NO:178

CGAGGTGCAGCTGGTGGAGTCCGGGGGAGGTGTGGTACGGCCTGGGGGGTCCCTG
AGACTCTCCTGTGCAGCCTCTGGATTACCTTTGACGATTATGGCATGAACCTGGG
TCCGCCAAGCTCCAGGCAAGGGCTGGAGTGGGTCTCTGGTGTATTTGGAATGG
TGGTACCAGAGATTATGCAGCCTCCGTGAAGGCCGATTCACCATCTCCAGAGAC
AACGCCAAGAACTCCCTGTATCTGCAAAATGAACAGTCTGAGAGCCGAGGACACGG
CCTTGATTACTGTCCGAGAGGATGGTATAGTGGGGCCGCGTGGACATGGGCTA
CTGGGGCCGAGGAACCTGGTCAACCGTCTCGAGTGGAGGCGGTTCAAGCGGA
GGTGGCTCTGGCGGTGGCGGAAGTGCACAGGCTGTGCTGACTCAGCCGTCTCCG
TGTCTGGGTCTCCTGGACAGTCGATCACCATCTCCTGCACCTGGAGCCAGCGGTGA
CGTTGGTGCTTATAACTTTGTCTCCTGGTACCAACAACACCCAGGCAAAACCCCC
AAACTCATAATTTATGATGTCAATAAGCGGCCCTCAGGGGTTTCTAATCGCTTCT
CTGGCTCCAAGCTAGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCCGA
GGACGAGTCTGATTATTACTGACGCTCATATACAAGCACCTTCTCTGTGGTATTT
GGCGGAGGACCAAGGTCACCGTCTCTAGGTGGCGCCGCACAT

FIG. 9(cont.)

367D04

SEQ ID NO:187

EVQLVESGGGVVRPGGSLRLSCAASGFTFDYGMNWVRQAPGKLEWVSG
VNWNGGTRDYAASVKGRTISRDNAKNSLYLQMNSLRAEDTALYYCARGW
YSGSPWSLGHWGRGLTVTVSSGGGGGGGGGGGGGGGGGGGGGGGGGGG
GGGSAQAVLTQPSVSGSPGQSVTISCTGASGDVGAYNEVSWYQQHPGK
TPKLIIDVNVKRPSGVSNRFSGSKSGNTASLTISRQAEDESDYCYCSYT
SRYTTEFGGGTKVTVLGAAAH

SEQ ID NO:196

GAGGTGAGCTGGTGGAGTCCGGGGGAGGTGTGGTACGGCCTGGGGGGGT
CCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTTGACGATTATGG
CATGAACTGGTCCGCCAAGCTCCAGGGAAGGGCTGGAGTGGGTCTCT
GGTGTTAATTGGAATGGTGATCCAGAGATTATGCAGCCTCCGTGAAGG
GCCGATTACCATCTCCAGAGACAACGCCAAGAACTCCCTGTATCTGCA
AATGAACAGCTGAGAGCCGAGGACACGGCCTTGTAATTACTGTCCGAGA
GGATGGTATAGTGGAGCCCGTGTCGCTGGGCCACTGGGGCCGAGGAA
CCCTGGTCACCGTCTCGAGTGGAGGGCGCGGTTCAGGGGAGGTGGCTC
TGCGGTAGCGGAGGTGGCTCTGGCGGTAGCGGAGGTGGCTCTAGCGGA
GGTGGCTCTGGCGGTGGCGGAAGTGCACAGGCTGTGCTGACTCAGCCGT
CCTCCGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCCTGCACCTGG
AGCCAGCGGTGACGTGGTGCTTATAACTTTGCTCCTGGTACCAACAA
CACCCAGGCAAAACCCCCAAACTCATAATTTATGATGTCAATAAGCGGC
CCTCAGGGGTTTCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGC
CTCCCTGACCATCTCTAGGCTCCAGGGCCGAGGACGAGTCTGATTATTAC
TGCAGCTCATATACATCGAGGTACACGACCGAGTTTGGCGGAGGGACCA
AGGTCACCGTCCTAGGTGGGGCCGCACAT

FIG. 9(cont.)

368D04

SEQ ID NO:205

EVQLVESGGGVVRPGSLRLSCAASGFTFDYGMNWVRQAPGKLEWVSG
VNWNGGTRDYAASVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCARGW
YSGAAMNMGYWGRGTLVTVSSGGGGSGGGSGGGSGGGSGGGSGGGGS
AQAVLTQPSVSGSPGQSITISCTGASGDVGAYNEFSWYQQHPGKTPKLI
IYDVNKRPSGVSNRFSGSKSGNTASLTISGLQAEDESDYYCASLVDSFSV
VFGGGTKVTVLGAAAH

SEQ ID NO:214

GAGGTGCAGCTGGTGGAGTCCGGGGGAGGTGTGGTACGGCCTGGGGGGT
CCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTTGACGATTATGG
CATGAACTGGGTCCGCCAAGCTCCAGGGAAGGGCTGGAGTGGTCTCT
GGTGTAAATTGGAATGGTGTACCAAGATTATGACGCCICCGTGAAGG
GCCGATTCA~~CC~~ATCTCCAGAGACAACGCCAAGAACTCCCTGTATCTGCA
AATGAACAGTCTGAGAGCCGAGGACACGGCCTTGTA~~TT~~ACTGTCCGAGA
GGATGGTATAGTGGGGCCCGTGGAAACATGGGCTACTGGGGCCGAGGAA
CCCTGGTCACCGTCTCGAGTGGAGGGCGGGGTT~~CAGCGGAGGTGGCTC~~
TGGTGGTAGCGGAGGTGGCTCTGGCGGTGGCGGAGGTGGCTCTGGCGGT
GGCGGAAGTGCACAGGCTGTGTGACTCAGCCGCTCCCTCGTGTCTGGGT
CCCCTGGACAGTCGATCACCATCTCCTGCAC~~TGGAGCCAGCGGTGACGT~~
TGGTGCCTTAACTTTGCTCTCTGGTACCAACAACACCCAGGCAAAACC
CCCAAACTCATAATTTATGATGTCAATAAGCGGCCCTCAGGGGTTCTTA
ATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTC
TGGGCTCCAGGCCGAGGACGAGTCTGATTATTACTGCGCCTCCCTCGTC
TCCGACTTCTCTGTGGTATTTGGCGGAGGGACCAAGGTCACCGTCTCTAG
GTGGCGCCGCACAT

FIG. 9(cont.)

166B06

SEQ ID NO:223

EVQLVQSGAEVKKPGASVKVSQASGYTFSDYYIHVVRQTPGQGFEMMGWV
NPDTGGTRYAOKFOGWTMTDRMSNTTAYMELPRLRDDDTAVYYCARDLTG
FDPFDIWGQGLVTVSSGGSSGGSSGGSSGSAQSVLTQPPSVSVAPGKTA
TITCGNFRNKRHVHWYQQRPGQAPVLVIYDSDRPSGIPERFSGSRSGNT
ATLTISRVEAGDEADFYCOVWDLFNDNGVFGGGTKLTVLGAAAH

SEQ ID NO:232

GAAGTCAGCTGGTCCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGTCTCCTGTCTAGGCTTCTGGATACACCTTCAGCGATTACTATA
TTCACCTGGGTGGACAGACCCCTGGACAAGGTTTGAGTGGATGGGATGG
GTCAACCCCTGACACTGGTGGCACAAGATACGGCGCAGAAGTTTCAGGGCTG
GGTCACAATGACCAGGGACATGTCCAACACCACAGCCTACATGGAGCTGC
CCAGGCTGAGAGACGACGACACGGCCGTATATTACTGTCCGAGAGATCTA
ACTGGATTGATCCTTTTGATATCTGGGGCCAGGGAACCCCTGGTCACCGT
CTCGAGTGGAGCGGCAGTTCAGGTGGAGGTGGCTCTGGCGGTGGCGGAA
GTGCACAGTCTGTGCTGACTACGCCACCCTCAGTGTCAGTGGCCCCCAGGA
AAGACGGCCACGATTACCTGTGGGGGAACAACITTCGAAATATAAAGAGT
ACACTGGTATCAGCAGAGGCCAGGCCAGGCCCTGTCTGGTCAATCTATT
ATGATTTCAGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCCCG
TCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAGGCCGGGATGA
GGCCGACTTTTACTGTCTCAGGTGTGGGATCTCTTCAACGACAACGGCGTGT
TCGGCGGAGGGACCAAGCTGACCGTCTTAGTGCGGCCGCACAT

FIG. 9(cont.)

166G05

SEQ ID NO:241

EVQLVQSGAEVKKPGASVKVSQASGYTFSDYIHWVRQTPGQGFEMGMV
NPDTGGTRYAOKFOGWVTMRDMSNTTAYMELPRLRDDDTAVYCARDLTG
FDPFDIWGQGLVTVSSGGGGSGGGGSAQSVLTQPPSVSVAPGKTA
TITCGGNFERNKRVHWYQQRPGQAPVLVIYDSDRPSGIPERFSGRSNGT
ATLTISRVEAGDEADFYQVWDFLTDSGFGGGTKLTVLGAAAH

SEQ ID NO:250

GAAGTCAGCTGGTCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGGTCTCCTGTGAGGCTTCTGGATACACCTTCAGCGATTACTATA
TTCACTGGGTGGCACAGACCCCTGGACAAGGGTTTGTGATGGATGGATGG
GTCAACCCCTGACACTGGTGGCACAAAGATACGGCGAGAAGTTTCAGGGCTG
GGTCACAAATGACCAGGGACATGTCCAACACCACAGCCTACATGGAGCTGC
CCAGGCTGAGAGACGACGACACGGCCGTATATTACTGTCCGAGAGATCTA
ACTGGATTGTATCCTTTTGATATCTGGGGCCAGGGAACCCGTGTCACCGT
CTCGAGTGGAGGGCGGGTTTCAGCGGAGGTGGCTCTGGCGTGCGGAA
GTGCACAGTCTGTGCTGACTCAGCCACCCTCAGTGTCACTGGCCCCAGGA
AAGACGGCCACAATTACCTGTGGGGGAAACAACCTTCGAAATAAAAGAGT
ACACTGGTATCAGCAGAGGCCAGGCCAGGGCCCTGTCTGGTCATCTATT
ATGATTACAGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCCCG
TCTGGGAACACGGCCACCCTGACCATCAGCAGGTCGAGGCCGGGATGA
GGCCGACTTTTACTGTGAGGTGTGGGATTTCTCTACCGACTCGGGGTCTGT
TCGGCGGAGGGACCAAGCTGACCGTCTTAGTGGCGCCGCACAT

FIG. 9(cont.)

375G06

SEQ ID NO:259

EVQLVQSGAEVKKPGASVKVSQASGYTFSDYIHWVRQTPGQGF~~EW~~MGW
VNPDTGGTRYAOKFOGWVTMTRDMSNTTAYMELPRLRDDDTAVYYCARDL
TG~~Y~~DIYDRWGQGLVTVSSGGGGGGGGGGGGGGGGGGGGGGGGGSAQ
SVLTQPPSM~~S~~VAPGKTATITCGGNFERNKRVHWYQQRPQAPVLVIYYDS
DRPSGIPERFSGRSRSGNTATLTISRVEAGDEADFYCQVWDEFLADEAMFEGG
GTKLTVLGAAAH

SEQ ID NO:268

GAAGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAACCTGGGGCCTC
AGTGAAGGTCTCCTGTCAAGCTTCTGGATACACCTTCAGCGATTACTATA
TTCAC~~T~~GGGTGGACAGACCCCTGGACAAGGTTTGAGTGGATGGATGG
GTCAA~~CC~~CTGACACTGGTGGCAAGAATACGGCGCAGAAAGTTTCAGGGCTG
GGTCACAATGACACGAGGACATGTCCAACACACAGCCCTACATGGAGCTGC
CCAGGCTGAGAGACGACGACACGCGCCGTATATTACTGTGCGAGAGATCTA
ACTGGATACGACTACTACGACCGGTGGGGCCAGGGAACCTGGTCACCGT
CTCGAGTGGAGCGCGGTTCAGCGGAGGTGGCTCTGGCGGTGGCGAAGTGCACAG
GTGGCTCTGGCGGTGGCGGAGGTGGCTCTGGCGGTGGCGAAGTGCACAG
TCTGTGCTGACTCAGCCGCCCTCAATGTCAGTGGCCCGCAGGAAAGACGGC
CACGATTACCTGTGGGGAAACAAC~~TT~~TCGAAATAAAAGAGTACACTGGT
ATCAGCAGAGGCCAGGCCAGGCCCTGTCTGGTCACTCTATTATGATTCA
GACCGG~~CCCT~~CAGGGATCCCTGAGCGATTCTCTGGCTCCCCCTCTGGGAA
CAGGGCCACCTGACCATCAGCAGGGTCGAGGCCGGGATGAGCCGACT
TTTACTGTCAAGGTGGGATTTCCTCGCCGACGAGCGGATGTTCTGGCCGA
GGGACCAAGCTGACCGTCTAGGTGGCGCGGCACAT

FIG. 9(cont.)

376B10

SEQ ID NO:277

EVQLVQSGAEVKKPGASVKVSCQASGYTFSDYYIHVVRQTPGQGFEMWMG
VNPDTGGTRYAOKFOGWNVTMRDMSNTTAYMELPGLRDDDTAVYYCARDL
TGYDQYTAWGQGLVTVSSGGSGGGGSAQSVLTQPPSVSVAPG
KTATITCGGNFRNKRHVHYQORPGQAPLVIVYDSDRPSGIPERFSGSR
SGNTATLTISRVEAGDEADFYCSTFDPTDRPLFGGGTKLTVLGAAAH

SEQ ID NO:286

GAAGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGGTCTCTGTCAAGCTTCTGGATACACCTTCAGCGATTACTATA
TTCACTGGGTCCGACAGACCCCGAGGCAAGGGTTTGAGTGGATGGGATGG
GTCAACCCCTGACACTGGTGGCAGAGATACCGGCAGAAAGTTTCAGGGCTG
GGTCACAAATGACCAGGGACATGTCCAACACCACAGCCTACATGGAGCTGC
CCGGCTGAGAGACGACGACACGGCCGTATATTA
CTGGGTACGACAGTACACGGCCTGGGGCCAGGAA
CTCGAGTGGAGCGCGGTTCAGGGGAGGTGGCTCTGGCGGTGGCGGAA
GTGCACAGTCTGTGCTGACTCAGCCACCCCTCAGTGTCA
AGACGGCCACGATTACCTGTGGGGAACAACCTTCGAAATAAAGAGT
ACACTGGTATCAGCAGAGGCCAGGCCCTGTCTGTCATCTAT
ATGATTACAGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCCCG
TCTGGGAACACGGCCACCCCTGACCATCAGCAGGTCGAGCCGGGATGA
GGCCGACTTTTACTGTAGCACCTTCGACCCCTTCACTGATCGTCGGCTGT
TCCGGCGAGGGACCAAGCTGACCCGTCTTAGTGGCGCCGCACAT

FIG. 9(cont.)

354A08

SEQ ID NO:295

QVQLVQSGAEKKPGASVKVSKASGYTFTDYYMHVVRQAPGQGLEWVGWIN
PYTGAFAIAOKFRGRVTMTSDTSINTAYMELSLGSDDTAVYYCAREPERE
GDSTGQVWGRGTMVTVSSGGGGGGGGSGGSRSAQAVLTQPSVSGAPRQR
VTISCTGSSSNIGAGYGVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSK
SGTSASLAITGLQAEDEADYYCYHWDKEQSGYVFGTGTQLTVLSA

SEQ ID NO:304

CAGGTCCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAGCCTGGGGCCTC
ACTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCGACTACTATA
TGCACCTGGGTGGACAGGCCCTGGACAAGGCTTGAGTGGTGGGATGG
ATCAACCCCTTATACTGGTGGCGCATTCCTATGCACAGAAATTTCGGGGCAG
GGTCACAATGACCAGGGACACGTCCATCAACACAGCCTACATGGAGCTAA
GCAGACTGGGATCTGACGACACGGCCGTGTATTATTGTGCGAGAGAACCT
GAAAGATTCCGGCGACTCCACGGGGCAGGTCTGGGGCCGGGGGACAAATGGT
CACCGTCTCGAGTGGGGCGGGCGGTTCAGGGGGAGGTGGCTCTGGCGGTA
GCAGAAAGTGCACAGGCTGTGTGACTCAGCCGTCCTCAGTGTCTGGGGCC
CCAAGGCAGAGGTCACCATCTCCTGCACCTGGGAGCAGCTCCAACATCGG
GGCAGGTTATGGTGTACACTGGTACCACAGCTTCCAGGAACAGCCCCCA
AACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGTCCCTGACCCGA
TTCTCTGGCTCCAAGTCTGGCACCTCAGCCCTCCCTGGCCATCACTGGGCT
CCAGGCTGAGGATGAGGCTGATTATTACTGCTACCACCTGGGACAAGGAGC
AGAGTGGTTATGTCTTCGGAACTGGGACCCAGCTCACCGTTTTTAAGTGGC

FIG. 9(cont.)

355B06

SEQ ID NO:313

EVQLVQSGAEVKKPGASVKVSCQASGYTFTDYMHVVRQAPGQGLEWVGWI
NPYTGSAFYAQKFRGRATWTRNTSINTAYMELSLGSDDTAVYYCAREPEK
FGESSGQLWGRGTMVTISSGGGGSGGGSGGSAQAALTPSSVSGAPGQ
RVTISCTGSSSNIGPGYGVHWYQQLPGTAPKLLIYGDSNRPSGVPDRFSGS
KSGTSASLAITGLQAEDEADYYCQSYDSGLSGYVFGTGTQLTVLSA

SEQ ID NO:322

GAAGTGCAGCTGGTGCAGTCTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCCTC
AGTGAAGGTCTCTCTGTCAGGCTTCTGGATACACCTTCACCGACTACTATA
TGCACTGGGTGCGACAGGCCCTGGACAAAGGCTTGAGTGGGTGGGTGG
ATCAACCCCTTATACTGGTAGCGCATTTCTATGCACAGAAAGTTTCGGGGGCAG
GGCCACAATGACCAGGAACACGTCCTCATCAACACAGCCTACATGGAGCTGA
GCAGACTGGGATCTGACGACACGGCCGTGTATTATTGTCCGAGAGAACCT
GAAAAATTCTGGCGAGTCCAGCGGCCAGTTGTGGGGCCGGGGACAAATGGT
CACCATCTCGAGTGGAGCGCGGTTTCAGCGGAGGTGGCTCTGGCGGTA
CGGAAGTGCACAGGTGTGCTGACTACGCCGTCCTCAGTGTCTGGGGCC
CCAGGGCAGAGGTCACCATCTCCTGCCACTGGGAGCAGCTCCAACATCGG
GGCAGGTTATGGTGTACACTGGTACCAACAGCTTCCAGGAACAGCCCCCA
AACTCCTCATCTATGGTGACAGCAATCGGCCCTCAGGGGTCCCTGACCGA
TTCTCTGGCTCCAAAGTCTGGCACCTCAGCTCCCTGGCCATCACTGGGCT
CCAGGCCGAGGATGAGGCTGATTATTACTGCCAGTCCCTATGACAGCGGCC
TGAGTGGTTATGCTCTTCGGAACCTGGGACCCAGCTCACCGTTTAAATGCG

FIG. 9(cont.)

355E04

SEQ ID NO:331

QVQLVQSGAEVKKPGASVKVSKASGYTFTHYMHVVRQAPGQGLEWVGWI
NPYTGGAFYAOKFOGRVTMTRDTSINTAYMELSRIGSDDTAVYICAREPEK
FDSPNAELWGRGTMVTISSEGGSGGGSGGSAQAVALTPSSVSGAPGQ
RVTISCTGSSSNIGAGYGVHWYQQLPGTAPKLLIYGNRNRPSPGVPDRFSGS
KSGTSASLAIITGLQAEDEADYYCOSYDSSLGVYFGTGTQLTVLSA

SEQ ID NO:340

CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAAAAGCCTGGGGCCTC
AGTGAAAGTCTCTGCAAGGCTTCTGGATACACCTTCACTACTATA
TGCACTGGGTGGACAGGCCCTGGACAAGGCTTGAGTGGGTGGATGG
ATCAACCCCTTACTGGTGGCGCATTTCTATGCACAGAAAGTTTCAGGGCAG
GGTCACAAATGACACGGGACACGTCCATCAACACAGCCTACATGGAGCTGA
GCAGACTGGGATCTGACGACACGGCCGTGTATTATTGTGCGAGAGAACCT
GAAAAATTCGACTCGCCGAACGCCGAGATCTGGGGCCGGGACAAATGGT
CACCATCTCGAGTGAAGCGGGCGGTTGAGGGGAGGTGGCTCTGGCGGTA
GCGGAAGTGACAGGCTGTGCTGACTCAGCCGTCCTCAGTGTCTGGGGCC
CCAGGGCAGAGGTCACCATCTCTGCACTGGGAGCAGCTCCAACATCGG
GGCAGGTTATGGTGTACACTGGTACCAACAGCTTCCAGGAACAGCCCCCA
AACTCCCTCATCTATGGTAACAGCAATCGGGCCCTCAGGGTCCCTGACCGA
TTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCT
CCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCTCTATGACAGCAGCC
TGAGTGGTTATGTCTTCGGAAACCGGGACCCAGCTCACCGTTTTTAAGTGGG

FIG. 9(cont.)

356A11

SEQ ID NO:349

QVQLVQSGAEVKKPKASVKVSKASGYTF^TNY^MHWVROAPGQGLEWVGWI
NPYTGSAFYAQKFRGRVTMT^RDT^SINTAYMELSLRGSDDTAVYYCAREPEK
FDSDSDVWGRGTMVTVSGGGSSGGSGGSAQA^VLTPPSVSGAPGQR
VTISCTGSSSNIGAGYGVHWYQQLPGTAPKLIYGDSSRPSGV^PDRFSGSK
SGTSASLAITGLQAEDEADYVYQSYD^NSLSGYVFGTGTQLTVLSA

SEQ ID NO:358

CAGGTTCAGCTGGTCAGTCTGGGGCTGAGCTGAAGAAGCC^TTGGGGCCTC
AGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAACTACTATA
TGCACTGGGTGGCAGACGGCCCTGGACAGGGCTT^GAGTGGGTGGGATGG
ATCAACCC^TTATACTGGTAGCGCATTCATCCACAGAA^GTTTCGGGGCAG
GGTTACAATGACCAGGGACACGTCCATCAACACAGCCTACATGGAGCTGA
GCAGACTGGGATCTGACGACACGGCCCGTGATTA^TTGTGCGAGAGAACCT
GAAAA^TTCGACTCCGACGACTCCGACGCTCGGGCCCGGGACAAATGGT
CACCGTCTCGGGTGGAGCGGCGAGTTCAGGCGGAGGTGGCTCTGGCGGTA
GCGGAAGTGACACAGGCTGTGCTGACTCAGCCGCCCTCAGTGTCTGGGGCC
CCAGGCGAGAGGTCACCATCTCCTGCAC^TGGAGCAGCTCCAAACATCGG
GGCAGGTTATGGTGTACACTG^TGTACCAACAGCTTCCAGGAACAGCCCCA
AACTCATCATCTATGGTGACAGCAGTCGGCCCTCAGGGGTCCCTGACCGA
TTCTCTGGCTCCAAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCT
CCAGGCTGAGGATGAGGCTGATTATTA^CTGCCAGTCCATGACAACAGCC
TGAGCGGTTATGTCTTCGGAACTGGGACCCAGCTCACCGTTTAAAGTGGC

FIG. 9(cont.)

GIL01

SEQ ID NO:367

QVQLVESGGGLVKPGGSLRLSCAASGFTFSDIYMSWIRQAPGKGLEWVSAIS
GSGSTYYADSVKGRITISRDNAKNSLYLQMNSLRAEDTAVYCARGLWVMD
PLDYWGRGTLVTVSSGGSGGGSGGSDIQMTQSPSTLSASVGDRVTIT
CRASEGIYHWLAWYQQKPGKAPKLLIYKASSLASGVPSRFSSGSGTDFTLT
ISSLPDDFATYYCQOYSNYPLTFGGGTKVEIKRA

SEQ ID NO:376

CAAGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTC
CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTGACTACTACA
TGAGCTGGATCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGCTCAGCT
ATTAGTGGTAGTGGTAGCACATACTACGCAGACTCCCGTGAAGGCCG
GATCACCATCTCCAGAGACAAAGCCCAAGAACTCACTGTATCTGCAATGA
ACAGCCTGAGAGCTGAGGACACGGCCGTGTATTACTGTGCGAGAGGGCTT
TGGGTTTGGGATCCCTCTGACTACTGGGGCAGAGGAACCCCTGGTCACCGT
CTCTTCAGGTGGAGCGGTTCAGCGGAGGTGGCAGCGGCGGTGGCGGAT
CGGACATCCAGATGACCCAGTCTCCTCCACCCTGTCTGCATCTGTTGGA
GACAGAGTCACCATCACCTGCCGGCCAGTGAGGGTATTATCACTGGTT
GGCCTGGTATCAGCAGAAGCCAGGGAAGCCCCTAAACTCCTGATCTATA
AGCCCTCTAGTTAGCCAGTGGGTCCCATCAAGTTCAGCGGCAGTGA
TCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGATGATT
TGCAACTTATTACTGCCAACAAATATAGTAATATCCGCTCACTTTCGGCG
GAGGGACCAAGGTGGAGATCAAAACGTGCG

FIG. 10

SEQ ID NO: 385

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGW
ISAYTGTNTYAQKFOGRVTMTDTSTAYMELSLRSDDTAVYCARDRGY
YDAFDIWGQGLTVTVSSGGGGGGGGGGSDIQMTQSPSTLSASVGD
RTITCRASEGIIYHWLAWYQQKPKAPKLLIYKASSLASGVPSRFSGSGSGTE
FTLTTISSLPDDFATYYCQQSYNPPLTFGGGTKVEIKRA

SEQ ID NO: 394

CAGGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAGCCTGGGGCCTC
AGTGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTTACCAGTTATGGTA
TCAGCTGGGTGCGACAGGCCCTTGACAAAGGGCTTGAGTGGATGGGATGG
ATCAGCGCTTACACTGGTAACACAAACTATGCCACAGAAGTTCACAGGCAG
AGTCACCATGACCCACAGACACATCCACGAGCACAGCCTACATGGAACTGA
GGAGCCTGAGATCTGCACGACAGGCCCGTGTAATTACTGTGCGAGAGATCGT
GGATACTATGATGCTTTTGATATCTGGGGCCAAAGCACCCCTGGTCAACCGT
CTCCTCAGGTGGAGCGGTTCAGGGGAGGTGGCAGCGCGGTGGCGGGAT
CGGACATCCAGATGACCCAGTCTCCTTCCACCTGTCTGCATCTGTTGGA
GACAGAGTCACCATCACCTGCGGGGCCAGTGAGGGTATTTATCACTGGTT
GGCCTGGTATCAGCAGAAGCCAGGGAAGCCCTAAACTCCTGATCTATA
AGGCCCTAGTTTAGCCAGTGGGGTCCCATCAAGTTTCAGCGGCAGTGGGA
TCTGGGACACAGATTCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTT
TGCAACTTATTACTGCCAACAAATAGTAATTATCCGCTCACTTTCGGCG
GAGGGACCAAGGTGGAGATCAAAACGTGCC

FIG. 10(cont.)

GIL45

SEQ ID NO:403

QMQLVESGGGVVQPGRSRLRLSCAAAGTTFSNYGMVWVRQAPGKGLEWVAHI
WYDGSNEKYADSVKGRMTVSRDNSKNTLYLQMNSLRAEDTAVYYCATEQHW
ITAFDIWGKGTLVTVSSGGGSGAGSGGGGSQSALTQPASVSGSPGQSIT
ISCTGTSSDVGGNYVSWYQQHPGKAPKLMIEGSKRPSGVSNRFSGSKSG
NTASLTISGLQAEDEADYYCSSYTTTRSVFGGGTKLTVLGA

SEQ ID NO:412

CAGATGCAGCTGGTGGAGTCTGGGGAGCGGTGGTCCAGCCTGGGAGGT
CCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTCACTTAACTATGG
CATGTACTGGGTCCGCCAGGCTCCAGGCAAGGGCTGGAGTGGGTGGCA
CATATTGGTATGATGGAAGTAATGAAAGTATGCAGACTCCCGTGAAGG
GCCGAATGACCGTCTCCAGAGACAATTCCAAGAACACGTTGTATTGCA
AATGAACAGCCTGAGAGCCGAGGACACGGCTGTTATTACTGTGCGACA
GAGCAACACTGGATTACTGCTTTTGATATAICTGGGGCAAGGCACCTGG
TCACCGTCTCCTCAGGTGGAGCGGGTTCAGGGCGCAGGTGGCAGCGCGGG
TGGCGGATCACAGTCTGGCGTGACTCAGCCTGCCTCCGTGCTGGGTCT
CCTGGACAGTCGATCACCATCTCCTGCACTGGAACCAAGCAGTACGTG
GTGGTTATAACTATGTCTCCTGGTACCAACAACACCCAGGCAAGCCCC
CAAACTCATGATTTATGAGGGCAGTAAGCGGCCCTCAGGGTTTCTAAT
CGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACAATCTCTG
GGCTCCAGGCTGAGGACGAGGCTGATTATTACTGCAGCTCATATACAAC
CAGGAGCACTCGAGTTTTCGGCGGAGGGACCAAGCTGACCCGTCTTAGGT
GCG

FIG. 10(cont.)

GIL60

SEQ ID NO:421

EVQLVESGGGVVRPGGSLRLSCAASGFTFDDYGMNWVRQAPGKGLEWVSG
VNWNGGTRDYAASVKGRFTISRDNAKNSLYLQMNLSRAEDTALYHCARGW
YSGSFYFYGWGRGTLVTVSSGGGGGGGGGSAQAALTQPASVSGS
PGQSITISCTGASGDVGAYNEFSWYQQHPGKAPKLIYDVNKRPSGVSNR
FSGSKSGNTASLTISGLQAEDEADYYCSSYTSTFVFGGGTKLTVLGA

SEQ ID NO:430

GAGGTGCAGCTGGTGGAGTCCGGGGGAGGTGTGGTACGGCCTGGGGGGTGC
CCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTTGACGATTATGGCA
TGAACCTGGTCCGCCAAGCTCCAGGAAGGGCTGGAGTGGGTCTCTGGT
GTTAATTGGAATGGTGGTACCAGAGATTATGCAGCCTCCGTGAAGGGCCG
ATTACCATCTCCAGAGACAACGCCAAGAACTCCCTGTATCTGCAATGA
ACAGTCTGAGAGCCGAGGACACGGCCTTGATCATCTGTCCGAGAGGATGG
TATAGTGGGAGCTTCTACTACTTTGGCTACTGGGGCCGAGGAACCCCTGGT
CACCGTCTCGAGTGGAGCGCGGGTTGAGCGGAGGTGGCTCTGGCGGTG
GCGGAAGTGACACAGGTGGCTGACTCAGCGGCCCTCCGTGTCTGGGTCT
CCTGGACAGTCGATCACCATCTCCTGCATCGAGCCAGCGGTGACGTTGG
TGCTTATAACTTTGTCTCCTGGTACCAACAACACCCAGGCAAGCCCCCA
AACTCATAAATTATGATGTCAATAAGCGGCCCTCAGGGGTTTCTAATCGC
TTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCT
CCAGGCCGAGGACGAGGCTGATTATTACTGAGCTCATATACAAGCACCT
TCTCTGTGGTATTGGCGGAGGACCAAGCTCACCGTCCCTAGGTGGC

FIG. 10(cont.)

GIL68

SEQ ID NO: 439

QVQLVQSGAEVKKPGASVKVSCKASGYTFSDYIHHVVRQAPGQGLEWMGNV
NPDTGGTRYAOKFQGRVTMTDMSISTAYMELSLRSDDTAVYYCARDLTG
FDPEDIWGQGLVTVSSGGGGGGGGSSASSVLTQPPSVSVAPGKTA
RITCGGNNFNRKRVHWYQQKPGQAPVLVIYYDSDRPSGIPERFSGSRSGNT
ATLTISRVEAGDEADYYCQVWDSS¹TDRLFGGGTKLTVLGA

SEQ ID NO: 448

CAAGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAGCCTGGGGCCTC
AGTGAAGGTCTCCTGTAAAGCTTCTGGATACACCTTCAGCGATTACTATA
TTCAC²TGGGTGGACAGGCCCTGGACAAGGTTGGAGTGGATGGGATGG
GTCAACCCCTGACACTGGTGGCACAAGATACGGGCAGAAAGTTTCAGGGCGG
GGTCACAATGACCAGGGACATGTCCATCTCCACAGCCTACATGGAGCTGT
CCAGGCTGAGAAGCGACGACAGGCCGTATATTACTGTGCGAGAGATCTA
ACTGGATTGTATCCTTTTGATATCTGGGGCCAGGGAACCCCTGGTCACCGT
CTCGAGTGGAGCGCGCGGTTCAGCGGAGGTGGCTCTGGCGGTGGCGGAA
GTGCAFCGTCTGTGCTGACTCAGCCACCCCTCAGTGTCAGTGGCCCCAGGA
AAGACGGCCCGCATTACCTGTGGGGGAACAAC³TTTCGAAATAAAAGAGT
ACACTGGTATCAGCAGAAGCCAGCCAGGCCCTGTCTGGTCATCTATT
ATGATTCAGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCCGC
TCTGGGAACACGGCCACCTGACCATCAGCAGGTCGAGGCCGGGATGA
GGCCGACTATTACTGTCAAGGTGTGGGATAGTAGTACTGATCGTCCGCTGT
TCGGCGGAGGACCAAGCTGACCGTCCTAGGTGGG

FIG. 10(cont.)

GIL92

SEQ ID NO:457

QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYMHVWRQAPGQGLEWVGWI
NPYTGGAFYAOKFRGRVTMTRDTSISTAYMELSLRLSDDTAVYYCAREPEK
FDFWGGDNWGRGTLVTVSSGGGGGGGGGSAQAVALTQPPSVSGAPGQ
RVTISCTGSSSNIGAGYGVHWYQQLPGTAPKLLIYGNSNRPSGVDPDRFSGS
KSGTSASLAITGLQAEDEADYYCQSYDSSISGVFGGGTQLTVLSA

SEQ ID NO:466

CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGTGAAGAAGCCTGGGGCCTC
AGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCGACTACTATA
TGCACTGGGTGGACAGGCCCTGGACAGGGCTTCACTGGGTGGGATGG
ATCAACCCCTTATACTGGTGGCGCATTTCTATGCACAGAAGTTTCGGGGCAG
GGTCACAAATGACCAAGGACACCGTCCATCAGCACAGCCTACATGGAGCTGA
GCAGACTGAGATCTGACACACGGCCGTGTATTATTGTGCGAGAGAACCT
GAAAAATTCGATTTTGGGGGGTGACAACTGGGGCCGGGGACATTGGT
CACCGTCTCGAGTGGAGGGGGGGTTCAGCGGAGGTGGCTCTGGCCGGTG
GCGGAAGTGCACAGGTGTGCTGACTCAGCCGCCGTCACTGTCTGGGGCC
CCAGGGCAGAGGTCACCATCTCCTGCACTGGGAGCAGCTCCAACATCGG
GGCAGGTTATGGTGTACACTGGTACCAACAGCTTCCAGGAACAGCCCCCA
AACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGA
TTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCT
CCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCCTATGACAGCAGCC
TGAGTGGTTATGCTCTCGGAGGTGGGACCCAGCTCACCGTTTAAGTGGG

FIG. 10(cont.)

SEQ ID NO: 475

[illegible]

SEQ ID NO: 484

CAGGTGCAGCTGGTGCACTCTGGAGCTGAGGTGAAGAAGCCTGGGGCCCTC
AGTGAAGGTCTCCTGCAAGGCTCTGGTTACACCTTTACCAGTTATGGTA
TCAGCTGGGTCCGACAGGCCCTTGACAAGGCTTGAGTGGATGGGATGG
GTGACGGCTTACACTGTTAAACACAACTATGCACAGAAGTTCAGGGGCAG
AGTCACCATGACACACAGACATCCACGAGCACGCCCTACATGGAACTGA
GGAGCCTGAGATCTGACGACACGGCCGTGTATTACTGTGCGAGAGATCGT
GGGATACATGATGCTTTTGATATCTGGGGCCAAAGCACCCCTGGTCAACCGT
CTCCTCAGGTGGAGGGCGGTTCAGGGCGGAGGTGGCAGCGGGGTGGCGGAT
CGGACATCCAGATGACCCAGTCTCCTTCCACCCCTGTCTGCATCTGTTGGA
GACAGAGTCACCATCACCTGCCGGGCCAGTGAGGGTATTTATCACTGGTT
GGCCTGGTATCAGCAGAAAGCCAGGAAAGCCCCCTAAACTCCTGATCTATA
AGGCCCTCTAGTTTAGCCAGTGGGTCCCATCAAGTTTCAGCGGCAGTGGGA
TCTTGGGACAGAGTTCACCTCAACCATCAGCAGCCTGCAGCCTGATGATTT
TGCAACTTATTACTGCCAACAAATGGGCGAGTACAAGCCACCTTCGGCG
CAGGGACCAAGGTGGAGATCAAAACGT

FIG. 10(cont.)

087B03

SEQ ID NO:493

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

SEQ ID NO:502

GAGGTGCAGCTGGTGAGAGCGGGGAGGTGTGTGTTACGGCCTGGGGGGTC
CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTGACGATTATGGCA
TGAACGGGTCCGCCAAGCTCCAGGGAAGGGCTGGAGTGGTCTCTGGT
GTTAATTGGAATGGTGTTACCAAGATTATGACGCTCCGTGAAGGCCG
ATTCACCATCTCCAGAGACACGCCCAAGAACTCCCTGTATCTGCAATGA
ACAGTCTGAGAGCCGAGGACACGGCCTTGATCACTGTGCGAGAGGATGG
TATAGTGGGGCCCGTGGAACATGGGCTACTGGGGCCGAGAACCTGGT
CACCGTCTCCTCAGAGGGCGGGTTACGGCGAGGTGGCTCTGGCGGTG
GCGAAGTGACAGGCTGCGCTGACTACGCCGGCTCCGTGTCTGGGTCT
CCTGGACAGTCGATCACCATCTCCTGCACTGGAGCCAGCGTGACGTGG
TGCTTATAACTTTGTCTCCTGGTACCAACAACACCCAGGCAAGCCCCA
AACTCATAAATTTATGATGTCAATAAGCGGCCCTCAGGGGTTTCTAATCGC
TTCTCTGGCTCCAAGCTGGCAACACGGCCTCCCTGACCATCTCTGGGCT
CCAGGCCGAGGACGAGCTGATTATTACTGCAGCTCATATACAAGCACCT
TCTCTGTGGTATTTGGCGGAGGACCAAGCTGACCGTCCCTAGGT

FIG. 10(cont.)

166B06

SEQ ID NO:511

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

SEQ ID NO:520

CAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCIC
AGTGAAGGTCTCCTGTAGGCTTCTGGATACACCTTCAGCGATTACTATA
TTCACTGGGTGGACAGGCCCCCTGGACAAGGTTGGAGTGGATGGATGG
GTCAACCTGACACTGGTGGCACAAGATACGCCAGAAGTTTCAGGGCCG
GGTCACAATGACCAGGGACATGTCCATCTCCACAGCCTACATGGAGCTGT
CCAGGCTGAGAAGCGACGACACGGCCGTATATTACTGTGCGAGAGATCTA
ACTGGATTGATCCTTTGATATCTGGGGCCAGGAAACCTGGTCACCGT
CTCCTCAGGAGGGCAGTTCAGGTGGAGGTGGCTCTGGCGGTGGCGGAA
GTGCATCGTCTGTGCTGACTCAGCCACCTCAGTGTCTAGTGGCCCCCAGGA
AAGACGGCCCGCATTAACCTGTGGGGGAAACAACCTTCGAAATAAAGAGT
ACACTGGTATCAGCAGAAGCCAGGCCAGGCCCTGTCTGTGTCATCTATT
ATGATTACAGACGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCCGC
TCTGGGAACACGGCCACCTGACCATCAGCAGGTCGAGGCCGGGATGA
GGCCGACTATTACTGTGAGGTGTGGGATCTCTTCAACGACAACGGCGTGT
TCGGCGGAGGGAACCAAGCTGACCGTCCCTAGGT

FIG. 10(cont.)

166G05

SEQ ID NO:529

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

SEQ ID NO:538

CAGGTCAGCTGGTGAGTCTGGGGCTGAGTGAAGAGCCTGGGGCCTC
AGTGAAGGTCCTGTAAGGCTTCTGGATACACCTTCAGCGATTACTATA
TTCACTGGGTGCGACAGGCCCTGGACAAGGTTGGAGTGGATGGATGG
GTCAACCCGTGACACTGGTGGCACAAGATACGGCAGAGTTTCAGGGCCG
GGTCACAATGACAGGGACATGTCCATCTCCACAGCCTACATCGAGCTGT
CCAGGCTGAGAAAGCGACACAGGCCGTATATTACTGTGCGAGAGATCTA
ACTGGATTGATCCTTTGATATCTGGGGCCAGGGAACCTGGTCACCGT
CTCCTCAGGAGGGCGGTTTCAGGGGAGGTGGCTCTGGCGGTGGCGGAA
GTGCATCGTCTGTGCTGACTCAGCCACCCTCAGTGTGAGTGGCCCCAGGA
AAGACGGCCCGCATTAACCTGTGGGGAAACAACCTTCGAAATAAAGAGT
ACACTGGTATCAGCAGAAGCCAGGCCAGGCCCTGTCTCTGGTCATCTATT
ATGATTCAGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCCGC
TCTGGGAACACGGCCACCCTGACCATCAGAGGTGAGGCCGGGATGA
GGCCGACTATTACTGTGAGGTGTGGGATTTCTCACCAGACTCGGGTCGT
TCGGCGGAGGGACCAAGCTGACCGTCTCTAGGT

FIG. 10(cont.)

354A08

SEQ ID NO:547

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

SEQ ID NO:556

CAGGTGCAGCTGGTGAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGGTCCTGCAAGGCTTCTGGATACACCTTACCGACTACTATA
TGCACTGGGTGGACAGGCCCTGGACAAGGCTTGAGTGGTGGGATGG
ATCAACCCCTTATACTGGTGGCGCATTTCTATGCACAGAAAGTTTCGGGGCAG
GGTCACAAATGACCAGGGACACGTCCATCAGCACAGCCTACATGGAGCTGA
GCAGACTGAGATCTGACGACACGGCCGTGATTATTGTCCGAGAGAACCT
GAAAGATTGGGACTCCACGGGGCAGGTCTGGGGCCGGGGACATTTGGT
CACCGTCTCCTCAGGGGGCGGGTTCAGCGGAGGTGGCTCTGGCGGTA
GCAGAGTGACAGGCTGTGCTGACTCAGCCGCCGTGAGTCTCTGGGGCC
CCAGGCAGAGGTCACCATCTCTGCACTGGGAGCAGCTCCAAACATCGG
GGCAGGTTATGGTGTAAGTGTACCAACAGCTTCCAGGAACAGCCCCCA
AACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGTCCCTGACCGA
TTCTCTGGCTCCAAAGTCTGGCACCTCAGCTCCCTGCCCATCACTGGCT
CCAGGCTGAGGATGAGGCTGATTATTACTGTACCACTGGGACAAGGAGC
AGAGTGGTTATGCTCTCGGAGGTGGGACCCAGCTCACCGTCCCTAGGT

FIG. 10(cont.)

355B06

SEQ ID NO:565

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

SEQ ID NO:574

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGGTCTCCGTCAAGGCTTCTGGATACACCTTCACCGACTACTATA
TGCACTGGGTCCGACAGGCCCCCTGGACAAGGCTTGAGTGGGTGGGATGG
ATCAACCCTTATACCTGGTAGCGCTTCTATGCACAGAAGTTTCGGGGCAG
GGTCACAATGACCAAGGACACGTCCTCATCAGCACAGCCTACATGGAGCTGA
GCAGACTGAGATCTGACGACACGGCCGTGTATTATTGCGGAGAGAACT
GAAATAATTCGGCGAGTCCAGCGGCCAGTTGTGGGCCGGGGACATTGGT
CACCGTCTCTCAGGAGGGCGGTTTCAGCGGAGGTGGCTCTGGCGGTA
GCGGAAGTGACAGGCTGTGTGACTCAGCCCGCTCAGTGTCTGGGGCC
CCAGGGCAGAGGTACCATCTCTGCACTGGGAGCAGCTCCAACATCGG
GGCAGGTTATGGTGTACACTGGTACCACAGCTTCCAGGAACAGCCCGCA
AACTCCTCATCTATGGTGACAGCAATCGGCCCTCAGGGGTCCCTGACCGA
TTCTCTGGCTCCAAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCT
CCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCTATGACAGCGGCC
TGAGTGGTTATGCTCTTCGGAGGTGGGACCCAGCTCACCCGCTCTAGGT

FIG. 10(cont.)

355E04

SEQ ID NO:583

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

SEQ ID NO:592

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCCTGGGGCCTC
AGTGAAGGTCTCTGCAAGGCTTCTGGATACACCTTCACCCACTACTATA
TGCACTGGGTGCGACAGGCCCTGGACAAGGCTTGAGTGGGTGGATGG
ATCAACCCCTTATCTGTTGGCGCATCTATGCACAGAAGTTTCAGGGCAG
GGTCACAAATGACCAGGGACACGTCCATCAGCACAGCCTACATGGAGCTGA
GCAGACTGAGATCTGACGACACGGCCGTGTATTATTGTGCGAGAGAACCT
GAAAATTCGACTCGCCGAACCGCGAGATCTGGGCGGGGACATTGGT
CACCGTCTCCTCAGAAGGGCGGTTCAGGCGAGGTGGCTCTGGCGGTA
GCGGAAGTGCACAGGCTGTGCTGACTCAGCCGCGTCAGTGTCTGGGGCC
CCAGGGCAGAGGTCACCATCTCCTGCACTGGGAGCAGTCCAACATCGG
GGCAGGTATGGTGTACACTGGTACCAACAGCTTCCAGGAACAGCCCCCA
AACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGA
TTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGT
CCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCTATGACAGCAGCC
TGAGTGGTTATGCTCTCGGAGGTGGGACCCAGCTCACCGTCTCTAGGT

FIG. 10(cont.)

356A11

SEQ ID NO:601

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

SEQ ID NO:610

CAGGTGCAGCTGGTGCACTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGTCTCTGCAAGGCTCTGGATACACCTTCACTACTATA
TGCACTGGGTGGACAGGCCCCCTGGACAAGGCTTGAAGTGGGTGGATGG
ATCAACCCCTTACTGGTAGCGCATCTATGCACAGAAGTTTCGGGGCAG
GGTCACAAATGACCAGGGACACGTCCATCAGCACAGCCTACATGGAGCTGA
GCAGACTGAGATCTGACGACACGGCCGTGTTATTGTCGAGAGAACCT
GAAAATTCGACTCCGACGACTCCGACGCTCTGGGGCCCGGGACATTGGT
CACCGTCTCCTCAGGAGCGGGCAGTTCAGGGGAGGTGGCTCTGGCGGTA
GCGGAAGTGCACAGGCTGTGCTGACTCAGCCGCGTCAGTGTCTGGGGCC
CCAGGGCAGAGGTCACCATCTCTGCACTGGGAGCAGTCCCAACATCGG
GGCAGGTTATGGTGTACACTGGTACCAACAGCTTCCAGGAACAGCCCCCA
AACTCCTCATCTATGGTGACAGCAATCGGCCCTCAGGGGTCCCTGACCGA
TTCTCTGGCTCCAAGTCTGGCACCTCAGCCCTCCCTGGCCATCACTGGGT
CCAGGCTGAGGATGAGGCTGATTACTGCCAGTCTATGACACAGCC
TGAGCGGTTATGCTCTTCGGAGGTGGGACCCAGCTCACCGTCCCTAGGT

FIG. 10(cont.)

368D04

SEQ ID NO:619

EVQLVESGGGVVRPGGSLRLSCAASGFTFDDYGMNVVRQAPGKLEWVSGV
NWNGGTRDYAASVKGRFTISRDNKNSLYLQMNSLRAEDTALYHCARGWYS
GAAWNMGYWGRGTLVTVSSGGGGSGGGSGGGSGGGGGGGGSAQA
ALTQPASVSGSPGQSITISCTGASGDVGAYNFVSWYQQHPGKAPKLIIDV
NKRPSGVSNRFGSKSGNTASLTISGLQAEDEADYYCASLVSDFSVVFGGG
TKLTVL

SEQ ID NO:628

GAGGTGCAGCTGGTGGAGAGCGCGGAGGCGTGGTGAGACCAGCGCGCA
GCCTGAGACTGAGCTGCGCCGCCAGCGGCTTACCTTCGACGACTACGG
CATGAAC TGGTGAGCAGGCCCCAGGCAAGGCCCTGGAGTGGGTGCC
GGCGTGAACTGGAAACGGCGGCCACAGAGACTACGCCCTCTGTGAAGG
GCAGATTACCATCAGCCGGGACAACGCCAAGAACAGCCTGTACTTGCA
GATGAACAGCCTGAGAGCCGAGGACACCGCCCTGTACCAC TCGCCAGA
GGCTGGTACAGCGGAGCCGCTGGAACATGGGCTACTGGGGCAGAGGCA
CCCTGGTGACCGTGTCCAGCGGAGGCGCGGTTCAAGCGGAGGTGGCTC
TGGTGGTAGCGGAGGTGGCTCTGGCGGTGGCGGAGGTGGCTCTGGCGGT
GGCGGAAGTGCAAGGCCGCCCTGACCCAGCCGCCAGGGTGTCTGGCA
GCCAGGCCAGAGCATCACCA TCAGCTGCACCGCGGCCAGCGGCGATGT
GGCGCCCTACAAC TCGTGTCTTGGTATCAGCAGCACCCCGCAAGGCC
CCCAAGCTGATCATCTACGACGTGAACAAGAGACCCAGCGGCGGTGCCA
ACAGATTACGGCGCAGCAAGACGGCAACACCGCCAGCCTGACCATCAG
CGGACTGCAGGCCGAGGACGAGGCCGACTACTACTGCGCCAGCCTGGTG
TCCGACTTCAGCGTGGTGTTCGGCGGAGGCCAACCAAGCTGACCGTGCTG

FIG. 10(cont.)