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	(28)(29)(30)(31)(32)(33)(34)(35)(36)(37)(38)(39)(40)(41)(42)(43)(44)(45)
	GTNRSSSKGRSLIGKVDGT
Comparator 1:	28 0.1 186 1.5 44 28 2.5 137 152 126 135
Comparator 3:	109 7 21 79 7 8 95 98 120 128 118
H4H581P:	118 106 5 0.2 0.1 24 56 1 20 121 112
H4H588N:	177 140 85 71 22 0.5 84 0.5 4.5 1 64

Fig. 5

(57) Abstract: The present invention provides antibodies that bind to protease-activated receptor-2 (PAR-2) and methods of using same. According to certain embodiments of the invention, the antibodies are fully human antibodies that bind to human PAR-2. The antibodies of the invention are useful, *inter alia*, for the treatment of diseases and disorders associated with one or more PAR-2 biological activities, including the treatment of pain conditions, inflammatory conditions and gastrointestinal conditions.

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HIGH AFFINITY HUMAN ANTIBODIES TO HUMAN PROTEASE-ACTIVATED RECEPTOR-2

FIELD OF THE INVENTION

[0001] The present invention relates to antibodies, and antigen-binding fragments thereof, which are specific for protease-activated receptor-2 (PAR-2).

BACKGROUND

[0002] Protease-activated receptors ("PARs") are a family of seven-transmembrane G-protein-coupled receptors. Among seven-transmembrane G-protein-coupled receptors PARs have a unique mode of activation; that is, PARs are activated by proteolytic cleavage at the amino terminus to generate a new N-terminal domain which serves as a "tethered ligand." The tethered ligand interacts with the extracellular loop-2 of the receptor thereby resulting in receptor activation. Currently, there are four known members of the PAR family, designated PAR-1, PAR-2, PAR-3 and PAR-4.

[0003] PAR-2 has also been referred to as "C140." (US 5,874,400). Both human and murine PAR-2 share the protease cleavage domain SKGRSLIG (residues 6-13 of SEQ ID NO:852, and residues 8-15 of SEQ ID NO:856). This sequence is cleaved between the R and S residues by a variety of proteases such as trypsin, as well as by mast cell tryptase, tissue factor/factor VIIa complex and factor Xa, neutrophil proteinase 3 (PR-3), human leukocyte elastase, and proteases originating from pathogenic organisms.

[0004] PAR-2 activity has been implicated in or associated with several diseases and conditions including inflammatory diseases, pain, gastrointestinal conditions, neurological diseases, and cardiovascular disorders (see, e.g., Linder et al., 2000, J. Immunol. 165:6504-6510; Vergnolle et al., 2001, Nature Medicine 7:821-826; Cenac et al., 2007, J. Clin. Investigation 117:636-647; Vergnolle, 2004, British J. Pharmacol. 141:1264-1274; Knight et al., 2001, J. Allergy Clin. Immunol. 108:797-803; Schmidlin et al., 2002, J. Immunol. 169:5315-5321). Antibodies that bind to PAR-2 have the potential to antagonize the activity of PAR-2 *in vivo*. Anti-PAR-2 antibodies are therefore potentially useful for treating and/or ameliorating a variety of disease conditions.

[0005] Antibodies that bind to PAR-2, and certain therapeutic uses thereof, are mentioned in US 5,874,400, US 2007/0237759, WO 2009/005726, and US 2010/0119506. Nonetheless, there remains a need in the art for novel PAR-2 modulating agents, including anti-PAR-2 antibodies, that can be used to treat PAR-2-mediated diseases and conditions.

BRIEF SUMMARY OF THE INVENTION

[0005a] According to a first aspect, the present invention provides an isolated human antibody or antigen-binding fragment thereof that specifically binds to human PAR-2 (SEQ ID NO:851), wherein the antibody or antigen-binding fragment thereof:

- (a) interacts with Ser-37, Leu-38, Ile-39, Gly-40, Val-42 and Asp-43 of human PAR-2;
- (b) does not interact with Lys-41 of human PAR-2;
- (c) blocks trypsin cleavage of human PAR-2 at the activating cleavage site located at the junction of residues Arg-36 and Ser-37 of human PAR-2;
- (d) does not block trypsin cleavage of human PAR-2 at the non-activating cleavage site located at the junction of residues Arg-31 and Ser-32; and
- (e) competes for binding to human PAR-2 with a reference antibody comprising heavy chain complementary determining regions (HCDR1-HCDR2-HCDR3) having the amino acid sequences of SEQ ID NOs:700-702-704; and the light chain CDRs (LCDR1-LCDR2-LCDR3) having the amino acid sequences of SEQ ID NOs:708-710-712.

[0005b] In a further aspect, the present invention provides a formulation, comprising:
a pharmaceutically acceptable carrier; and

an effective amount of an antibody or antigen-binding fragment thereof that specifically binds human protease-activated receptor 2 (PAR2) (SEQ ID NO:851), wherein the antibody or antigen-binding fragment thereof:

- (a) interacts with Ser-37, Leu-38, Ile-39, Gly-40, Val-42 and Asp-43 of human PAR2;
- (b) does not interact with Lys-41 of human PAR2;
- (c) blocks trypsin cleavage of human PAR2 at the activating cleavage site located at the junction of residues Arg-36 and Ser-37 of human PAR2;
- (d) does not block trypsin cleavage of human PAR2 at the non-activating cleavage site located at the junction of residues Arg-31 and Ser-32; and
- (e) competes for binding to human PAR2 with a reference antibody comprising heavy chain CDRs (HCDR1-HCDR2-HCDR3) having the amino acid sequences of SEQ ID NOs:700-702-704; and the light chain CDRs (LCDR1-LCDR2-LCDR3) having the amino acid sequences of SEQ ID NOs:708-710-712.

[0005c] In a further aspect, the present invention provides a method for treating pruritus, the method comprising administering to a patient in need thereof an effective amount of an antibody or antigen-binding fragment thereof that specifically binds human protease-activated receptor 2 (PAR2) (SEQ ID NO:851), wherein the antibody or antigen-binding fragment thereof:

- (a) interacts with Ser-37, Leu-38, Ile-39, Gly-40, Val-42 and Asp-43 of human PAR2; (b) does not interact with Lys-41 of human PAR2; (c) blocks trypsin cleavage of human PAR2 at the activating cleavage site located at the junction of residues Arg-36 and Ser-37 of human PAR2; (d) does not block trypsin cleavage of human PAR2 at the non-activating cleavage site located at the junction of residues Arg-31 and Ser-32; and (e) competes for binding to human PAR2 with a reference antibody comprising heavy chain CDRs (HCDR1-HCDR2-HCDR3) having the amino acid sequences of SEQ ID NOs:700-702-704; and the light chain CDRs (LCDR1-LCDR2-LCDR3) having the amino acid sequences of SEQ ID NOs:708-710-712

[0006] The present invention provides human antibodies that bind to human PAR-2. The

antibodies of the invention are useful, *inter alia*, for inhibiting PAR-2-mediated signaling and for treating diseases and disorders caused by or related to PAR-2 activation.

[0007] The present invention includes antibodies which interact with the N-terminal region of PAR-2 and block proteolytic cleavage at the activating PAR-2 protease cleavage site (as defined herein) but do not block proteolytic cleavage at one or more non-activating protease cleavage sites. According to certain embodiments, anti-PAR-2 antibodies which exhibit such proteolytic cleavage blocking properties interact with specific amino acids in the vicinity of the activating PAR-2 protease cleavage site. For example, the present invention provides anti-PAR-2 antibodies with protease cleavage blocking activity and which interact with Val-42 and Asp-43 of human PAR-2 (SEQ ID NO:851), and may further interact with one or more human PAR-2 residues selected from the group consisting of Ser-37, Leu-38, Ile-39, Gly-40, and Gly-44.

[0008] According to other embodiments, the anti-PAR-2 antibodies of the present invention specifically bind to human PAR-2 and monkey PAR-2 but do not bind to at least one member selected from the group consisting of mouse, rat, rabbit, dog and pig PAR-2. The present invention also includes antibodies that are capable of inhibiting or attenuating proteolytic activation of PAR-2 but do not block proteolytic cleavage of PAR-2. Exemplary methods for measuring/assessing an antibody's ability to block PAR-2 cleavage or proteolytic activation are described herein.

[0009] The antibodies of the invention can be full-length (for example, an IgG1 or IgG4 antibody) or may comprise only an antigen-binding portion (for example, a Fab, F(ab')₂ or scFv fragment), and may be modified to affect functionality, e.g., to eliminate residual effector functions (Reddy et al., 2000, J. Immunol. 164:1925-1933).

[0010] The present invention provides an antibody or antigen-binding fragment of an antibody comprising a heavy chain variable region (HCVR) having an amino acid sequence selected from the group consisting of SEQ ID NO: 2, 18, 22, 26, 42, 46, 50, 66, 70, 74, 90, 94, 98, 114, 118, 122, 138, 142, 146, 162, 166, 170, 186, 190, 194, 210, 214, 218, 234, 238, 242, 258, 262, 266, 282, 286, 290, 306, 310, 314, 330, 334, 338, 354, 358, 362, 378, 382, 386, 402, 406, 410, 426, 430, 434, 450, 454, 458, 474, 478, 482, 498, 502, 506, 522, 526, 530, 546, 550, 554, 570, 574, 578, 594, 598, 602, 618, 622, 626, 642, 646, 650, 666, 670, 674, 690, 694, 698, 714, 718, 722, 738, 742, 746, 762, 766, 770, 786, 790, 794, 810, 814, 818, 834, and 838, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity. According to certain embodiments, the antibody or antigen-binding portion of an antibody comprises a HCVR having an amino acid sequence selected from the group consisting of SEQ ID NO: 98, 146, 338, and 714.

[0011] The present invention also provides an antibody or antigen-binding fragment of an antibody comprising a light chain variable region (LCVR) having an amino acid sequence selected from the group consisting of SEQ ID NO: 10, 20, 24, 34, 44, 48, 58, 68, 72, 82, 92, 96, 106, 116, 120, 130, 140, 144, 154, 164, 168, 178, 188, 192, 202, 212, 216, 226, 236, 240, 250, 260, 264, 274, 284, 288, 298, 308, 312, 322, 332, 336, 346, 356, 360, 370, 380, 384, 394, 404,

408, 418, 428, 432, 442, 452, 456, 466, 476, 480, 490, 500, 504, 514, 524, 528, 538, 548, 552, 562, 572, 576, 586, 596, 600, 610, 620, 624, 634, 644, 648, 658, 668, 672, 682, 692, 696, 706, 716, 720, 730, 740, 744, 754, 764, 768, 778, 788, 792, 802, 812, 816, 826, 836, and 840, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity. According to certain embodiments, the antibody or antigen-binding portion of an antibody comprises a LCVR having an amino acid sequence selected from the group consisting of SEQ ID NO: 106, 154, 346, and 692.

[0012] The present invention also provides an antibody or antigen-binding fragment thereof comprising a HCVR and LCVR (HCVR/LCVR) sequence pair selected from the group consisting of SEQ ID NO: 2/10, 18/20, 22/24, 26/34, 42/44, 46/48, 50/58, 66/68, 70/72, 74/82, 90/92, 94/96, 98/106, 114/116, 118/120, 122/130, 138/140, 142/144, 146/154, 162/164, 166/168, 170/178, 186/188, 190/192, 194/202, 210/212, 214/216, 218/226, 234/236, 238/240, 242/250, 258/260, 262/264, 266/274, 282/284, 286/288, 290/298, 306/308, 310/312, 314/322, 330/332, 334/336, 338/346, 354/356, 358/360, 362/370, 378/380, 382/384, 386/394, 402/404, 406/408, 410/418, 426/428, 430/432, 434/442, 450/452, 454/456, 458/466, 474/476, 478/480, 482/490, 498/500, 502/504, 506/514, 522/524, 526/528, 530/538, 546/548, 550/552, 554/562, 570/572, 574/576, 578/586, 594/596, 598/600, 602/610, 618/620, 622/624, 626/634, 642/644, 646/648, 650/658, 666/668, 670/672, 674/682, 690/692, 694/696, 698/706, 714/716, 714/692, 718/720, 722/730, 738/740, 742/744, 746/754, 762/764, 766/768, 770/778, 786/788, 790/792, 794/802, 810/812, 814/816, 818/826, 834/836, and 838/840. According to certain embodiments, the antibody or fragment thereof comprises a HCVR and LCVR selected from the amino acid sequence pairs of SEQ ID NO: 98/106, 146/154, 338/346, and 714/692.

[0013] The present invention also provides an antibody or antigen-binding fragment of an antibody comprising a heavy chain CDR3 (HCDR3) domain having an amino acid sequence selected from the group consisting of SEQ ID NO: 8, 32, 56, 80, 104, 128, 152, 176, 200, 224, 248, 272, 296, 320, 344, 368, 392, 416, 440, 464, 488, 512, 536, 560, 584, 608, 632, 656, 680, 704, 728, 752, 776, 800, and 824, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity; and a light chain CDR3 (LCDR3) domain having an amino acid sequence selected from the group consisting of SEQ ID NO: 16, 40, 64, 88, 112, 136, 160, 184, 208, 232, 256, 280, 304, 328, 352, 376, 400, 424, 448, 472, 496, 520, 544, 568, 592, 616, 640, 664, 688, 712, 736, 760, 784, 808, and 832, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

[0014] In certain embodiments, the antibody or antigen-binding portion of an antibody comprises a HCDR3/LCDR3 amino acid sequence pair selected from the group consisting of SEQ ID NO: 8/16, 32/40, 56/64, 80/88, 104/112, 128/136, 152/160, 176/184, 200/208, 224/232, 248/256, 272/280, 296/304, 320/328, 344/352, 368/376, 392/400, 416/424, 440/448, 464/472, 488/496, 512/520, 536/544, 560/568, 584/592, 608/616, 632/640, 656/664, 680/688, 704/712,

728/736, 752/760, 776/784, 800/808, and 824/832. According to certain embodiments, the antibody or antigen-binding portion of an antibody comprises a HCDR3/LCDR3 amino acid sequence pair selected from the group consisting of SEQ ID NO: 104/112, 152/160, 344/352 and 704/712. Non-limiting examples of anti-PAR-2 antibodies having these HCDR3/LCDR3 pairs are the antibodies designated H4H588N, H4H591N, H4H618N, and H4H581P, respectively.

[0015] The present invention also provides an antibody or fragment thereof further comprising a heavy chain CDR1 (HCDR1) domain having an amino acid sequence selected from the group consisting of SEQ ID NO: 4, 28, 52, 76, 100, 124, 148, 172, 196, 220, 244, 268, 292, 316, 340, 364, 388, 412, 436, 460, 484, 508, 532, 556, 580, 604, 628, 652, 676, 700, 724, 748, 772, 796, and 820, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity; a heavy chain CDR2 (HCDR2) domain having an amino acid sequence selected from the group consisting of SEQ ID NO: 6, 30, 54, 78, 102, 126, 150, 174, 198, 222, 246, 270, 294, 318, 342, 366, 390, 414, 438, 462, 486, 510, 534, 558, 582, 606, 630, 654, 678, 702, 726, 750, 774, 798, and 822, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity; a light chain CDR1 (LCDR1) domain having an amino acid sequence selected from the group consisting of SEQ ID NO: 12, 36, 60, 84, 108, 132, 156, 180, 204, 228, 252, 276, 300, 324, 348, 372, 396, 420, 444, 468, 492, 516, 540, 564, 588, 612, 636, 660, 684, 708, 732, 756, 780, 804, and 828, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity; and a light chain CDR2 (LCDR2) domain having an amino acid sequence selected from the group consisting of SEQ ID NO: 14, 38, 62, 86, 110, 134, 158, 182, 206, 230, 254, 278, 302, 326, 350, 374, 398, 422, 446, 470, 494, 518, 542, 566, 590, 614, 638, 662, 686, 710, 734, 758, 782, 806, and 830, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

[0016] Certain non-limiting, exemplary antibodies and antigen-binding fragments of the invention comprise HCDR1, HCDR2, HCDR3, LCDR1, LCDR2 and LCDR3 domains, respectively, selected from the group consisting of: (i) SEQ ID NO: 100, 102, 104, 108, 110 and 112 (e.g., H4H588N); (ii) SEQ ID NO: 148, 150, 152, 156, 158 and 160 (e.g., H4H591N); (iii) SEQ ID NO: 340, 342, 344, 348, 350 and 352 (e.g., H4H618N); and (iv) SEQ ID NO: 700, 702, 704, 708, 710 and 712 (e.g., H4H581P). The amino acid sequences of these exemplary CDRs are depicted in Figs. 2 and 3.

[0017] In a related embodiment, the invention comprises an antibody or antigen-binding fragment of an antibody which specifically binds PAR-2, wherein the antibody or fragment comprises the heavy and light chain CDR domains contained within heavy and light chain sequences selected from the group consisting of SEQ ID NO: 2/10, 18/20, 22/24, 26/34, 42/44, 46/48, 50/58, 66/68, 70/72, 74/82, 90/92, 94/96, 98/106, 114/116, 118/120, 122/130, 138/140, 142/144, 146/154, 162/164, 166/168, 170/178, 186/188, 190/192, 194/202, 210/212, 214/216,

218/226, 234/236, 238/240, 242/250, 258/260, 262/264, 266/274, 282/284, 286/288, 290/298, 306/308, 310/312, 314/322, 330/332, 334/336, 338/346, 354/356, 358/360, 362/370, 378/380, 382/384, 386/394, 402/404, 406/408, 410/418, 426/428, 430/432, 434/442, 450/452, 454/456, 458/466, 474/476, 478/480, 482/490, 498/500, 502/504, 506/514, 522/524, 526/528, 530/538, 546/548, 550/552, 554/562, 570/572, 574/576, 578/586, 594/596, 598/600, 602/610, 618/620, 622/624, 626/634, 642/644, 646/648, 650/658, 666/668, 670/672, 674/682, 690/692, 694/696, 698/706, 714/716, 714/692, 718/720, 722/730, 738/740, 742/744, 746/754, 762/764, 766/768, 770/778, 786/788, 790/792, 794/802, 810/812, 814/816, 818/826, 834/836, and 838/840.

According to certain embodiments, the antibody or fragment thereof comprises the CDR sequences contained within HCVRs and LCVRs selected from the amino acid sequence pairs of SEQ ID NO: 98/106, 146/154, 338/346, and 714/692. Methods and techniques for identifying CDRs within HCVR and LCVR amino acid sequences are well known in the art and can be used to identify CDRs within the specified HCVR and/or LCVR amino acid sequences disclosed herein. Exemplary conventions that can be used to identify the boundaries of CDRs include, e.g., the Kabat definition, the Chothia definition, and the AbM definition. In general terms, the Kabat definition is based on sequence variability, the Chothia definition is based on the location of the structural loop regions, and the AbM definition is a compromise between the Kabat and Chothia approaches. See, e.g., Kabat, "Sequences of Proteins of Immunological Interest," National Institutes of Health, Bethesda, Md. (1991); Al-Lazikani *et al.*, *J. Mol. Biol.* 273:927-948 (1997); and Martin *et al.*, *Proc. Natl. Acad. Sci. USA* 86:9268-9272 (1989). Public databases are also available for identifying CDR sequences within an antibody.

[0018] In another aspect, the invention provides nucleic acid molecules encoding anti-PAR-2 antibodies or fragments thereof. Recombinant expression vectors carrying the nucleic acids of the invention, and host cells into which such vectors have been introduced, are also encompassed by the invention, as are methods of producing the antibodies by culturing the host cells under conditions permitting production of the antibodies, and recovering the antibodies produced.

[0019] In one embodiment, the invention provides an antibody or fragment thereof comprising a HCVR encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1, 17, 21, 25, 41, 45, 49, 65, 69, 73, 89, 93, 97, 113, 117, 121, 137, 141, 145, 161, 165, 169, 185, 189, 193, 209, 213, 217, 233, 237, 241, 257, 261, 265, 281, 285, 289, 305, 309, 313, 329, 333, 337, 353, 357, 361, 377, 381, 385, 401, 405, 409, 425, 429, 433, 449, 453, 457, 473, 477, 481, 497, 501, 505, 521, 525, 529, 545, 549, 553, 569, 573, 577, 593, 597, 601, 617, 621, 625, 641, 645, 649, 665, 669, 673, 689, 693, 697, 713, 717, 721, 737, 741, 745, 761, 765, 769, 785, 789, 793, 809, 813, 817, 833, and 837, or a substantially identical sequence having at least 90%, at least 95%, at least 98%, or at least 99% homology thereof. According to certain embodiments, the antibody or fragment thereof comprises a HCVR encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO: 97, 145, 337, and 713.

[0020] The present invention also provides an antibody or fragment thereof comprising a LCVR encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO: 9, 19, 23, 33, 43, 47, 57, 67, 71, 81, 91, 95, 105, 115, 119, 129, 139, 143, 153, 163, 167, 177, 187, 191, 201, 211, 215, 225, 235, 239, 249, 259, 263, 273, 283, 287, 297, 307, 311, 321, 331, 335, 345, 355, 359, 369, 379, 383, 393, 403, 407, 417, 427, 431, 441, 451, 455, 465, 475, 479, 489, 499, 503, 513, 523, 527, 537, 547, 551, 561, 571, 575, 585, 595, 599, 609, 619, 623, 633, 643, 647, 657, 667, 671, 681, 691, 695, 705, 715, 719, 729, 739, 743, 753, 763, 767, 777, 787, 791, 801, 811, 815, 825, 835, and 839, or a substantially identical sequence having at least 90%, at least 95%, at least 98%, or at least 99% homology thereof. According to certain embodiments, the antibody or fragment thereof comprises a LCVR encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO: 105, 153, 345, and 715.

[0021] The present invention also provides an antibody or antigen-binding fragment of an antibody comprising a HCDR3 domain encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 7, 31, 55, 79, 103, 127, 151, 175, 199, 223, 247, 271, 295, 319, 343, 367, 391, 415, 439, 463, 487, 511, 535, 559, 583, 607, 631, 655, 679, 703, 727, 751, 775, 799, and 823, or a substantially identical sequence having at least 90%, at least 95%, at least 98%, or at least 99% homology thereof; and a LCDR3 domain encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 15, 39, 63, 87, 111, 135, 159, 183, 207, 231, 255, 279, 303, 327, 351, 375, 399, 423, 447, 471, 495, 519, 543, 567, 591, 615, 639, 663, 687, 711, 735, 759, 783, 807, and 831, or a substantially identical sequence having at least 90%, at least 95%, at least 98%, or at least 99% homology thereof. According to certain embodiments, the antibody or fragment thereof comprises HCDR3 and LCDR3 sequences encoded by the nucleic acid sequence pairs selected from the group consisting of SEQ ID NO: 103/111, 151/159, 343/351, and 703/711.

[0022] The present invention also provides an antibody or fragment thereof which further comprises a HCDR1 domain encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 3, 27, 51, 75, 99, 123, 147, 171, 195, 219, 243, 267, 291, 315, 339, 363, 387, 411, 435, 459, 483, 507, 531, 555, 579, 603, 627, 651, 675, 699, 723, 747, 771, 795, and 819, or a substantially identical sequence having at least 90%, at least 95%, at least 98%, or at least 99% homology thereof; a HCDR2 domain encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 5, 29, 53, 77, 101, 125, 149, 173, 197, 221, 245, 269, 293, 317, 341, 365, 389, 413, 437, 461, 485, 509, 533, 557, 581, 605, 629, 653, 677, 701, 725, 749, 773, 797, and 821, or a substantially identical sequence having at least 90%, at least 95%, at least 98%, or at least 99% homology thereof; a LCDR1 domain encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 11, 35, 59, 83, 107, 131, 155, 179, 203, 227, 251, 275, 299, 323, 347, 371, 395, 419, 443, 467, 491, 515, 539, 563, 587, 611, 635, 659, 683, 707, 731, 755, 779, 803, and 827, or a substantially identical sequence having at least 90%, at least 95%, at least 98%, or at least 99% homology thereof; and a

LCDR2 domain encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 13, 37, 61, 85, 109, 133, 157, 181, 205, 229, 253, 277, 301, 325, 349, 373, 397, 421, 445, 469, 493, 517, 541, 565, 589, 613, 637, 661, 685, 709, 733, 757, 781, 805, 829, or a substantially identical sequence having at least 90%, at least 95%, at least 98%, or at least 99% homology thereof.

[0023] According to certain embodiments, the antibody or fragment thereof comprises the heavy and light chain CDR sequences encoded by the nucleic acid sequences of SEQ ID NO: 97 and 105; SEQ ID NO: 145 and 153; SEQ ID NO: 337 and 345; or SEQ ID NO: 713 and 715.

[0024] The present invention also provides an isolated antibody or antigen-binding fragment of an antibody that specifically binds PAR-2, comprising a HCDR3 and a LCDR3, wherein the HCDR3 comprises an amino acid sequence of the formula $X^1 - X^2 - X^3 - X^4 - X^5 - X^6 - X^7 - X^8 - X^9 - X^{10} - X^{11} - X^{12}$ (SEQ ID NO:843) wherein X^1 is Ala or Val, X^2 is Lys, X^3 is Gly or Glu, X^4 is Asp or Gly, X^5 is Phe or Asp, X^6 is Trp or Ser, X^7 is Ser or Gly, X^8 is Gly or Tyr, X^9 is Tyr or Asp, X^{10} is Phe or Leu, X^{11} is Asp or Ala, and X^{12} is Tyr; and the LCDR3 comprises an amino acid sequence of the formula $X^1 - X^2 - X^3 - X^4 - X^5 - X^6 - X^7 - X^8 - X^9$ (SEQ ID NO:846) wherein X^1 is Met or Gln, X^2 is Gln, X^3 is Ala or Tyr, X^4 is Thr or Lys, X^5 is Gln, Ser or Ile, X^6 is Phe or Ser, X^7 is Pro, X^8 is Thr or Leu, and X^9 is Thr or absent.

[0025] In a more specific embodiment, the invention features an isolated antibody or fragment thereof that specifically binds PAR-2, comprising a HCDR1 sequence of the formula $X^1 - X^2 - X^3 - X^4 - X^5 - X^6 - X^7 - X^8$ (SEQ ID NO:841), wherein X^1 is Gly, X^2 is Phe, X^3 is Thr, X^4 is Phe, X^5 is Ser or Arg, X^6 is Ser or Arg, X^7 is Tyr, and X^8 is Gly, Ala or Thr; a HCDR2 sequence of the formula $X^1 - X^2 - X^3 - X^4 - X^5 - X^6 - X^7 - X^8$ (SEQ ID NO:842), wherein X^1 is Ile, X^2 is Ser, Gly or Thr, X^3 is Tyr, Gly or Asp, X^4 is Asp, Gly or Ser, X^5 is Gly or Arg, X^6 is Ile, Gly or Ala, X^7 is Asn, Ser, Arg or Gly, and X^8 is Lys, Ala or Thr; a HCDR3 sequence of the formula $X^1 - X^2 - X^3 - X^4 - X^5 - X^6 - X^7 - X^8 - X^9 - X^{10} - X^{11} - X^{12}$ (SEQ ID NO:843) wherein X^1 is Ala or Val, X^2 is Lys, X^3 is Gly or Glu, X^4 is Asp or Gly, X^5 is Phe or Asp, X^6 is Trp or Ser, X^7 is Ser or Gly, X^8 is Gly or Tyr, X^9 is Tyr or Asp, X^{10} is Phe or Leu, X^{11} is Asp or Ala, and X^{12} is Tyr; a LCDR1 sequence of the formula $X^1 - X^2 - X^3 - X^4 - X^5 - X^6 - X^7 - X^8 - X^9 - X^{10} - X^{11}$ (SEQ ID NO:844) wherein X^1 is Gln, X^2 is Ser or Gly, X^3 is Leu or Ile, X^4 is Val or Ser, X^5 is His, Asn or Thr, X^6 is Ser, Asn or Tyr, X^7 is Asp or absent; X^8 is Gly or absent, X^9 is Asn or absent, X^{10} is Thr or absent, and X^{11} is Tyr or absent; a LCDR2 sequence of the formula $X^1 - X^2 - X^3$ (SEQ ID NO:845) wherein X^1 is Lys or Ala, X^2 is Ile, Ala or Thr, and X^3 is Ser; and a LCDR3 comprises an amino acid sequence of the formula $X^1 - X^2 - X^3 - X^4 - X^5 - X^6 - X^7 - X^8 - X^9$ (SEQ ID NO:846) wherein X^1 is Met or Gln, X^2 is Gln, X^3 is Ala or Tyr, X^4 is Thr or Lys, X^5 is Gln, Ser or Ile, X^6 is Phe or Ser, X^7 is Pro, X^8 is Thr or Leu, and X^9 is Thr or absent.

[0026] The invention encompasses anti-PAR-2 antibodies having a modified glycosylation pattern. In some applications, modification to remove undesirable glycosylation sites may be useful, or an antibody lacking a fucose moiety present on the oligosaccharide chain, for

example, to increase antibody dependent cellular cytotoxicity (ADCC) function (see Shield et al. (2002) JBC 277:26733). In other applications, modification of galactosylation can be made in order to modify complement dependent cytotoxicity (CDC).

[0027] In another aspect, the invention provides a pharmaceutical composition comprising a recombinant human antibody or fragment thereof which specifically binds PAR-2 and a pharmaceutically acceptable carrier. In a related aspect, the invention features a composition which is a combination of a PAR-2 inhibitor and a second therapeutic agent. In one embodiment, the PAR-2 inhibitor is an antibody or fragment thereof. In one embodiment, the second therapeutic agent is any agent that is advantageously combined with a PAR-2 inhibitor. Exemplary agents that may be advantageously combined with a PAR-2 inhibitor include, without limitation, other agents that inhibit PAR-2 activity (including other antibodies or antigen-binding fragments thereof, peptide inhibitors, small molecule antagonists, etc) and/or agents which interfere with PAR-2 upstream or downstream signaling.

[0028] In yet another aspect, the invention provides methods for inhibiting PAR-2 activity using the anti-PAR-2 antibody or antigen-binding portion of an antibody of the invention, wherein the therapeutic methods comprise administering a therapeutically effective amount of a pharmaceutical composition comprising an antibody or antigen-binding fragment of an antibody of the invention. The disorder treated is any disease or condition which is improved, ameliorated, inhibited or prevented by removal, inhibition or reduction of PAR-2 activity. The anti-PAR-2 antibody or antibody fragment of the invention may function to block the interaction between PAR-2 and a protease (e.g., trypsin or trypsin-like serine proteases) or otherwise inhibit protease-mediated activation of PAR-2. Alternatively, or additionally, the anti-PAR-2 antibodies of the invention may interfere with the interaction between the PAR-2 tethered ligand and one or more of the PAR-2 extracellular loops (see, e.g., MacFarlane et al., 2001, Pharmacological Reviews 53:245-282 for a general discussion of PAR-2 proteolytic cleavage and activation). The antibody or antibody fragment may be used alone or in combination with one or more additional therapeutic agents.

[0029] The present invention also includes the use of an anti-PAR-2 antibody or antigen binding portion of an antibody of the invention in the manufacture of a medicament for the treatment of a disease or disorder related to or caused by PAR-2 activity in a patient.

[0030] Other embodiments will become apparent from a review of the ensuing detailed description.

BRIEF DESCRIPTION OF THE FIGURES

[0031] **Fig. 1.** Sequence comparison table of heavy chain variable regions and CDRs of antibodies H4H581P, H4H588N, H4H591N and H4H618N.

[0032] **Fig. 2.** Sequence comparison table of light chain variable regions and CDRs of antibodies H4H581P, H4H588N, H4H591N and H4H618N.

[0033] Fig. 3. The top panel (A) shows C- and N-terminal biotin labeled peptides corresponding to the sequence surrounding the activating PAR-2 protease cleavage site (GTNRSSKGRSLIGKVDGT; SEQ ID NO:852). The protease cleavage sites are designated by number 1 (an upstream, non-activating protease cleavage site) and number 2 (the activating PAR-2 protease cleavage site). The expected sizes of the uncleaved and cleaved fragments are indicated in the top table. The bottom panel (B) shows the fragment sizes that were observed following 0, 5, and 15 minutes of trypsin treatment in the presence of anti-PAR-2 antibodies or negative control.

[0034] Fig. 4. The top panel (A) shows the mouse, rat and human peptides corresponding to the sequence surrounding the activating PAR-2 protease cleavage sites (SEQ ID NOs:883, 858 and 852, respectively). The protease cleavage sites are designated by numbers 1 and 2 (upstream, non-activating protease cleavage sites) and number 3 (the activating PAR-2 protease cleavage site). The expected sizes of the uncleaved and cleaved fragments are indicated in the top table. The bottom panel (B) shows the fragment sizes that were observed following 0 and 5 minutes of trypsin treatment in the presence of anti-PAR-2 antibodies or negative control.

[0035] Fig. 5. Depiction of alanine scanning epitope mapping results for antibody binding to the sequence surrounding the PAR-2 activating protease cleavage site (SEQ ID NO:852). Open triangles represent protease cleavage sites located upstream from the activating PAR-2 protease cleavage site. The activating PAR-2 protease cleavage site is designated by a closed triangle. The numbers in parentheses indicate the amino acid numbering in the full-length human PAR-2 sequence (SEQ ID NO:851). Numbers in circles under the amino acid residues indicate the percent of T_{1/2} of antibody binding to alanine-scan mutant peptide relative to the T_{1/2} of antibody binding to wild-type peptide, as shown in Tables 24-26 and 28. If duplicate experiments were conducted, the average T_{1/2} percentage is shown in the circle. Black circles with white numbers indicate amino acids that, when changed to alanine, reduce the T_{1/2} of antibody binding to 30% or less of the T_{1/2} of antibody binding to wild-type peptide. Such amino acids are defined herein as residues with which the antibody interacts.

DETAILED DESCRIPTION

[0036] Before the present invention is described, it is to be understood that this invention is not limited to particular methods and experimental conditions described, as such methods and conditions may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting, since the scope of the present invention will be limited only by the appended claims.

[0037] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. As used herein, the term "about," when used in reference to a particular recited

numerical value, means that the value may vary from the recited value by no more than 1%. For example, as used herein, the expression "about 100" includes 99 and 101 and all values in between (e.g., 99.1, 99.2, 99.3, 99.4, etc.).

[0038] Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, the preferred methods and materials are now described.

Definitions

[0039] As used herein, the terms "proteinase-activated receptor-2," "protease-activated receptor-2," and "PAR-2", refer to full-length PAR-2 protein. Human PAR-2 is encoded by the nucleic acid sequence shown in SEQ ID NO:850 and has the amino acid sequence of SEQ ID NO:851. Amino acid sequences of PAR-2 molecules from non-human species (e.g., mouse, monkey, rabbit, dog, pig, etc.) are available from public sources.

[0040] The term "PAR-2 fragment," as used herein, means a peptide or polypeptide comprising 4, 5, 6, 7, 8, 9, 10 or more contiguous amino acids located upstream from (*i.e.*, N-terminal to) the activating PAR-2 protease cleavage site (as defined herein below) and/or 4, 5, 6, 7, 8, 9, 10 or more contiguous amino acids located downstream from (*i.e.*, C-terminal to) the activating PAR-2 protease cleavage site. Exemplary PAR-2 fragments are illustrated in Example 2, Table 2 (designated Peptides "A" through "J"; *i.e.*, SEQ ID NOs:852 through 861, respectively).

[0041] The expressions "PAR-2" and "PAR-2 fragment," as used herein refer to the human PAR-2 protein or fragment unless specified as being from a non-human species (e.g., "mouse PAR-2," "mouse PAR-2 fragment," "monkey PAR-2," "monkey PAR-2 fragment," etc.).

[0042] As used in the context of the present disclosure, the expression "activating PAR-2 protease cleavage site" means the junction of residues Arg-36 and Ser-37 of human PAR-2 (SEQ ID NO:851). The activating PAR-2 protease cleavage site is the site which, when cleaved, results in the formation of the PAR-2 tethered ligand in the naturally occurring protein.

[0043] The term "PAR-2 protease," as used herein, means an enzyme which is capable of cleaving a PAR-2 or PAR-2 fragment at the activating PAR-2 protease cleavage site. Exemplary PAR-2 proteases include trypsin, cathepsin G, acrosin, tissue factor VIIa, tissue factor Xa, human airway trypsin-like protease, tryptase, membrane-type serine protease-1 (MT-SP1), TMPRSS2, protease-3, elastase, kallikrein-5, kallikrein-6, kallikrein-14, activated protein C, duodenase, gingipains-R, Der p1, Der p3, Der p9, thermolysin, serralysin, and *T. denticla* protease.

[0044] The term "antibody", as used herein, is intended to refer to immunoglobulin molecules comprising four polypeptide chains, two heavy (H) chains and two light (L) chains interconnected by disulfide bonds, as well as multimers thereof (e.g., IgM). Each heavy chain comprises a heavy chain variable region (abbreviated herein as HCVR or V_H) and a heavy chain constant region. The heavy chain constant region comprises three domains, C_H1, C_H2 and C_H3.

Each light chain comprises a light chain variable region (abbreviated herein as LCVR or V_L) and a light chain constant region. The light chain constant region comprises one domain (C_L1). The V_H and V_L regions can be further subdivided into regions of hypervariability, termed complementarity determining regions (CDRs), interspersed with regions that are more conserved, termed framework regions (FR). Each V_H and V_L is composed of three CDRs and four FRs, arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4. In different embodiments of the invention, the FRs of the anti-Ang-2 antibody (or antigen-binding portion thereof) may be identical to the human germline sequences, or may be naturally or artificially modified. An amino acid consensus sequence may be defined based on a side-by-side analysis of two or more CDRs.

[0045] The term "antibody," as used herein, also includes antigen-binding fragments of full antibody molecules. The terms "antigen-binding portion" of an antibody, "antigen-binding fragment" of an antibody, and the like, as used herein, include any naturally occurring, enzymatically obtainable, synthetic, or genetically engineered polypeptide or glycoprotein that specifically binds an antigen to form a complex. Antigen-binding fragments of an antibody may be derived, e.g., from full antibody molecules using any suitable standard techniques such as proteolytic digestion or recombinant genetic engineering techniques involving the manipulation and expression of DNA encoding antibody variable and optionally constant domains. Such DNA is known and/or is readily available from, e.g., commercial sources, DNA libraries (including, e.g., phage-antibody libraries), or can be synthesized. The DNA may be sequenced and manipulated chemically or by using molecular biology techniques, for example, to arrange one or more variable and/or constant domains into a suitable configuration, or to introduce codons, create cysteine residues, modify, add or delete amino acids, etc.

[0046] Non-limiting examples of antigen-binding fragments include: (i) Fab fragments; (ii) $F(ab')_2$ fragments; (iii) Fd fragments; (iv) Fv fragments; (v) single-chain Fv (scFv) molecules; (vi) dAb fragments; and (vii) minimal recognition units consisting of the amino acid residues that mimic the hypervariable region of an antibody (e.g., an isolated complementarity determining region (CDR)). Other engineered molecules, such as diabodies, triabodies, tetrabodies and minibodies, are also encompassed within the expression "antigen-binding fragment," as used herein.

[0047] An antigen-binding fragment of an antibody will typically comprise at least one variable domain. The variable domain may be of any size or amino acid composition and will generally comprise at least one CDR which is adjacent to or in frame with one or more framework sequences. In antigen-binding fragments having a V_H domain associated with a V_L domain, the V_H and V_L domains may be situated relative to one another in any suitable arrangement. For example, the variable region may be dimeric and contain V_H - V_H , V_H - V_L or V_L - V_L dimers. Alternatively, the antigen-binding fragment of an antibody may contain a monomeric V_H or V_L domain.

[0048] In certain embodiments, an antigen-binding fragment of an antibody may contain at least one variable domain covalently linked to at least one constant domain. Non-limiting, exemplary configurations of variable and constant domains that may be found within an antigen-binding fragment of an antibody of the present invention include: (i) V_H-C_H1; (ii) V_H-C_H2; (iii) V_H-C_H3; (iv) V_H-C_H1-C_H2; (v) V_H-C_H1-C_H2-C_H3; (vi) V_H-C_H2-C_H3; (vii) V_H-C_L; (viii) V_L-C_H1; (ix) V_L-C_H2; (x) V_L-C_H3; (xi) V_L-C_H1-C_H2; (xii) V_L-C_H1-C_H2-C_H3; (xiii) V_L-C_H2-C_H3; and (xiv) V_L-C_L. In any configuration of variable and constant domains, including any of the exemplary configurations listed above, the variable and constant domains may be either directly linked to one another or may be linked by a full or partial hinge or linker region. A hinge region may consist of at least 2 (e.g., 5, 10, 15, 20, 40, 60 or more) amino acids which result in a flexible or semi-flexible linkage between adjacent variable and/or constant domains in a single polypeptide molecule. Moreover, an antigen-binding fragment of an antibody of the present invention may comprise a homo-dimer or hetero-dimer (or other multimer) of any of the variable and constant domain configurations listed above in non-covalent association with one another and/or with one or more monomeric V_H or V_L domain (e.g., by disulfide bond(s)).

[0049] As with full antibody molecules, antigen-binding fragments may be monospecific or multispecific (e.g., bispecific). A multispecific antigen-binding fragment of an antibody will typically comprise at least two different variable domains, wherein each variable domain is capable of specifically binding to a separate antigen or to a different epitope on the same antigen. Any multispecific antibody format, including the exemplary bispecific antibody formats disclosed herein, may be adapted for use in the context of an antigen-binding fragment of an antibody of the present invention using routine techniques available in the art.

[0050] The constant region of an antibody is important in the ability of an antibody to fix complement and mediate cell-dependent cytotoxicity. Thus, the isotype of an antibody may be selected on the basis of whether it is desirable for the antibody to mediate cytotoxicity.

[0051] The term "human antibody", as used herein, is intended to include antibodies having variable and constant regions derived from human germline immunoglobulin sequences. 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. However, the term "human antibody", as used herein, is not intended to include antibodies in which CDR sequences derived from the germline of another mammalian species, such as a mouse, have been grafted onto human framework sequences.

[0052] The term "recombinant human antibody", as used herein, is intended to include all human antibodies that are prepared, expressed, created or isolated by recombinant means, such as antibodies expressed using a recombinant expression vector transfected into a host cell (described further below), antibodies isolated from a recombinant, combinatorial human antibody library (described further below), antibodies isolated from an animal (e.g., a mouse)

that is transgenic for human immunoglobulin genes (see e.g., Taylor et al. (1992) Nucl. Acids Res. 20:6287-6295) or antibodies prepared, expressed, created or isolated by any other means that involves splicing of human immunoglobulin gene sequences to other DNA sequences. Such recombinant human antibodies have variable and constant regions derived from human germline immunoglobulin sequences. In certain embodiments, however, such recombinant human antibodies are subjected to *in vitro* mutagenesis (or, when an animal transgenic for human Ig sequences is used, *in vivo* somatic mutagenesis) and thus the amino acid sequences of the VH and VL regions of the recombinant antibodies are sequences that, while derived from and related to human germline VH and VL sequences, may not naturally exist within the human antibody germline repertoire *in vivo*.

[0053] Human antibodies can exist in two forms that are associated with hinge heterogeneity. In one form, an immunoglobulin molecule comprises a stable four chain construct of approximately 150-160 kDa in which the dimers are held together by an interchain heavy chain disulfide bond. In a second form, the dimers are not linked via inter-chain disulfide bonds and a molecule of about 75-80 kDa is formed composed of a covalently coupled light and heavy chain (half-antibody). These forms have been extremely difficult to separate, even after affinity purification.

[0054] The frequency of appearance of the second form in various intact IgG isotypes is due to, but not limited to, structural differences associated with the hinge region isotype of the antibody. A single amino acid substitution in the hinge region of the human IgG4 hinge can significantly reduce the appearance of the second form (Angal et al. (1993) Molecular Immunology 30:105) to levels typically observed using a human IgG1 hinge. The instant invention encompasses antibodies having one or more mutations in the hinge, CH2 or CH3 region which may be desirable, for example, in production, to improve the yield of the desired antibody form.

[0055] An "isolated antibody," as used herein, means an antibody that has been identified and separated and/or recovered from at least one component of its natural environment. For example, an antibody that has been separated or removed from at least one component of an organism, tissue or cell in which the antibody naturally exists or is naturally produced is an "isolated antibody" for purposes of the present invention. An isolated antibody also includes an antibody *in situ* within a recombinant cell, as well as an antibody that has been subjected to at least one purification or isolation step. According to certain embodiments, an isolated antibody may be substantially free of other cellular material and/or chemicals.

[0056] The term "specifically binds," or the like, means that an antibody or antigen-binding fragment thereof forms a complex with an antigen that is relatively stable under physiologic conditions. Specific binding can be characterized by a dissociation constant of 1×10^{-6} M or less. Methods for determining whether two molecules specifically bind are well known in the art and include, for example, equilibrium dialysis, surface plasmon resonance, and the like. For

example, an antibody that "specifically binds" human PAR-2, as used in the context of the present invention, includes antibodies that bind human PAR-2 or portion thereof (e.g., a PAR-2 fragment comprising the activating protease cleavage site) with a K_D of less than about 1000 nM, less than about 500 nM, less than about 300 nM, less than about 200 nM, less than about 100 nM, less than about 90 nM, less than about 80 nM, less than about 70 nM, less than about 60 nM, less than about 50 nM, less than about 40 nM, less than about 30 nM, less than about 20 nM, less than about 10 nM, less than about 5 nM, less than about 4 nM, less than about 3 nM, less than about 2 nM, less than about 1 nM or less than about 0.5 nM, as measured in a surface plasmon resonance assay. (See, e.g., Example 4, herein). An isolated antibody that specifically binds human PAR-2 may, however, have cross-reactivity to other antigens, such as PAR-2 molecules from other species.

[0057] A "neutralizing" or "blocking" antibody, as used herein, is intended to refer to an antibody whose binding to PAR-2: (i) interferes with the interaction between PAR-2 or a PAR-2 fragment and one or more proteases, (ii) prevents cleavage of PAR-2 or a PAR-2 fragment by a PAR-2 protease, (iii) inhibits the interaction between the PAR-2 tethered ligand and a PAR-2 extracellular loop, and/or (iv) results in inhibition of at least one biological function of PAR-2. The inhibition caused by a PAR-2 neutralizing or blocking antibody need not be complete so long as it is detectable using an appropriate assay. Exemplary assays for detecting PAR-2 inhibition are described herein.

[0058] The fully-human anti-PAR-2 antibodies disclosed herein may comprise one or more amino acid substitutions, insertions and/or deletions in the framework and/or CDR regions of the heavy and light chain variable domains as compared to the corresponding germline sequences. Such mutations can be readily ascertained by comparing the amino acid sequences disclosed herein to germline sequences available from, for example, public antibody sequence databases. The present invention includes antibodies, and antigen-binding fragments thereof, which are derived from any of the amino acid sequences disclosed herein, wherein one or more amino acids within one or more framework and/or CDR regions are back-mutated to the corresponding germline residue(s) or to a conservative amino acid substitution (natural or non-natural) of the corresponding germline residue(s) (such sequence changes are referred to herein as "germline back-mutations"). A person of ordinary skill in the art, starting with the heavy and light chain variable region sequences disclosed herein, can easily produce numerous antibodies and antigen-binding fragments which comprise one or more individual germline back-mutations or combinations thereof. In certain embodiments, all of the framework and/or CDR residues within the V_H and/or V_L domains are mutated back to the germline sequence. In other embodiments, only certain residues are mutated back to the germline sequence, e.g., only the mutated residues found within the first 8 amino acids of FR1 or within the last 8 amino acids of FR4, or only the mutated residues found within CDR1, CDR2 or CDR3. Furthermore, the antibodies of the present invention may contain any combination of two or more germline back-mutations

within the framework and/or CDR regions, *i.e.*, wherein certain individual residues are mutated back to the germline sequence while certain other residues that differ from the germline sequence are maintained. Once obtained, antibodies and antigen-binding fragments that contain one or more germline back-mutations can be easily tested for one or more desired property such as, improved binding specificity, increased binding affinity, improved or enhanced antagonistic or agonistic biological properties (as the case may be), reduced immunogenicity, etc. Antibodies and antigen-binding fragments obtained in this general manner are encompassed within the present invention.

[0059] The present invention also includes anti-PAR-2 antibodies comprising variants of any of the HCVR, LCVR, and/or CDR amino acid sequences disclosed herein having one or more conservative substitutions. For example, the present invention includes anti-PAR-2 antibodies having HCVR, LCVR, and/or CDR amino acid sequences with, *e.g.*, 10 or fewer, 8 or fewer, 6 or fewer, 4 or fewer, etc. conservative amino acid substitutions relative to any of the HCVR, LCVR, and/or CDR amino acid sequences disclosed herein. In one embodiment, the antibody comprises an HCVR having the amino acid sequence of SEQ ID NO:698 with 8 or fewer conservative amino acid substitutions. In another embodiment, the antibody comprises an HCVR having the amino acid sequence of SEQ ID NO:698 with 6 or fewer conservative amino acid substitutions. In another embodiment, the antibody comprises an HCVR having the amino acid sequence of SEQ ID NO:698 with 4 or fewer conservative amino acid substitutions. In another embodiment, the antibody comprises an HCVR having the amino acid sequence of SEQ ID NO:698 with 2 or fewer conservative amino acid substitutions. In one embodiment, the antibody comprises an LCVR having the amino acid sequence of SEQ ID NO:706 with 8 or fewer conservative amino acid substitutions. In another embodiment, the antibody comprises an LCVR having the amino acid sequence of SEQ ID NO:706 with 6 or fewer conservative amino acid substitutions. In another embodiment, the antibody comprises an LCVR having the amino acid sequence of SEQ ID NO:706 with 4 or fewer conservative amino acid substitutions. In another embodiment, the antibody comprises an LCVR having the amino acid sequence of SEQ ID NO:706 with 2 or fewer conservative amino acid substitutions.

[0060] The term "surface plasmon resonance", as used herein, refers to an optical phenomenon that allows for the analysis of real-time interactions by detection of alterations in protein concentrations within a biosensor matrix, for example using the BIAcore™ system (Biacore Life Sciences division of GE Healthcare, Piscataway, NJ).

[0061] The term " K_D ", as used herein, is intended to refer to the equilibrium dissociation constant of a particular antibody-antigen interaction.

[0062] The term "epitope" refers to an antigenic determinant that interacts with a specific antigen binding site in the variable region of an antibody molecule known as a paratope. A single antigen may have more than one epitope. Thus, different antibodies may bind to different areas on an antigen and may have different biological effects. Epitopes may be either

conformational or linear. A conformational epitope is produced by spatially juxtaposed amino acids from different segments of the linear polypeptide chain. A linear epitope is one produced by adjacent amino acid residues in a polypeptide chain. In certain circumstance, an epitope may include moieties of saccharides, phosphoryl groups, or sulfonyl groups on the antigen.

[0063] The term "substantial identity" or "substantially identical," when referring to a nucleic acid or fragment thereof, indicates that, when optimally aligned with appropriate nucleotide insertions or deletions with another nucleic acid (or its complementary strand), there is nucleotide sequence identity in at least about 95%, and more preferably at least about 96%, 97%, 98% or 99% of the nucleotide bases, as measured by any well-known algorithm of sequence identity, such as FASTA, BLAST or Gap, as discussed below. A nucleic acid molecule having substantial identity to a reference nucleic acid molecule may, in certain instances, encode a polypeptide having the same or substantially similar amino acid sequence as the polypeptide encoded by the reference nucleic acid molecule.

[0064] As applied to polypeptides, the term "substantial similarity" or "substantially similar" means that two peptide sequences, when optimally aligned, such as by the programs GAP or BESTFIT using default gap weights, share at least 95% sequence identity, even more preferably at least 98% or 99% sequence identity. Preferably, residue positions which are not identical differ by conservative amino acid substitutions. A "conservative amino acid substitution" is one in which an amino acid residue is substituted by another amino acid residue having a side chain (R group) with similar chemical properties (e.g., charge or hydrophobicity). In general, a conservative amino acid substitution will not substantially change the functional properties of a protein. In cases where two or more amino acid sequences differ from each other by conservative substitutions, the percent sequence identity or degree of similarity may be adjusted upwards to correct for the conservative nature of the substitution. Means for making this adjustment are well-known to those of skill in the art. See, e.g., Pearson (1994) *Methods Mol. Biol.* 24: 307-331. Examples of groups of amino acids that have side chains with similar chemical properties include (1) aliphatic side chains: glycine, alanine, valine, leucine and isoleucine; (2) aliphatic-hydroxyl side chains: serine and threonine; (3) amide-containing side chains: asparagine and glutamine; (4) aromatic side chains: phenylalanine, tyrosine, and tryptophan; (5) basic side chains: lysine, arginine, and histidine; (6) acidic side chains: aspartate and glutamate, and (7) sulfur-containing side chains are cysteine and methionine. Preferred conservative amino acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, glutamate-aspartate, and asparagine-glutamine. Alternatively, a conservative replacement is any change having a positive value in the PAM250 log-likelihood matrix disclosed in Gonnet *et al.* (1992) *Science* 256: 1443-1445. A "moderately conservative" replacement is any change having a nonnegative value in the PAM250 log-likelihood matrix.

[0065] Sequence similarity for polypeptides, which is also referred to as sequence identity, is

typically measured using sequence analysis software. Protein analysis software matches similar sequences using measures of similarity assigned to various substitutions, deletions and other modifications, including conservative amino acid substitutions. For instance, GCG software contains programs such as Gap and Bestfit which can be used with default parameters to determine sequence homology or sequence identity between closely related polypeptides, such as homologous polypeptides from different species of organisms or between a wild type protein and a mutein thereof. See, e.g., GCG Version 6.1. Polypeptide sequences also can be compared using FASTA using default or recommended parameters, a program in GCG Version 6.1. FASTA (e.g., FASTA2 and FASTA3) provides alignments and percent sequence identity of the regions of the best overlap between the query and search sequences (Pearson (2000) *supra*). Another preferred algorithm when comparing a sequence of the invention to a database containing a large number of sequences from different organisms is the computer program BLAST, especially BLASTP or TBLASTN, using default parameters. See, e.g., Altschul *et al.* (1990) *J. Mol. Biol.* 215:403-410 and Altschul *et al.* (1997) *Nucleic Acids Res.* 25:3389-402.

Preparation of Human Antibodies

[0066] Methods for generating monoclonal antibodies, including fully human monoclonal antibodies are known in the art. Any such known methods can be used in the context of the present invention to make human antibodies that specifically bind to human PAR-2.

[0067] Using VELOCIMMUNE™ technology or any other known method for generating monoclonal antibodies, high affinity chimeric antibodies to PAR-2 are initially isolated having a human variable region and a mouse constant region. As in the experimental section below, the antibodies are characterized and selected for desirable characteristics, including affinity, selectivity, epitope, etc. The mouse constant regions are replaced with a desired human constant region to generate the fully human antibody of the invention, for example wild-type or modified IgG1 or IgG4. While the constant region selected may vary according to specific use, high affinity antigen-binding and target specificity characteristics reside in the variable region.

Bioequivalents

[0068] The anti-PAR-2 antibodies and antibody fragments of the present invention encompass proteins having amino acid sequences that vary from those of the described antibodies, but that retain the ability to bind human PAR-2. Such variant antibodies and antibody fragments comprise one or more additions, deletions, or substitutions of amino acids when compared to parent sequence, but exhibit biological activity that is essentially equivalent to that of the described antibodies. Likewise, the anti-PAR-2 antibody-encoding DNA sequences of the present invention encompass sequences that comprise one or more additions, deletions, or substitutions of nucleotides when compared to the disclosed sequence, but that encode an anti-PAR-2 antibody or antibody fragment that is essentially bioequivalent to an anti-PAR-2 antibody or antibody fragment of the invention. Examples of such variant amino acid and DNA sequences

are discussed above.

[0069] Two antigen-binding proteins, or antibodies, are considered bioequivalent if, for example, they are pharmaceutical equivalents or pharmaceutical alternatives whose rate and extent of absorption do not show a significant difference when administered at the same molar dose under similar experimental conditions, either single dose or multiple dose. Some antibodies will be considered equivalents or pharmaceutical alternatives if they are equivalent in the extent of their absorption but not in their rate of absorption and yet may be considered bioequivalent because such differences in the rate of absorption are intentional and are reflected in the labeling, are not essential to the attainment of effective body drug concentrations on, e.g., chronic use, and are considered medically insignificant for the particular drug product studied.

[0070] In one embodiment, two antigen-binding proteins are bioequivalent if there are no clinically meaningful differences in their safety, purity, and potency.

[0071] In one embodiment, two antigen-binding proteins are bioequivalent if a patient can be switched one or more times between the reference product and the biological product without an expected increase in the risk of adverse effects, including a clinically significant change in immunogenicity, or diminished effectiveness, as compared to continued therapy without such switching.

[0072] In one embodiment, two antigen-binding proteins are bioequivalent if they both act by a common mechanism or mechanisms of action for the condition or conditions of use, to the extent that such mechanisms are known.

[0073] Bioequivalence may be demonstrated by in vivo and in vitro methods. Bioequivalence measures include, e.g., (a) an in vivo test in humans or other mammals, in which the concentration of the antibody or its metabolites is measured in blood, plasma, serum, or other biological fluid as a function of time; (b) an in vitro test that has been correlated with and is reasonably predictive of human in vivo bioavailability data; (c) an in vivo test in humans or other mammals in which the appropriate acute pharmacological effect of the antibody (or its target) is measured as a function of time; and (d) in a well-controlled clinical trial that establishes safety, efficacy, or bioavailability or bioequivalence of an antibody.

[0074] Bioequivalent variants of anti-PAR-2 antibodies of the invention may be constructed by, for example, making various substitutions of residues or sequences or deleting terminal or internal residues or sequences not needed for biological activity. For example, cysteine residues not essential for biological activity can be deleted or replaced with other amino acids to prevent formation of unnecessary or incorrect intramolecular disulfide bridges upon renaturation. In other contexts, bioequivalent antibodies may include anti-PAR-2 antibody variants comprising amino acid changes which modify the glycosylation characteristics of the antibodies, e.g., mutations which eliminate or remove glycosylation.

Biological Characteristics of the Antibodies

[0075] The antibodies of the present invention may function through complement-dependent cytotoxicity (CDC) or antibody-dependent cell-mediated cytotoxicity (ADCC). "Complement-dependent cytotoxicity" (CDC) refers to lysis of antigen-expressing cells by an antibody of the invention in the presence of complement. "Antibody-dependent cell-mediated cytotoxicity" (ADCC) refers to a cell-mediated reaction in which nonspecific cytotoxic cells that express Fc receptors (FcRs) (e.g., Natural Killer (NK) cells, neutrophils, and macrophages) recognize bound antibody on a target cell and thereby lead to lysis of the target cell. CDC and ADCC can be measured using assays that are well known and available in the art. (See, e.g., U.S. 5,500,362 and 5,821,337, and Clynes *et al.* (1998) Proc. Natl. Acad. Sci. (USA) 95:652-656).

[0076] Alternatively, or additionally, the antibodies of the invention may be therapeutically useful in blocking a PAR-2 interaction or inhibiting receptor component interaction. In the case of the PAR-2 antibodies of the present invention, the antibodies may function by, *inter alia*, blocking or obscuring the activating PAR-2 protease cleavage site. Alternatively, the antibodies of the invention may function by interfering with the interaction between the tethered ligand and one or more extracellular loops (e.g., loop-1, loop-2 and/or loop-3).

[0077] More specifically, the anti-PAR-2 antibodies of the invention may exhibit one or more of the following characteristics: (1) ability to bind to a human PAR-2 or human PAR-2 fragment and to a non-human (e.g., mouse, monkey, rat, rabbit, dog, pig, etc.) PAR-2 or PAR-2 fragment; (2) ability to bind to a human PAR-2 or human PAR-2 fragment but not to a non-human (e.g., mouse, monkey, rat, rabbit, dog, pig, etc.) PAR-2 or PAR-2 fragment; (3) ability to bind to a human PAR-2 or human PAR-2 fragment and to a monkey PAR-2 or monkey PAR-2 fragment, but not to a mouse, rat, rabbit, dog or pig PAR-2 or PAR-2 fragment; (4) ability to bind to a human PAR-2 or human PAR-2 fragment and to a human PAR-1, PAR-3 or PAR-4 or fragment thereof; (5) ability to bind to a human PAR-2 or human PAR-2 fragment but not to a human PAR-1, PAR-3, or PAR-4 or fragment thereof; (6) ability to bind to a human PAR-2 or human PAR-2 fragment and to a non-human (e.g., mouse, monkey, rat, rabbit, dog, pig, etc.) PAR-1, PAR-3 or PAR-4 or fragment thereof; (7) ability to bind to a human PAR-2 or human PAR-2 fragment but not to a non-human (e.g., mouse, monkey, rat, rabbit, dog, pig, etc.) PAR-1, PAR-3 or PAR-4 or fragment thereof; (8) ability to block proteolytic cleavage of a PAR-2 or a PAR-2 fragment; (9) ability to block proteolytic cleavage of a human PAR-2 or human PAR-2 fragment and a non-human (e.g., mouse, monkey, rat, rabbit, dog, pig, etc.) PAR-2 or PAR-2 fragment; (10) ability to block proteolytic cleavage of a human PAR-2 or human PAR-2 fragment but not a non-human (e.g., mouse, monkey, rat, rabbit, dog, pig, etc.) PAR-2 or PAR-2 fragment; (11) ability to block proteolytic cleavage of a human PAR-2 or human PAR-2 fragment and a human PAR-1, PAR-3 or PAR-4 or fragment thereof; (12) ability to block proteolytic cleavage of a human PAR-2 or human PAR-2 fragment but not a human PAR-1, PAR-3 or PAR-4 or fragment thereof; (13) ability to block proteolytic cleavage of a human PAR-2 or human PAR-2 fragment

and a non-human (e.g., mouse, monkey, rat, rabbit, dog, pig, etc.) PAR-1, PAR-3 or PAR-4 or fragment thereof; and/or (14) ability to block proteolytic cleavage of a human PAR-2 or human PAR-2 fragment but not a non-human (e.g., mouse, monkey, rat, rabbit, dog, pig, etc.) PAR-1, PAR-3 or PAR-4 or fragment thereof.

[0078] As used in items (8) – (14) above, the term "proteolytic cleavage" means cleavage of a PAR molecule (PAR-1, PAR-2, PAR-3 or PAR-4) or fragment thereof by a PAR-2 protease or other enzyme that is capable of cleaving PAR-2 at the activating PAR-2 protease cleavage site.

[0079] The N-terminal region of human PAR-2 has at least two "non-activating" protease cleavage sites, *i.e.*, sites that are capable of being cleaved by trypsin but do not result in activation of the receptor. The N-terminal non-activating protease cleavage sites are located: (a) at the junction of residues Arg-31 and Ser-32 of human PAR-2 (SEQ ID NO:851); and (b) at the junction of residues Lys-34 and Gly-35 of human PAR-2 (SEQ ID NO:851). The activating and non-activating cleavage sites at the N-terminus of PAR-2 are illustrated in Fig. 5 (white triangles indicate the non-activating protease cleavage sites and the black triangle indicates the activating PAR-2 protease cleavage site); see *also* Fig. 4. The present invention includes anti-PAR-2 antibodies that block the activating PAR-2 protease cleavage site but do not block one or both of the non-activating protease cleavage sites. Whether a candidate antibody blocks or does not block a particular protease cleavage site can be determined by a person of ordinary skill in the art using any suitable assay such as the exemplary *in vitro* blocking assays set forth in Example 8 herein. As illustrated in Example 8, the exemplary antibody H4H581P was shown to block trypsin cleavage at the activating PAR-2 protease cleavage site and at the non-activating protease cleavage site located at the junction of residues Lys-34 and Gly-35 of human PAR-2 (SEQ ID NO:851), but did not block cleavage at the non-activating protease cleavage site located at the junction of residues Arg-31 and Ser-32 of human PAR-2 (SEQ ID NO:851). By contrast, the comparator antibody used in Example 8 blocked cleavage at the activating PAR-2 protease cleavage site and at both non-activating sites. The differential blocking capabilities of these exemplary anti-PAR-2 antibodies most likely reflects differences in the particular regions of the PAR-2 molecule with which these antibodies bind (see, e.g., Example 9 herein).

[0080] As used herein, an antibody "does not bind" to a specified target molecule (e.g., mouse PAR-2, rat PAR-2, rabbit PAR-2, dog PAR-2, pig PAR-2, or fragment thereof) if the antibody, when tested for binding to the target molecule at 25°C in a surface plasmon resonance assay, exhibits a K_D of greater than 500 nM, or if tested for binding to the target molecule at 25°C in an enzyme-linked immunosorbent assay (ELISA) exhibits an EC_{50} of greater than 50 nM, or fails to exhibit any binding in either type of assay or equivalent thereof.

[0081] Certain anti-PAR-2 antibodies of the present invention are able to inhibit or attenuate PAR-2 activation in an *in vitro* cellular assay. A non-limiting, exemplary *in vitro* cellular assay for PAR-2 activation is illustrated in Example 6, herein. In this Example, cells are used which

express PAR-2 and harbor a construct comprising NF- κ B fused to a reporter molecule (e.g., luciferase). Briefly, such cells are combined with an anti-PAR-2 antibody, followed by treatment with a PAR-2 protease. Cells that are treated with the protease in the presence of an inhibitory anti-PAR-2 antibody will exhibit significantly less or no reporter signal as compared to cells treated with the protease in the absence of an inhibitory anti-PAR-2 antibody. The concentration of antibody necessary to achieve half-maximal inhibition of reporter signal (IC_{50}) can be calculated using such an assay. The present invention includes inhibitory anti-PAR-2 antibodies that exhibit an IC_{50} of less than 300 nM when tested in an *in vitro* cellular assay for PAR-2 activation as described above. For example, the invention includes anti-PAR-2 antibodies with an IC_{50} of less than 300, 290, 280, 270, 260, 250, 240, 230, 220, 210, 200, 190, 180, 170, 160, 150, 140, 130, 120, 110, 100, 90, 80, 70, 60, 50, 40, 30, 20, 10, 18, 16, 14, 12, 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 nM when tested in an *in vitro* cellular assay for PAR-2 activation as described above in which the cells are incubated with the antibody for 1 h at 37°C followed by treatment with 20 nM trypsin (or other PAR-2 protease) for 5 h at 37°C.

[0082] The present invention includes anti-PAR-2 antibodies and antigen binding fragments thereof which bind to one or more of the following peptides: Peptide A (GTNRSSKGRSLIGKVDGT, SEQ ID NO:852); Peptide B (SLIGKVDGTSHVTG, SEQ ID NO:853); Peptide C (SLIGKV, SEQ ID NO:854); Peptide D (N-terminal domain of human PAR-2 – mouse IgG, SEQ ID NO:855); Peptide E (LAPGRNNSKGRSLIGRLETQ, SEQ ID NO:856); Peptide F (GTNRSSKGRSLIGRVDGT, SEQ ID NO:857); Peptide G (GPNSKGRSLIGRLDTP, SEQ ID NO:858); Peptide H (GTNKTSGRSLIGRNTGS, SEQ ID NO:859); Peptide I (GTNRTSKGRSLIGKTDSS, SEQ ID NO:860); Peptide J (GTSRPSKGRSLIGKADNT, SEQ ID NO:861); Peptide K (ATNATLDPRSFLLRNPND, SEQ ID NO:862); Peptide L (DTNNLAKPTLPIKTRGA, SEQ ID NO:863); or Peptide M (ESGSTGGGDDSTPSILPAP, SEQ ID NO:864). Additional information regarding these peptides can be found in Example 3 herein. These peptides may contain no additional labels or moieties, or they may contain an N-terminal or C-terminal label or moiety. In one embodiment, the label or moiety is biotin. In a binding assay, the location of a label (if any) may determine the orientation of the peptide relative to the surface upon which the peptide is bound. For example, if a surface is coated with avidin, a peptide containing an N-terminal biotin will be oriented such that the C-terminal portion of the peptide will be distal to the surface.

[0083] With regard to the aforementioned Peptides, the present invention includes anti-PAR-2 antibodies with one or more of the following binding profiles: (1) binding to Peptides A and B, but not binding to Peptide C; (2) binding to Peptides A, B and D, but not binding to Peptide C; (3) binding to Peptides A, B, D and F, but not binding to Peptide C; (4) binding to Peptides A, B, D and F, but not binding to either of Peptides C or E; (5) binding to Peptides A, B and D, but not binding to any of Peptides K, L or M; (6) binding to Peptides A, B and F, but not binding to any of Peptides K, L or M; (7) binding to Peptides A, B, D and F, but not binding to any of Peptides

K, L or M; and/or (8) binding to at least three of Peptides A, B, C, D, E, F, G, I and J, but not binding to Peptide H. Other binding profiles of the antibodies of the invention will be evident from the examples herein.

Epitope Mapping and Related Technologies

[0084] To screen for antibodies that bind to a particular epitope (e.g., those which block binding of IgE to its high affinity receptor), a routine cross-blocking assay such as that described Antibodies, Harlow and Lane (Cold Spring Harbor Press, Cold Spring Harb., NY) can be performed. Other methods include alanine scanning mutants, peptide blots (Reineke, 2004, *Methods Mol Biol* 248:443-463), or peptide cleavage analysis. In addition, methods such as epitope excision, epitope extraction and chemical modification of antigens can be employed (Tomer, 2000, *Protein Science* 9:487-496).

[0085] The term "epitope" refers to a site on an antigen to which B and/or T cells respond. B-cell epitopes can be formed both from contiguous amino acids or noncontiguous amino acids juxtaposed by tertiary folding of a protein. Epitopes formed from contiguous amino acids are typically retained on exposure to denaturing solvents, whereas epitopes formed by tertiary folding are typically lost on treatment with denaturing solvents. An epitope typically includes at least 3, and more usually, at least 5 or 8-10 amino acids in a unique spatial conformation.

[0086] Modification-Assisted Profiling (MAP), also known as Antigen Structure-based Antibody Profiling (ASAP) is a method that categorizes large numbers of monoclonal antibodies (mAbs) directed against the same antigen according to the similarities of the binding profile of each antibody to chemically or enzymatically modified antigen surfaces (US 2004/0101920). Each category may reflect a unique epitope either distinctly different from or partially overlapping with epitope represented by another category. This technology allows rapid filtering of genetically identical antibodies, such that characterization can be focused on genetically distinct antibodies. When applied to hybridoma screening, MAP may facilitate identification of rare hybridoma clones that produce mAbs having the desired characteristics. MAP may be used to sort the anti-PAR-2 antibodies of the invention into groups of antibodies binding different epitopes.

[0087] The present invention includes anti-PAR-2 antibodies which bind to an epitope at or near (e.g., within 5, 10, 15 or 20 amino acids of) the activating PAR-2 protease cleavage site. In certain embodiments, the anti-PAR-2 antibodies bind to an epitope located upstream from (*i.e.*, N-terminal to) the activating PAR-2 protease cleavage site. In certain other embodiments of the invention, the anti-PAR-2 antibodies bind to an epitope located downstream from (*i.e.*, C-terminal to) the activating PAR-2 protease cleavage site. In yet other embodiments, the anti-PAR-2 antibodies of the invention may bind an epitope that includes both amino acid sequences located upstream from the activating PAR-2 protease cleavage site and amino acid sequences located downstream from the activating PAR-2 protease cleavage site.

[0088] Alternatively, the anti-PAR-2 antibodies of the invention may, in certain embodiments, bind to an epitope located on one or more extracellular loops of the PAR-2 protein (e.g.,

extracellular loop 1, extracellular loop 2 and/or extracellular loop 3).

[0089] The present invention includes isolated human antibodies or antigen-binding fragments thereof that interact with certain amino acid residues located downstream from the activating PAR-2 protease cleavage site. For example, the present invention includes isolated human antibodies or antigen-binding fragments thereof that interact with Val-42 and Asp-43 of human PAR-2 (SEQ ID NO:851). In addition to these two residues, the isolated human antibodies or antigen-binding fragments thereof may also interact with one or more of the following residues located downstream from the activating PAR-2 protease cleavage site: Ser-37, Leu-38, Ile-39, Gly-40 or Gly-44 of human PAR-2 (SEQ ID NO:851). In certain embodiments, the isolated human antibody or antigen binding fragment thereof does not interact with Lys-41 of human PAR-2 (SEQ ID NO:851). For example, the present invention includes isolated human antibodies or antigen-binding fragments thereof that interact with Ser-37, Leu-38, Ile-39, Gly-40, Val-42 and Asp-43 of human PAR-2 (SEQ ID NO:851), and do not interact with Lys-41 of human PAR-2 (SEQ ID NO:851). The experimental procedures illustrated in Example 9 can be used to determine if a candidate anti-PAR-2 antibody "interacts with" or "does not interact with" a particular amino acid residue of PAR-2. For example, if a candidate antibody is tested for binding to a peptide having SEQ ID NO:879 (corresponding to the N-terminal region of PAR-2 wherein Val-42 of PAR-2 is mutated to alanine, see, e.g., Tables 24-28) using the procedure of Example 9, and the $T_{1/2}$ of the antibody is less than 30% the $T_{1/2}$ observed when the candidate antibody is tested for binding to the wild-type peptide (SEQ ID NO:871), then for purposes of the present disclosure, the candidate antibody is deemed to "interact with" the amino acid that was mutated to alanine (in this case, Val-42); that is, binding of the candidate antibody is substantially reduced when the amino acid corresponding to Val-42 is mutated to alanine (such residues are depicted by black circles in Figure 5). On the other hand, if a candidate antibody is tested for binding to a peptide having SEQ ID NO:878 (corresponding to the N-terminal region of PAR-2 wherein Lys-41 of PAR-2 is mutated to alanine, see, e.g., Tables 24-28) using the procedure of Example 9, and the $T_{1/2}$ of the antibody is greater than or equal to 30% the $T_{1/2}$ observed when the candidate antibody is tested for binding to the wild-type peptide (SEQ ID NO:871), then for purposes of the present disclosure, the candidate antibody is deemed to "not interact with" the amino acid that was mutated to alanine (in this case, Lys-41); that is, binding of the candidate antibody is not substantially reduced when the amino acid corresponding to Lys-41 is mutated to alanine (such residues are depicted by white circles in Figure 5).

[0090] The present invention includes anti-PAR-2 antibodies that bind to the same epitope as any of the specific exemplary antibodies described herein (e.g., H4H581P, H4H588N, H4H591N or H4H618N). Likewise, the present invention also includes anti-PAR-2 antibodies that cross-compete for binding to PAR-2 or a PAR-2 fragment with any of the specific exemplary antibodies described herein (e.g., H4H581P, H4H588N, H4H591N or H4H618N).

[0091] One can easily determine whether an antibody binds to the same epitope as, or

competes for binding with, a reference anti-PAR-2 antibody by using routine methods known in the art. For example, to determine if a test antibody binds to the same epitope as a reference anti-PAR-2 antibody of the invention, the reference antibody is allowed to bind to a PAR-2 protein or peptide under saturating conditions. Next, the ability of a test antibody to bind to the PAR-2 molecule is assessed. If the test antibody is able to bind to PAR-2 following saturation binding with the reference anti-PAR-2 antibody, it can be concluded that the test antibody binds to a different epitope than the reference anti-PAR-2 antibody. On the other hand, if the test antibody is not able to bind to the PAR-2 molecule following saturation binding with the reference anti-PAR-2 antibody, then the test antibody may bind to the same epitope as the epitope bound by the reference anti-PAR-2 antibody of the invention. Additional routine experimentation (e.g., peptide mutation and binding analyses) can then be carried out to confirm whether the observed lack of binding of the test antibody is in fact due to binding to the same epitope as the reference antibody or if steric blocking (or another phenomenon) is responsible for the lack of observed binding. Experiments of this sort can be performed using ELISA, RIA, Biacore, flow cytometry or any other quantitative or qualitative antibody-binding assay available in the art. In accordance with certain embodiments of the present invention, two antibodies bind to the same (or overlapping) epitope if, e.g., a 1-, 5-, 10-, 20- or 100-fold excess of one antibody inhibits binding of the other by at least 50% but preferably 75%, 90% or even 99% as measured in a competitive binding assay (see, e.g., Junghans et al., Cancer Res. 1990:50:1495-1502). Alternatively, two antibodies are deemed to bind to the same epitope if essentially all amino acid mutations in the antigen that reduce or eliminate binding of one antibody reduce or eliminate binding of the other. Two antibodies are deemed to have "overlapping epitopes" if only a subset of the amino acid mutations that reduce or eliminate binding of one antibody reduce or eliminate binding of the other.

[0092] To determine if an antibody competes for binding with a reference anti-PAR-2 antibody, the above-described binding methodology is performed in two orientations: In a first orientation, the reference antibody is allowed to bind to a PAR-2 molecule under saturating conditions followed by assessment of binding of the test antibody to the PAR-2 molecule. In a second orientation, the test antibody is allowed to bind to a PAR-2 molecule under saturating conditions followed by assessment of binding of the reference antibody to the PAR-2 molecule. If, in both orientations, only the first (saturating) antibody is capable of binding to the PAR-2 molecule, then it is concluded that the test antibody and the reference antibody compete for binding to PAR-2. As will be appreciated by a person of ordinary skill in the art, an antibody that competes for binding with a reference antibody may not necessarily bind to the same epitope as the reference antibody, but may sterically block binding of the reference antibody by binding an overlapping or adjacent epitope.

Species Selectivity and Species Cross-Reactivity

[0093] According to certain embodiments of the invention, the anti-PAR-2 antibodies bind to

human PAR-2 but not to PAR-2 from other species. Alternatively, the anti-PAR-2 antibodies of the invention, in certain embodiments, bind to human PAR-2 and to PAR-2 from one or more non-human species. For example, the anti-PAR-2 antibodies of the invention may bind to human PAR-2 and may bind or not bind, as the case may be, to one or more of mouse, rat, guinea pig, hamster, gerbil, pig, cat, dog, rabbit, goat, sheep, cow, horse, camel, cynomolgous, marmoset, rhesus or chimpanzee PAR-2.

Immunoconjugates

[0094] The invention encompasses anti-PAR-2 monoclonal antibodies conjugated to a therapeutic moiety ("immunoconjugate"), such as a cytotoxin, a chemotherapeutic drug, an immunosuppressant or a radioisotope. Cytotoxic agents include any agent that is detrimental to cells. Examples of suitable cytotoxic agents and chemotherapeutic agents for forming immunoconjugates are known in the art, see for example, WO 05/103081).

Multispecific Antibodies

[0095] The antibodies of the present invention may be monospecific, bi-specific, or multispecific. Multispecific antibodies may be specific for different epitopes of one target polypeptide or may contain antigen-binding domains specific for more than one target polypeptide. See, e.g., Tutt et al., 1991, J. Immunol. 147:60-69; Kufer *et al.*, 2004, Trends Biotechnol. 22:238-244. The anti-PAR-2 antibodies of the present invention can be linked to or co-expressed with another functional molecule, e.g., another peptide or protein. For example, an antibody or fragment thereof can be functionally linked (e.g., by chemical coupling, genetic fusion, noncovalent association or otherwise) to one or more other molecular entities, such as another antibody or antibody fragment to produce a bi-specific or a multispecific antibody with a second binding specificity. For example, the present invention includes bi-specific antibodies wherein one arm of an immunoglobulin is specific for human PAR-2 or a fragment thereof, and the other arm of the immunoglobulin is specific for a second therapeutic target or is conjugated to a therapeutic moiety such as a trypsin inhibitor.

[0096] An exemplary bi-specific antibody format that can be used in the context of the present invention involves the use of a first immunoglobulin (Ig) C_H3 domain and a second Ig C_H3 domain, wherein the first and second Ig C_H3 domains differ from one another by at least one amino acid, and wherein at least one amino acid difference reduces binding of the bispecific antibody to Protein A as compared to a bi-specific antibody lacking the amino acid difference. In one embodiment, the first Ig C_H3 domain binds Protein A and the second Ig C_H3 domain contains a mutation that reduces or abolishes Protein A binding such as an H95R modification (by IMGT exon numbering; H435R by EU numbering). The second C_H3 may further comprise a Y96F modification (by IMGT; Y436F by EU). Further modifications that may be found within the second C_H3 include: D16E, L18M, N44S, K52N, V57M, and V82I (by IMGT; D356E, L358M, N384S, K392N, V397M, and V422I by EU) in the case of IgG1 antibodies; N44S, K52N, and

V82I (IMGT; N384S, K392N, and V422I by EU) in the case of IgG2 antibodies; and Q15R, N44S, K52N, V57M, R69K, E79Q, and V82I (by IMGT; Q355R, N384S, K392N, V397M, R409K, E419Q, and V422I by EU) in the case of IgG4 antibodies. Variations on the bi-specific antibody format described above are contemplated within the scope of the present invention.

Therapeutic Formulation and Administration

[0097] The invention provides therapeutic compositions comprising the anti-PAR-2 antibodies or antigen-binding fragments thereof of the present invention. The administration of therapeutic compositions in accordance with the invention will be administered with suitable carriers, excipients, and other agents that are incorporated into formulations to provide improved transfer, delivery, tolerance, and the like. A multitude of appropriate formulations can be found in the formulary known to all pharmaceutical chemists: Remington's Pharmaceutical Sciences, Mack Publishing Company, Easton, PA. These formulations include, for example, powders, pastes, ointments, jellies, waxes, oils, lipids, lipid (cationic or anionic) containing vesicles (such as LIPOFECTIN™), DNA conjugates, anhydrous absorption pastes, oil-in-water and water-in-oil emulsions, emulsions carbowax (polyethylene glycols of various molecular weights), semi-solid gels, and semi-solid mixtures containing carbowax. See also Powell et al. "Compendium of excipients for parenteral formulations" PDA (1998) J Pharm Sci Technol 52:238-311.

[0098] The dose of antibody may vary depending upon the age and the size of a subject to be administered, target disease, conditions, route of administration, and the like. The preferred dose is typically calculated according to body weight or body surface area. When an antibody of the present invention is used for treating a condition or disease associated with PAR-2 activity in an adult patient, it may be advantageous to intravenously administer the antibody of the present invention normally at a single dose of about 0.01 to about 20 mg/kg body weight, more preferably about 0.02 to about 7, about 0.03 to about 5, or about 0.05 to about 3 mg/kg body weight. Depending on the severity of the condition, the frequency and the duration of the treatment can be adjusted. Effective dosages and schedules for administering PAR-2 antibodies may be determined empirically; for example, patient progress can be monitored by periodic assessment, and the dose adjusted accordingly. Moreover, interspecies scaling of dosages can be performed using well-known methods in the art (e.g., Mordenti *et al.*, 1991, *Pharmaceut. Res.* 8:1351).

[0099] Various delivery systems are known and can be used to administer the pharmaceutical composition of the invention, e.g., encapsulation in liposomes, microparticles, microcapsules, recombinant cells capable of expressing the mutant viruses, receptor mediated endocytosis (see, e.g., Wu et al., 1987, *J. Biol. Chem.* 262:4429-4432). Methods of introduction include, but are not limited to, intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal, epidural, and oral routes. The composition may be administered by any convenient route, for example by infusion or bolus injection, by absorption through epithelial or mucocutaneous linings (e.g., oral mucosa, rectal and intestinal mucosa, etc.) and may be

administered together with other biologically active agents. Administration can be systemic or local.

[0100] A pharmaceutical composition of the present invention can be delivered subcutaneously or intravenously with a standard needle and syringe. In addition, with respect to subcutaneous delivery, a pen delivery device readily has applications in delivering a pharmaceutical composition of the present invention. Such a pen delivery device can be reusable or disposable. A reusable pen delivery device generally utilizes a replaceable cartridge that contains a pharmaceutical composition. Once all of the pharmaceutical composition within the cartridge has been administered and the cartridge is empty, the empty cartridge can readily be discarded and replaced with a new cartridge that contains the pharmaceutical composition. The pen delivery device can then be reused. In a disposable pen delivery device, there is no replaceable cartridge. Rather, the disposable pen delivery device comes prefilled with the pharmaceutical composition held in a reservoir within the device. Once the reservoir is emptied of the pharmaceutical composition, the entire device is discarded.

[0101] Numerous reusable pen and autoinjector delivery devices have applications in the subcutaneous delivery of a pharmaceutical composition of the present invention. Examples include, but are not limited to AUTOPEN™ (Owen Mumford, Inc., Woodstock, UK), DISETRONIC™ pen (Disetronic Medical Systems, Bergdorf, Switzerland), HUMALOG MIX 75/25™ pen, HUMALOG™ pen, HUMALIN 70/30™ pen (Eli Lilly and Co., Indianapolis, IN), NOVOPEN™ I, II and III (Novo Nordisk, Copenhagen, Denmark), NOVOPEN JUNIOR™ (Novo Nordisk, Copenhagen, Denmark), BD™ pen (Becton Dickinson, Franklin Lakes, NJ), OPTIPEN™, OPTIPEN PRO™, OPTIPEN STARLET™, and OPTICLIK™ (sanofi-aventis, Frankfurt, Germany), to name only a few. Examples of disposable pen delivery devices having applications in subcutaneous delivery of a pharmaceutical composition of the present invention include, but are not limited to the SOLOSTAR™ pen (sanofi-aventis), the FLEXPEN™ (Novo Nordisk), and the KWIKPEN™ (Eli Lilly), the SURECLICK™ Autoinjector (Amgen, Thousand Oaks, CA), the PENLET™ (Haselmeier, Stuttgart, Germany), the EPIPEN (Dey, L.P.), and the HUMIRA™ Pen (Abbott Labs, Abbott Park IL), to name only a few.

[0102] In certain situations, the pharmaceutical composition can be delivered in a controlled release system. In one embodiment, a pump may be used (see Langer, *supra*; Sefton, 1987, CRC Crit. Ref. Biomed. Eng. 14:201). In another embodiment, polymeric materials can be used; see, Medical Applications of Controlled Release, Langer and Wise (eds.), 1974, CRC Pres., Boca Raton, Florida. In yet another embodiment, a controlled release system can be placed in proximity of the composition's target, thus requiring only a fraction of the systemic dose (see, e.g., Goodson, 1984, in Medical Applications of Controlled Release, *supra*, vol. 2, pp. 115-138). Other controlled release systems are discussed in the review by Langer, 1990, Science 249:1527-1533.

[0103] The injectable preparations may include dosage forms for intravenous, subcutaneous,

intracutaneous and intramuscular injections, drip infusions, etc. These injectable preparations may be prepared by methods publicly known. For example, the injectable preparations may be prepared, e.g., by dissolving, suspending or emulsifying the antibody or its salt described above in a sterile aqueous medium or an oily medium conventionally used for injections. As the aqueous medium for injections, there are, for example, physiological saline, an isotonic solution containing glucose and other auxiliary agents, etc., which may be used in combination with an appropriate solubilizing agent such as an alcohol (e.g., ethanol), a polyalcohol (e.g., propylene glycol, polyethylene glycol), a nonionic surfactant [e.g., polysorbate 80, HCO-50 (polyoxyethylene (50 mol) adduct of hydrogenated castor oil)], etc. As the oily medium, there are employed, e.g., sesame oil, soybean oil, etc., which may be used in combination with a solubilizing agent such as benzyl benzoate, benzyl alcohol, etc. The injection thus prepared is preferably filled in an appropriate ampoule.

[0104] Advantageously, the pharmaceutical compositions for oral or parenteral use described above are prepared into dosage forms in a unit dose suited to fit a dose of the active ingredients. Such dosage forms in a unit dose include, for example, tablets, pills, capsules, injections (ampoules), suppositories, etc. The amount of the aforesaid antibody contained is generally about 5 to about 500 mg per dosage form in a unit dose; especially in the form of injection, it is preferred that the aforesaid antibody is contained in about 5 to about 100 mg and in about 10 to about 250 mg for the other dosage forms.

Therapeutic Uses of the Antibodies

[0105] The antibodies of the invention are useful, *inter alia*, for the treatment, prevention and/or amelioration of any disease or disorder associated with PAR-2 activity, including diseases or disorders associated with the proteolytic activation of PAR-2. Exemplary diseases and disorders that can be treated with the anti-PAR-2 antibodies of the present invention include pain conditions such as nociceptive pain and visceral pain, as well as pain associated with conditions such as inflammation, post-operative incision, neuropathy, bone fracture, burn, osteoporotic fracture, bone cancer, gout, migraine headache, fibromyalgia, etc. The antibodies of the invention may also be used to treat, prevent and/or ameliorate inflammatory conditions such as joint inflammation, airway inflammation (e.g., asthma), skin inflammation, dermatitis (e.g., atopic dermatitis, allergic contact dermatitis, etc.), inflammatory bowel disease (IBD), glomerulonephritis, interstitial cystitis, bladder inflammation, hyperalgesia, rheumatoid arthritis, osteoarthritis, inflammatory arthritis, multiple sclerosis, anti-phospholipid syndrome, alpha-1-antitrypsin deficiency, etc. The antibodies of the present invention may be used to treat fibrotic conditions, including, e.g., scleroderma, biliary cirrhosis, post-transplant fibrosis, renal fibrosis, lung fibrosis, liver fibrosis, pancreatic fibrosis, testicular fibrosis, hypertrophic scarring and cutaneous keloids. In certain embodiments, the antibodies of the invention are useful for the treatment of gastrointestinal conditions (e.g., celiac disease, Crohn's disease, ulcerative colitis, idiopathic gastroparesis, pancreatitis, irritable bowel syndrome (IBS) and ulcers (including

gastric and duodenal ulcers)); acute lung injury; acute renal injury; and sepsis. The anti-PAR-2 antibodies of the present invention are also useful for the treatment of pruritus; e.g., dermal/pruritoceptive, neuropathic, neurogenic, and psychogenic itch, as well as pruritus associated with atopic dermatitis, psoriasis, burn scarring (burn-related itch), hypertrophic scarring, keloids, renal failure and hepatic failure. Other therapeutic uses of the anti-PAR-2 antibodies of the present invention include the treatment, prevention and/or amelioration of Alzheimer's disease, Netherton's disease, pathological angiogenesis, chronic urticaria, angioedema, mastocytosis, endometriosis, infertility (e.g., male infertility associated with testicular fibrosis), mast cell-mediated diseases, *Clostridium difficile* Toxin-A induced enteritis, and cancer (e.g., blood cell cancer, brain cancer, breast cancer, colon cancer, head and neck cancer, liver cancer, lung cancer, ovarian cancer, pancreatic cancer, prostate cancer, skin cancer, stomach cancer, etc.).

Combination Therapies

[0106] The present invention includes therapeutic administration regimens which comprise administering an anti-PAR-2 antibody of the present invention in combination with at least one additional therapeutically active component. Non-limiting examples of such additional therapeutically active components include other PAR-2 antagonists (e.g., anti-PAR-2 antibody or small molecule inhibitor of PAR-2 (e.g., N1-3-methylbutyryl-N4-6-aminohexanoyl-piperazine; ENMD-1068)), cytokine inhibitors (e.g., an interleukin-1 (IL-1) inhibitor (such as rilonacept or anakinra, a small molecule IL-1 antagonist, or an anti-IL-1 antibody); IL-18 inhibitor (such as a small molecule IL-18 antagonist or an anti-IL-18 antibody); IL-4 inhibitor (such as a small molecule IL-4 antagonist, an anti-IL-4 antibody or an anti-IL-4 receptor antibody); IL-6 inhibitor (such as a small molecule IL-6 antagonist, an anti-IL-6 antibody or an anti-IL-6 receptor antibody); antiepileptic drugs (e.g., gabapentin); nerve growth factor (NGF) inhibitors (e.g., a small molecule NGF antagonist or an anti-NGF antibody); low dose cochicine; aspirin; NSAIDs; steroids (e.g., prednisone, methotrexate, etc.); low dose cyclosporine A; tumor necrosis factor (TNF) or TNF receptor inhibitors (e.g., a small molecule TNF or TNFR antagonist or an anti-TNF or TNFR antibody); uric acid synthesis inhibitors (e.g., allopurinol); uric acid excretion promoters (e.g., probenecid, sulfinpyrazone, benzbromarone, etc.); other inflammatory inhibitors (e.g., inhibitors of caspase-1, p38, IKK1/2, CTLA-4lg, etc.); and/or corticosteroids. The additional therapeutically active component(s) may be administered prior to, concurrent with, or after the administration of the anti-PAR-2 antibody of the present invention.

Diagnostic Uses of the Antibodies

[0107] The anti-PAR-2 antibodies of the present invention may also be used to detect and/or measure PAR-2 in a sample, e.g., for diagnostic purposes. For example, an anti-PAR-2 antibody, or fragment thereof, may be used to diagnose a condition or disease characterized by aberrant expression (e.g., over-expression, under-expression, lack of expression, etc.) of PAR-

2. Exemplary diagnostic assays for PAR-2 may comprise, *e.g.*, contacting a sample, obtained from a patient, with an anti-PAR-2 antibody of the invention, wherein the anti-PAR-2 antibody is labeled with a detectable label or reporter molecule. Alternatively, an unlabeled anti-PAR-2 antibody can be used in diagnostic applications in combination with a secondary antibody which is itself detectably labeled. The detectable label or reporter molecule can be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I ; a fluorescent or chemiluminescent moiety such as fluorescein isothiocyanate, or rhodamine; or an enzyme such as alkaline phosphatase, β -galactosidase, horseradish peroxidase, or luciferase. Specific exemplary assays that can be used to detect or measure PAR-2 in a sample include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and fluorescence-activated cell sorting (FACS).

[0108] Samples that can be used in PAR-2 diagnostic assays according to the present invention include any tissue or fluid sample obtainable from a patient which contains detectable quantities of PAR-2 protein, or fragments thereof, under normal or pathological conditions. Generally, levels of PAR-2 in a particular sample obtained from a healthy patient (*e.g.*, a patient not afflicted with a disease or condition associated with abnormal PAR-2 levels or activity) will be measured to initially establish a baseline, or standard, level of PAR-2. This baseline level of PAR-2 can then be compared against the levels of PAR-2 measured in samples obtained from individuals suspected of having a PAR-2 related disease or condition.

EXAMPLES

[0109] The following examples are put forth so as to provide those of ordinary skill in the art with a complete disclosure and description of how to make and use the methods and compositions of the invention, and are not intended to limit the scope of what the inventors regard as their invention. Efforts have been made to ensure accuracy with respect to numbers used (*e.g.*, amounts, temperature, etc.) but some experimental errors and deviations should be accounted for. Unless indicated otherwise, parts are parts by weight, molecular weight is average molecular weight, temperature is in degrees Centigrade, and pressure is at or near atmospheric.

Example 1. Generation of Human Antibodies to Human PAR-2

[0110] An immunogen comprising human PAR-2 peptide having the amino acid sequence GTNRSSKGRSLIGKVDGT (SEQ ID NO:852) was administered directly, with an adjuvant to stimulate the immune response, to a VELOCIMMUNE[®] mouse comprising DNA encoding human Immunoglobulin heavy and kappa light chain variable regions. The antibody immune response was monitored by a PAR-2-specific immunoassay. When a desired immune response was achieved splenocytes were harvested and fused with mouse myeloma cells to preserve their viability and form hybridoma cell lines. The hybridoma cell lines were screened and selected to identify cell lines that produce PAR-2-specific antibodies. Using this technique several anti-PAR-2 chimeric antibodies (*i.e.*, antibodies possessing human variable domains

and mouse constant domains) were obtained; exemplary antibodies generated in this manner were designated as follows: H2M588, H2M589, H1M590, H2M591, H1M592, H1M595, H2M609, H2M610, H2M611, H1M612, H1M613, H2M614, H1M615, H1M616, H3M617, H2M618, H1M619, and H3M620.

[0111] Anti-PAR-2 antibodies were also isolated directly from antigen-positive B cells without fusion to myeloma cells, as described in U.S. 2007/0280945A1. Using this method, several fully human anti-PAR-2 antibodies (*i.e.*, antibodies possessing human variable domains and human constant domains) were obtained; exemplary antibodies generated in this manner were designated as follows: H1H571, H1H572, H1H573, H1H574, H1H575, H1H576, H1H577, H1H578, H1H579, H1H580, H1H581, H1H583, H1H584, H1H585, H1H586, and H1H587.

[0112] The biological properties of the exemplary anti-PAR-2 antibodies generated in accordance with the methods of this Example are described in detail in the Examples set forth below.

Example 2. Heavy and Light Chain Variable Region Amino Acid Sequences

[0113] Table 1 sets forth the heavy and light chain variable region amino acid sequence pairs of selected anti-PAR-2 antibodies and their corresponding antibody identifiers. The N, P and G designations refer to antibodies having heavy and light chains with identical CDR sequences but with sequence variations in regions that fall outside of the CDR sequences (*i.e.*, in the framework regions). Thus, N, P and G variants of a particular antibody have identical CDR sequences within their heavy and light chain variable regions but differ from one another within their framework regions.

Table 1

Name	HCVR/LCVR SEQ ID NOs	Name	HCVR/LCVR SEQ ID NOs	Name	HCVR/LCVR SEQ ID NOs
H1H571N	458/466	H1H571P	474/476	H1H571G	478/480
H1H572N	482/490	H1H572P	498/500	H1H572G	502/504
H1H573N	506/514	H1H573P	522/524	H1H573G	526/528
H1H574N	530/538	H1H574P	546/548	H1H574G	550/552
H1H575N	554/562	H1H575P	570/572	H1H575G	574/576
H1H576N	578/586	H1H576P	594/596	H1H576G	598/600
H1H577N	602/610	H1H577P	618/620	H1H577G	622/624
H1H578N	626/634	H1H578P	642/644	H1H578G	646/648
H1H579N	650/658	H1H579P	666/668	H1H579G	670/672
H1H580N	674/682	H1H580P	690/692	H1H580G	694/696
H1H581N	698/706	H1H581P	714/692	H1H581G	718/720
H1H583N	722/730	H1H583P	738/740	H1H583G	742/744
H1H584N	746/754	H1H584P	762/764	H1H584G	766/768
H1H585N	770/778	H1H585P	786/788	H1H585G	790/792
H1H586N	794/802	H1H586P	810/812	H1H586G	814/816

H1H587N	818/826	H1H587P	834/836	H1H587G	838/840
H2M588N	98/106	H2M588P	114/116	H2M588G	118/120
H2M589N	122/130	H2M589P	138/140	H2M589G	142/144
H1M590N	218/226	H1M590P	234/236	H1M590G	238/240
H2M591N	146/154	H2M591P	162/164	H2M591G	166/168
H1M592N	242/250	H1M592P	258/260	H1M592G	262/264
H1M595N	266/274	H1M595P	282/284	H1M595G	286/288
H2M609N	170/178	H2M609P	186/188	H2M609G	190/192
H2M610N	194/202	H2M610P	210/212	H2M610G	214/216
H2M611N	290/298	H2M611P	306/308	H2M611G	310/312
H1M612N	2/10	H1M612P	18/20	H1M612G	22/24
H1M613N	410/418	H1M613P	426/428	H1M613G	430/432
H2M614N	314/322	H2M614P	330/332	H2M614G	334/336
H1M615N	26/34	H1M615P	42/44	H1M615G	46/48
H1M616N	50/58	H1M616P	66/68	H1M616G	70/72
H3M617N	362/370	H3M617P	378/380	H3M617G	382/384
H2M618N	338/346	H2M618P	354/356	H2M618G	358/360
H1M619N	74/82	H1M619P	90/92	H1M619G	94/96
H3M620N	386/394	H3M620P	402/404	H3M620G	406/408
FP3B12F6N	434/442	FP3B12F6P	450/452	FP3B12F6G	454/456

Example 3. Antibody Binding to PAR-2 Peptides

[0114] Synthetic peptides (Celtek Bioscience, Nashville, TN) of PAR-2 and PAR-2 related sequences were generated to characterize the binding profiles of anti-PAR-2 antibodies. Both biotinylated and unbiotinylated forms for the various peptides were generated for the examples set forth below. For biotinylated forms, biotin moieties were covalently attached to the peptide at either the C-terminus or the N-terminus via a G₄S linker. Table 2 sets forth the sequence and derivation of these peptides.

Table 2

Designation	Species	Gene	Sequence	SEQ ID NO:
Peptide A	Human	PAR-2	GTNRSSKGRSLIGKVDGT	852
Peptide B	Human	PAR-2	SLIGKVDGTSHVTG	853
Peptide C	Human	PAR-2	SLIGKV	854
Peptide D	Human	PAR-2	SLIGKVDGTSHVTGKGVTVE TVFSVDEFSASVLTGKLTTVF LP – mouse IgG2a	855
Peptide E	Mouse (<i>Mus musculus</i>)	PAR-2	LAPGRNNSKGRSLIGRLETQ	856
Peptide F	Monkey (<i>Macaca mulatta</i>)	PAR-2	GTNRSSKGRSLIGRVDGT	857
Peptide G	Rat (<i>Rattus norvegicus</i>)	PAR-2	GPNSKGRSLIGRLDTP	858

Peptide H	Rabbit (<i>Oryctolagus cuniculus</i>)	PAR-2	GTNKTSKGRSLIGRNTGS	859
Peptide I	Dog (<i>Canis familiaris</i>)	PAR-2	GTNRTSKGRSLIGKTDSS	860
Peptide J	Pig (<i>Sus scrofa</i>)	PAR-2	GTSRPSKGRSLIGKADNT	861
Peptide K	Human	PAR-1	ATNATLDPRSFLLRNPND	862
Peptide L	Human	PAR-3	DTNNLAKPTLPIKTRGA	863
Peptide M	Human	PAR-4	ESGSTGGGDDSTPSILPAP	864

[0115] Anti-PAR-2 antibodies were tested for their ability to bind to the PAR-2 peptides. Various PAR-2 Peptides (Table 3) were coated onto 96-well plates at a concentration of 2 µg/ml and incubated overnight followed by blocking in a suitable blocking agent for one hour. In a similar fashion, for biotinylated peptides (N-Term: N-terminal biotinylated; C-Term: C-terminal biotinylated), avidin was coated on plates at 2 µg/ml followed by incubation with biotinylated PAR-2 peptides at a concentration of 0.2 µg/ml and incubated for one hour. Purified anti-PAR-2 antibodies were added to the plate coated with PAR-2 peptides to a final concentration ranging from 0.2 to 2.0 µg/ml and incubated for one hour at room temperature. Detection of bound antibodies was determined with Horse-Radish Peroxidase (HRP) conjugated anti-mouse or human IgG (Jackson Immuno Research Lab, West Grove, PA) and developed by standard colorimetric response using tetramethylbenzidine (TMB) substrate. Absorbance was read at OD₄₅₀ for 0.1 second.

[0116] Relative binding (+++, ++, +) to unbiotinylated (No Biotin) or biotinylated Peptides A, B and C as compared to no binding (-) for each anti-PAR-2 antibody tested according to the observed OD₄₅₀ value (1.0 – 4.0, 0.50 – 0.99, 0.1 – 0.49, 0.0 – 0.09, respectively) is shown in Table 3. Control: "Sam11," a commercially available mouse monoclonal antibody that binds human PAR-2 (Santa Cruz Biotechnology, Santa Cruz, CA).

Table 3

Antibody	Peptide A			Peptide B			Peptide C	
	No Biotin	N-Term	C-Term	No Biotin	N-Term	C-Term	N-Term	C-Term
H2M588N	+++	+++	+++	+++	+++	+++	-	-
H2M589N	+++	+++	+++	+++	+++	+++	-	-
H1M590N	+++	+++	+++	-	-	-	-	-
H2M591N	+++	+++	+++	+++	+++	+++	-	-
H1M592N	+++	+++	+++	-	++	+++	+++	+++
H1M595N	+++	+++	+++	-	-	-	++	-
H2M609N	+++	+++	+++	-	-	-	-	-
H2M610N	+++	+++	+++	-	-	-	-	-
H2M611N	+++	+++	+++	+++	+++	+++	-	-
H1M612N	+++	+++	+++	-	-	-	-	-

H1M613N	+++	+++	+++	-	++	+++	+++	+++
H2M614N	++	+++	+++	-	-	-	-	-
H1M615N	+++	+++	+++	-	-	-	-	-
H1M616N	+++	+++	+++	-	-	-	-	-
H2M618N	+++	+++	+++	+++	+++	+++	-	-
H1M619N	+++	+++	+++	-	-	-	-	-
H3M620N	+++	++	+++	-	-	-	-	-
Control	-	-	-	+++	+++	+++	-	-

[0117] In a similar experiment, selected anti-PAR-2 antibodies cloned onto a mutant human IgG4 (SEQ ID NO:849) were tested for their ability to bind unbiotinylated and biotinylated forms of human PAR-2 peptides (as described above). Results are shown in Table 4.

Table 4

Antibody	Peptide A			Peptide B			Peptide C	
	No Biotin	N-Term	C-Term	No Biotin	N-Term	C-Term	N-Term	C-Term
H4H572P	-	-	-	-	-	-	-	-
H4H573P	+++	+++	+++	-	-	-	-	-
H4H576P	+	-	-	-	-	-	-	-
H4H578P	+++	+++	+++	-	-	-	-	-
H4H579P	+++	+++	+++	+++	+++	+++	-	-
H4H580P	+++	+++	+++	+++	+++	+++	-	-
H4H581P	+++	+++	+++	+++	+++	+++	++	+
H4H583P	+++	+++	+++	-	-	-	-	-
H4H584P	+++	+++	+++	+++	+++	+++	-	-
H4H585P	+++	+++	+++	+++	+++	+++	+	+
H4H587P	-	-	-	-	-	-	-	+
H4H588N	+++	+++	+++	+++	+++	+++	-	-
H4H591N	+++	+++	+++	+++	+++	+++	-	-
H4H618N	+++	+++	+++	+++	+++	+++	-	-
Control	-	-	-	+++	+++	+++	-	-

[0118] In another experiment, selected anti-PAR-2 antibodies were tested for binding to unbiotinylated Peptides D, K, L and M (as described above). Results for chimeric antibodies (e.g. H2M588N) and fully human antibodies (e.g. H4H572P) are shown in Tables 5 and 6, respectively. For Peptide D, detection of bound antibodies was determined with Horse-Radish Peroxidase (HRP) conjugated anti-mouse κ (Southern Biotech, Birmingham, AL).

Table 5

Antibody	Peptide D	Peptide K	Peptide L	Peptide M
H2M588N	+++	-	-	-
H2M589N	+++	-	-	-
H1M590N	-	-	-	-
H2M591N	+++	-	-	-
H1M592N	+	-	-	-
H1M595N	-	-	-	-
H2M609N	+	-	-	-
H2M610N	-	-	-	-
H2M611N	+	-	-	-
H1M612N	-	-	-	-
H1M613N	+	-	-	-
H2M614N	-	-	-	-
H1M615N	-	-	-	-
H1M616N	-	-	-	-
H2M618N	+++	-	-	-
H1M619N	-	-	-	-
H3M620N	-	-	-	-
Control	+++	-	-	-

Table 6

Antibody	Peptide D	Peptide K	Peptide L	Peptide M
H4H572P	+	-	-	-
H4H573P	+	-	-	-
H4H576P	+	-	-	-
H4H578P	+	-	-	-
H4H579P	+++	-	-	-
H4H580P	+++	-	-	-
H4H581P	+++	+	+	+
H4H583P	++	-	-	-
H4H584P	+++	-	-	-
H4H585P	+++	+	+	+
H4H587P	+	-	-	-
H4H588N	+++	-	-	-
H4H591N	+++	+	+	+
H4H618N	+++	-	-	-
Control	+++	-	-	-

[0119] In another experiment, selected anti-PAR-2 antibodies were tested for binding to N-

terminal biotinylated mouse (Peptide E N-Term) and monkey (Peptide F N-Term) PAR-2 peptides (as described above).

Table 7

Antibody	Peptide E N-Term	Peptide F N-Term
H2M588N	-	+++
H2M589N	-	+++
H1M590N	+++	+++
H2M591N	-	+++
H1M592N	-	-
H1M595N	+++	+++
H2M609N	+++	+++
H2M610N	+++	+++
H2M611N	-	+++
H1M612N	+++	+++
H1M613N	-	-
H2M614N	+++	+++
H1M615N	+++	+++
H1M616N	+++	+++
H2M618N	-	+++
H1M619N	+++	+++
H3M620N	+++	++
Control	-	-

[0120] In another experiment, selected anti-PAR-2 antibodies cloned onto human IgG4 were tested for binding to unbiotinylated and biotinylated forms of Peptides E through J (as described above). Results are shown in Table 8.

Table 8

Antibody	Peptide E		Peptide F N-Term	Peptide G			Peptide H	Peptide I	Peptide J
	No Biotin	N-Term		No Biotin	N-Term	C-Term			
H4H572P	+	-	-	-	-	+	-	-	-
H4H573P	+++	+++	+++	+++	+++	++	+++	+++	+++
H4H576P	+	-	-	-	-	+	-	-	-
H4H578P	+++	+++	+++	+++	+++	+	+++	+++	+++
H4H579P	+++	+++	+++	+++	+++	+++	+	+++	+
H4H580P	+++	+++	+++	+++	+++	+++	-	+++	+
H4H581P	+++	+++	+++	+++	+++	+++	-	+++	+++
H4H583P	+++	+++	+++	+++	+++	+++	+++	+++	+++
H4H584P	+++	+++	+++	+++	+++	+++	-	+++	++
H4H585P	+++	+++	+++	+++	+++	+++	+	+++	+++

H4H587P	-	-	-	-	+	-	-	-	+
H4H588N	-	-	+++	-	+	-	-	-	-
H4H591N	+	+	+++	+	+	+	+	-	+
H4H618N	-	-	+++	-	-	-	-	-	-
Control	-	-	-	-	-	-	-	-	-

[0121] In another experiment, selected anti-PAR-2 antibodies cloned onto human IgG4 were tested for binding to unbiotinylated and biotinylated forms of PAR-2 peptides (Peptides A, E, F and G; as described above). In this experiment, anti-PAR-2 antibodies, serially diluted three-fold from 13.3 nM to 0.22 pM, were incubated on the peptide-coated plates for one hour at room temperature. Absorbance values at 450 nm were analyzed using a sigmoidal dose-response model in GraphPad Prism (GraphPad Software, Inc., La Jolla, CA) and EC₅₀ values were reported (Table 9). EC₅₀ values are defined as the antibody concentration required to achieve 50% maximal binding to PAR-2 peptide.

Table 9

Antibody	EC ₅₀ (nM)								
	Peptide A			Peptide E		Peptide F N-Term	Peptide G		
	No Biotin	C-Term	N-Term	No Biotin	N-Term		No Biotin	C-Term	N-Term
H4H572P	>50	>50	>50	>50	>50	>50	>50	>50	>50
H4H573P	0.093	0.022	0.093	0.355	0.016	0.018	0.014	10.130	0.017
H4H576P	>50	>50	>50	>50	>50	>50	>50	>50	>50
H4H578P	0.034	0.040	0.062	2.778	0.090	0.036	0.046	>50	0.081
H4H579P	0.038	0.076	0.077	0.713	0.540	0.061	0.055	0.044	0.059
H4H580P	0.090	0.202	0.160	2.533	0.932	0.148	0.139	0.100	0.142
H4H581P	0.012	0.028	0.020	0.029	0.032	0.020	0.020	0.013	0.019
H4H583P	0.008	0.018	0.015	0.019	0.014	0.013	0.012	0.630	0.015
H4H584P	0.012	0.015	0.019	2.152	0.511	0.012	0.013	0.015	0.012
H4H585P	0.017	0.021	0.026	0.308	0.189	0.017	0.018	0.021	0.017
H4H587P	>50	>50	>50	>50	>50	>50	>50	>50	>50
H4H588N	0.010	0.016	0.019	>50	>50	0.012	>50	>50	>50
H4H591N	0.010	0.016	0.022	>50	>50	0.011	>50	>50	>50
H4H618N	0.009	0.016	0.021	>50	>50	0.011	>50	>50	>50
Control	>50	>50	>50	>50	>50	>50	>50	>50	>50

[0122] As indicated by the foregoing experiments, antibodies H4H581P, H4H588N, H4H591N or H4H618N all show substantial binding to human Peptides A, B and D, which comprise the sequence SLIGKVDGT (amino acids 10-18 of SEQ ID NO:852), as well as to monkey Peptide F, which comprises the sequence SLIGRVDGT (amino acids 10-18 of SEQ ID NO:857). For antibodies H4H588N, H4H591N and H4H618N, the sequence VDDGT, located downstream from

the activating PAR-2 protease cleavage site, appears to be particularly important for binding since changes to this sequence resulted in substantially reduced or no binding by these antibodies (see, e.g., binding data for Peptides E (mouse), G (rat), H (rabbit), I (dog) and J (pig)).

Example 4. Antigen Binding Affinity Determination

[0123] Equilibrium dissociation constants (K_D values) for antigen binding to selected purified PAR-2 antibodies were determined by surface kinetics using a real-time surface plasmon resonance biosensor assay. Antibody was captured on either a rabbit anti-mouse IgG polyclonal antibody (GE Healthcare, Piscataway, NJ) surface or a goat anti-human IgG polyclonal antibody (Jackson Immuno Research Lab, West Grove, PA) surface created through direct amine chemical coupling to a BIACORE™ CM5 sensor chip to form a captured antibody surface. Various concentrations (ranging from 15.6 to 250 nM) of monomeric human PAR-2 peptides (Peptides A and B) were injected at a rate of 100 μ l/min over the captured antibody surface for 90 seconds. Antigen-antibody binding and dissociation were monitored in real time at room temperature. Kinetic analysis was performed to calculate K_D and half-life of antigen/antibody complex dissociation (Table 10). For those antibodies where no $T_{1/2}$ value is shown, steady state analysis was used to calculate the K_D value. NB: no binding observed under current experimental conditions. ND: not determined.

Table 10

Antibody	Peptide A		Peptide B	
	K_D (nM)	$T_{1/2}$ (min)	K_D (nM)	$T_{1/2}$ (min)
H4H572P	NB	-	ND	-
H4H573P	749	-	ND	-
H4H576P	NB	-	ND	-
H4H578P	245	0.17	ND	-
H4H579P	15	4	>500	-
H4H580P	103	0.88	ND	-
H4H581P	9.44	1.4	>500	-
H4H583P	37.1	0.37	NB	-
H4H584P	22	0.73	>500	-
H4H585P	8.78	3.7	>500	-
H4H587P	NB	-	ND	-
H1M590N	173	-	ND	-
H1M592N	2100	-	ND	-
H1M595N	510	-	ND	-
H1M612N	180	-	ND	-
H1M613N	2100	-	ND	-
H1M615N	162	-	ND	-

H1M616N	144	-	ND	-
H1M619N	164	-	ND	-
H2M588N	4.47	60.8	61.7	7.7
H2M589N	3.75	51.3	128	7.3
H2M591N	4.22	42.7	151	8.1
H2M610N	71.3	-	360	0.8
H2M611N	72.8	4.1	1090	1.2
H2M614N	470	-	ND	-
H2M618N	9.62	6.7	126	3.5
Control	NB	-	149	0.1

[0124] In a similar experiment, K_D values for binding to unbiotinylated monomeric mouse (Peptide E) and N-terminal biotinylated monkey (Peptide F N-Term) PAR-2 peptides of selected antibodies cloned onto human IgG4 were determined (as described above) (Table 11). Antibodies H4H588N, H4H591N, and H4H618N did not bind Peptide E, while the Control antibody did not bind to either Peptide E or F.

Table 11

Antibody	Peptide F N-Term	
	K_D (nM)	$T_{1/2}$ (min)
H4H588N	7.10	24
H4H591N	8.54	21
H4H618N	13.8	5

[0125] In another series of experiments, equilibrium dissociation constants (K_D values) for purified antibody binding to selected biotinylated and unbiotinylated forms of PAR-2 peptides were determined by surface kinetics using a real-time surface plasmon resonance biosensor assay. Neutravidin (Pierce, Rockford, IL) was covalently coupled to the surface of a Biacore™ C1 chip or CM5 chip using amine coupling chemistry. Biotinylated (N-Term or C-Term) PAR-2 peptides (Peptides A and B) were immobilized on the surface via the high affinity binding interaction between biotin and the amine coupled Neutravidin.

[0126] In a first experiment using this format, varying concentrations (ranging from 5 to 100 $\mu\text{g/ml}$) of purified antibody were injected at a rate of 50 $\mu\text{l/min}$ over a surface coated with immobilized peptide at low-density (<1RU) for 300 seconds. Antibody-peptide binding and dissociation was monitored in real time 25°C (Table 12).

Table 12

Antibody	Peptide A C-Term		Peptide B C-Term	
	K _D (nM)	T _{1/2} (min)	K _D (nM)	T _{1/2} (min)
H2M588N	0.826	169	1.49	140
H1M590N	1.27	13	NB	-
H2M591N	0.545	209	1.82	94
H2M618N	1.8	79	2.32	60
Control	NB	-	0.99	19

[0127] In another similar experiment, K_D values for binding to a low-density surface (<1RU) of biotinylated forms of Peptides A, B, C, E, F and G of selected antibodies cloned onto human IgG4 were determined (as described above). Results for binding to C-terminal and N-terminal biotinylated PAR-2 peptides are shown in Tables 13-14, respectively. In this experiment, only antibody H4H581P demonstrated affinity for N-terminal biotinylated Peptide C (K_D of >100 nM), while all other antibodies tested, including the control, showed no binding to this peptide.

Table 13

Antibody	Peptide A C-Term		Peptide B C-Term	
	K _D (nM)	T _{1/2} (min)	K _D (nM)	T _{1/2} (min)
H4H579P	0.143	479	0.453	96
H4H581P	0.237	134	0.346	49
H4H583P	0.898	34	NB	-
H4H584P	0.688	55	1.66	15
H4H585P	0.151	493	0.376	123
H4H588N	0.517	141	1.03	70
H4H590N	3.56	3	NB	-
Control	NB	-	0.935	14

Table 14

Antibody	Peptide A N-Term		Peptide B N-Term		Peptide E N-Term		Peptide F N-Term		Peptide G N-Term	
	K _D (nM)	T _{1/2} (min)	K _D (nM)	T _{1/2} (min)	K _D (nM)	T _{1/2} (min)	K _D (nM)	T _{1/2} (min)	K _D (nM)	T _{1/2} (min)
H4H579P	1.61	46	5.44	55	3.40	20	0.796	70	1.16	38
H4H581P	0.498	41	2.72	38	1.13	21	0.272	78	0.354	62
H4H583P	0.412	46	NB	-	1.68	11	0.291	73	1.49	13
H4H584P	0.525	43	3.20	30	>100	-	0.565	40	1.39	15
H4H585P	1.69	48	5.41	63	>100	-	0.899	66	1.36	35

H4H588N	1.05	189	0.0272	>1155	NB	-	1.81	94	NB	-
H4H590N	1.52	3	NB	-	1.28	7	1.84	2	2.94	2
Control	NB	-	0.279	32	NB	-	NB	-	NB	-

[0128] In a similar experiment, K_D values for binding to monomeric biotinylated and unbiotinylated forms of PAR-2 peptides (Peptides A, B, E – M) for selected antibodies cloned onto human IgG4 were determined (as described above for the captured antibody surface). Results are shown in Tables 15-16. None of the antibodies tested showed binding to Peptides K, L or M.

Table 15

Antibody	Peptide A		Peptide B		Peptide E	
	K_D (nM)	$T_{1/2}$ (min)	K_D (nM)	$T_{1/2}$ (min)	K_D (nM)	$T_{1/2}$ (min)
H4H579P	15	4.1	>500	-	>500	-
H4H581P	9.44	1.4	>500	-	>500	-
H4H583P	37.1	0.37	NB	-	>500	-
H4H584P	22	0.73	NB	-	NB	-
H4H585P	8.78	3.7	>500	-	>500	-
H4H588N	4.95	25.1	84	9	NB	-
H4H590N	>500	-	NB	-	>500	-
Control	ND	-	149	0.1	ND	-

Table 16

Antibody	Peptide F N-Term		Peptide G		Peptide H		Peptide I		Peptide J	
	K_D (nM)	$T_{1/2}$ (min)	K_D (nM)	$T_{1/2}$ (min)	K_D (nM)	$T_{1/2}$ (min)	K_D (nM)	$T_{1/2}$ (min)	K_D (nM)	$T_{1/2}$ (min)
H4H579P	49.4	2	134	0.45	NB	-	311	0.26	NB	-
H4H581P	36.6	0.53	40.2	0.63	NB	-	143	0.07	NB	-
H4H583P	112	0.47	530	0.07	189	0.17	320	0.16	190	0.16
H4H584P	93.3	0.23	246	0.13	NB	-	>500	-	NB	-
H4H585P	46.2	2	162	0.33	NB	-	372	0.19	NB	-
H4H588N	10.8	20	NB	-	NB	-	NB	-	NB	-
H4H590N	>500	-	>500	-	>500	-	>500	-	>500	-

Example 5. Antibody Binding to Cells Engineered to Express PAR-2

[0129] To further characterize anti-PAR-2 antibodies, cells of the human embryonic kidney 293 cell line (HEK293) were genetically engineered to overexpress either full length human (SEQ ID NO:851) or mouse (SEQ ID NO:866) PAR-2.

[0130] HEK293 cells were transfected with an NF- κ B-luciferase-IRES-eGFP reporter plasmid.

Stability of transfected cells was demonstrated by response to IL-1 β as detected by eGFP expression through flow cytometry and luciferase activity. A clonal cell line, named D9, having low background levels of luciferase activity and high levels of eGFP when induced with IL-1 β was made by a series of successive sorts of cell populations using flow cytometry. The 293/D9 cell line was then separately transfected with human PAR-2 or mouse PAR-2 to create the stable cell lines 293/D9/hPAR-2rec and 293/D9/mPAR-2rec, respectively.

[0131] Binding of anti-PAR-2 antibodies to 293/D9/hPAR-2rec cells was determined by ELISA. 293/D9 and 293/D9/hPAR-2rec cells were plated at a density of 5×10^4 cells/well in media and incubated overnight at 37°C and 5% CO₂. Purified antibody was added to the cells to a final concentration of 10 μ g/ml and incubated at room temperature for one hour. Cells were then fixed and washed before detection of bound antibodies with HRP conjugated anti-mouse IgG and developed by standard colorimetric response using TMB substrate. Absorbance was read at OD₄₅₀ for 0.1 second. The A₄₅₀ ratio of antibody binding to 293/D9/hPAR-2rec cells compared to 293/D9 cells is shown in Table 17.

Table 17

Antibody	A ₄₅₀ ratio
H2M588N	2.50
H2M589N	2.03
H1M590N	1.81
H2M591N	2.25
H1M592N	1.25
H1M595N	1.80
H2M609N	1.54
H2M610N	1.66
H2M611N	1.76
H1M612N	1.90
H1M613N	1.27
H2M614N	1.17
H1M615N	2.18
H1M616N	2.78
H2M618N	2.44
H1M619N	1.51
H3M620N	1.24
Control	1.49

[0132] In a similar experiment, anti-PAR-2 antibodies were tested for binding to 293/D9, 293/D9/hPAR-2rec and 293/D9/mPAR-2rec cells using electro-chemiluminescence technology (Meso Scale Discovery, MSD, Gaithersburg, MD). Cells were plated on MSD high-bind 96 well

plates at a density of 4×10^4 cells/well in PBS and incubated for one hour at room temperature. Cells were then blocked in PBS with 2% BSA and incubated at room temperature for one hour. Anti-PAR-2 antibodies (ranging from 100 nM to 0.098 nM) were serially diluted two-fold in PBS with 0.5% BSA and incubated with the cells for one hour at room temperature followed by washing in PBS with 0.5% BSA. Sulfo-tagged anti-human IgG antibody (MSD) at a concentration of 0.1 $\mu\text{g/ml}$ was then added to the cell/antibody mixture and incubated at room temperature for an additional hour. After another wash, a 1X non-surfactant containing read buffer was added and electro-chemiluminescent signal was read on the MSD Sector Imager. Signal of antibody binding to 293/D9 cells was subtracted from signal to 293/D9/hPAR-2rec or 293/D9/mPAR-2rec cells. Subtracted data were analyzed using a sigmoidal dose-response model in GraphPad Prism and EC_{50} and B_{max} values were reported (Table 18). EC_{50} values are defined as the antibody concentration required to achieve 50% maximal binding (B_{max}) to cells.

Table 18

Antibody	293/D9/hPAR-2rec		293/D9/mPAR-2rec	
	EC_{50} (nM)	B_{max} (MSD Unit)	EC_{50} (nM)	B_{max} (MSD Unit)
H4H579P	1.86	25049	NB	-
H4H580P	8.69	30177	NB	-
H4H581P	0.652	28224	NB	-
H4H583P	2.12	13252	9.28	7219
H4H584P	1.45	26044	NB	-
H4H585P	1.95	22540	NB	-
H4H588N	5.95	27549	NB	-
H4H590N	9.72	6554	5.76	13255

Example 6. *In vitro* Blocking of Human PAR-2 Activation By Anti-PAR-2 Antibodies

[0133] Blocking of PAR-2 activation (signaling) was determined by binding of selected purified anti-PAR-2 antibodies to 293/D9/hPAR-2rec cells (see Example 5) by a luciferase assay. 293/D9/hPAR-2rec cells were plated at a concentration ranging from 5×10^4 to 10^5 cells/well in a 96 well plate in low serum media and incubated overnight at 37°C with 5% CO_2 . The media was removed and purified anti-PAR-2 antibodies were added to the cells at various concentrations (ranging from 51 pM to 1 μM) and incubated for one hour at 37°C with 5% CO_2 . Various concentrations of different serine proteases (Trypsin, Human Trypsin 1, Factor Xa and Lung Tryptase) were then added separately to the cell/antibody mixture and incubated for five hours at 37°C with 5% CO_2 . Proteolytic cleavage of PAR-2 in this assay leads to expression of the NF- κB -luciferase reporter construct, whereas a reduced or attenuated level of luciferase signal indicates inhibition of PAR-2 cleavage. IC_{50} values are shown in Table 19. ND: not determined.

Table 19

Antibody	IC ₅₀ (nM)							
	Trypsin					10 nM Human Trypsin 1	200 nM Factor Xa	750 nM Lung Tryptase
	250 nM	75 nM	30 nM	20 nM	10 nM			
H2M588N	2.3	5.7	33.0	26.8	10.4	164.9	45.3	1.0
H2M589N	6.3	3.7	ND	ND	ND	ND	ND	ND
H1M591N	4.5	ND	ND	121.8	24.2	149.6	51.5	88.1
H2M618N	6.6	7.8	ND	70	12.4	153.5	54.2	7.0

[0134] As shown in Table 20, antibodies H4H581P, H4H588N, H4H591N and H4H618N were able to significantly block protease activation of PAR-2 in reporter cells. By contrast, anti-PAR-2 antibodies H4H592N, H4H595N, H4H611N, H4H613N, H4H614N, H4H615N, H4H616N, H4H617N and H4H619N did not demonstrate any measurable blocking of PAR-2 cleavage/activation in this assay (data not shown).

Table 20

Antibody	20 nM Trypsin IC ₅₀ (nM)
H4H579P	4.1
H4H580P	3.5
H4H581P	1.1
H4H583P	14
H4H584P	5.6
H4H585P	8.9
H4H588N	16.9
H4H591N	204.1
H4H618N	50.2

[0135] Under the experimental conditions used in this Example, no blocking of PAR-2 signaling was observed for antibodies H4H572P, H4H573P, H4H576P, H4H578P or H4H587P, whereas significant blockage (to varying degrees) was observed with antibodies H4H579P, H4H580P, H4H581P, H4H583P, H4H584P, H4H585P, H4H588N, H4H591N and H4H618N.

[0136] In another similar experiment, antibody blocking of PAR-2 signaling mediated by human Trypsin 1, Factor Xa and Lung Tryptase was determined for selected purified anti-PAR-2 antibodies cloned onto human IgG4 (as described above). Results are shown in Table 21.

Table 21. IC₅₀ (nM)

Antibody	10 nM Human Trypsin 1	200 nM Factor Xa	750 nM Lung Tryptase
H4H581P	7.4	5.3	1.1
H4H588N	42.7	17.1	1.6
H4H591N	104.7	74.6	62.9
H4H618N	92.2	47.2	8.5

[0137] HEK293/NFκB-luciferase cells expressing human, monkey, mouse or rat PAR-2 were treated with various proteases after preincubation with increasing amounts of anti-PAR-2 antibody H4H581P, and the IC₅₀ was determined. Results are summarized in Table 22.

Table 22

Activator (6h)	PAR-2 Species	EC ₅₀ (nM)	H4H581P IC ₅₀ (nm)
Human Pancreatic Trypsin	Human	0.8	1.9
	mouse	1.4	491.0
	monkey	2.4	5.4
	rat	6.0	700.0
Human Kallikrein 5	Human	28.0	0.9
	mouse	ND	ND
	monkey	16.8	11
Human Kallikrein 14	Human	5.0	1.2
	mouse	8.0	256.0
	monkey	6.3	11.6
Bovine Factor Xa	Human	27.2	2.5
	mouse	46.3	340.4
	monkey	58.2	0.9
Human Factor Xa	Human	46.3	1.1
	mouse	78.7	109
	monkey	ND	ND
Tryptase	Human	61.1	3.5
	mouse	ND	ND
	monkey	ND	ND

[0138] Under the particular experimental conditions used, the H4H581P antibody effectively inhibited protease-activation of human and monkey PAR-2, but not mouse or rat PAR-2.

Example 7. *In vitro* Antibody Blocking of Human PAR-2 Dependent Calcium Mobilization

[0139] Blocking of trypsin-stimulated PAR-2 activation (signaling) was determined by treating

HEK293 cells with selected purified anti-PAR-2 antibodies cloned onto human IgG4 in a calcium mobilization FLIPR assay (Molecular Devices, Sunnyvale, CA). Also tested in this assay was a non-PAR-2 specific control antibody.

[0140] Briefly, 8×10^4 HEK293 cells were plated on Poly-D-Lysine plates (BD Biosciences, San Jose, CA) in low serum media (DME with 0.5% FBS) and incubated overnight at 37°C with 5% CO₂. The following day cells were incubated with various concentrations (ranging from 0 to 1 μ M) of selected anti-PAR-2 antibodies, or a control antibody, followed by the addition of trypsin. Trypsin-mediated activation of PAR-2 is indicated by calcium mobilization. In-cell measurement of calcium signaling was measured using a Fluo-4 NW Calcium Assay Kit (Invitrogen, Carlsbad, CA) on a FlexStation 3 (Molecular Devices, Sunnyvale, CA). The antibody concentration necessary to cause half-maximal inhibition of trypsin-mediated calcium signaling (IC₅₀) was measured for each experimental and control antibody. Results are shown in Table 23 as IC₅₀ (nM).

Table 23

Antibody	100 nM Trypsin
H4H581P	54.96
H4H588N	29.47
Non-Specific Control	> 1000

[0141] As shown in this Example, antibodies H4H581P and H4H588N each inhibited trypsin-stimulated calcium signaling to a significant extent as compared to the control antibody.

Example 8. *In vitro* Blocking of Trypsin-mediated Cleavage of PAR-2 Peptides

[0142] A Matrix Assisted Laser Desorption Ionization – Time of Flight (MALDI-TOF) assay was developed to determine the ability of selected purified anti-PAR-2 antibodies to block Trypsin-mediated cleavage of human PAR-2 peptide (Peptide A, SEQ ID NO:852). Biotinylated versions of Peptide A (containing C-terminal or N-terminal biotin) were mixed with anti-PAR-2 antibody to achieve a 3:1 molar ratio of antibody to peptide, and then trypsin was added to the peptide-antibody mixture. Biotinylated peptides were recovered by immuno-precipitation (IP) via mono-avidin and analyzed by MALDI-TOF.

[0143] In a typical experiment, selected purified anti-PAR-2 antibodies cloned onto human IgG4 (H4H581P and H4H588N) were tested for their ability to block Trypsin-mediated cleavage of the biotinylated PAR-2 peptides. A non-PAR-2-specific antibody of the same isotype was used as a negative control ("Neg Ctrl" in Fig. 3). For H4H581P and the negative control antibody, biotinylated peptides were used at a final concentration of 4.75 μ M and antibodies were used at 14.25 μ M. For H4H588N, biotinylated peptides were used at a final concentration of 2.45 μ M and the antibody at 7.35 μ M. Peptide and antibody were mixed in PBS and allowed to come to equilibrium for 1 hr at room temperature. Trypsin (96 ng) was then added and the

mixture incubated at 37°C for 0, 5, 10 and 15 minutes. At each time point an aliquot equaling 100 ng of biotinylated peptide was removed and mixed with 10 µl of monomeric avidin resin (Pierce) for 1 minute. The bound peptides were rinsed 3x with 200 µl of PBS and then eluted with 20 µl of 100 mM glycine pH 2.5. Salt was removed from the eluted peptide mixture using ZipTips (Millipore). The molecular weights of the major biotinylated PAR-2 peptides produced after trypsin cleavage, as revealed by MALDI-TOF analysis, are summarized in Fig. 3.

[0144] The PAR-2 peptides used in these experiments contain two R/S protease cleavage sites. The first site (designated site "(1)" in Fig. 3) is an "upstream" cleavage site located N-terminal to the activating PAR-2 protease cleavage site. The activating PAR-2 protease cleavage site (designated site "(2)" in Fig. 3) is the site which, when cleaved, results in the formation of the PAR-2 tethered ligand in the naturally occurring protein. The sizes of the peptides detected following cleavage at the different sites are shown in the top portion of Fig. 3 (panel A).

[0145] As indicated in Fig. 3 (panel B), the C-terminal biotin PAR-2 peptide, when treated with the isotype-matched control antibody, followed by trypsin incubation, produced a cleavage fragment of 1558 Da (containing residues 10-18 of SEQ ID NO:852). The 1558 Da fragment is the result of cleavage at the activating PAR-2 protease cleavage site (2). This cleavage pattern was also observed in the experiment using the H4H588N anti-PAR-2 antibody. Thus, according to this assay, neither the control antibody nor the H4H588N antibody inhibit trypsin cleavage at the activating PAR-2 protease cleavage site (2).

[0146] By contrast, the C-terminal biotin PAR-2 peptide, when treated with the H4H581P antibody, followed by trypsin incubation, produced a cleavage fragment of 2073 Da (containing residues 5-18 of SEQ ID NO:852). The 2073 Da fragment is the fragment produced by cleavage at the upstream cleavage site (1) only. Thus, cleavage at the activating PAR-2 protease cleavage site (2) was apparently blocked by the H4H581P antibody.

[0147] Experiments with the N-terminal biotin PAR-2 peptide showed trypsin cleavage at the upstream cleavage site (1) and thus produced a 988 Da N-biotinylated fragment (containing residues 1-4 of SEQ ID NO:852) in the presence of all antibodies tested. Therefore, none of the antibodies tested blocked cleavage at the upstream cleavage site (1) under these experimental conditions.

[0148] As shown in Examples 6 and 7 above, both H4H581P and H4H588N blocked PAR-2 activation by trypsin in cell-based assays. In the present Example, however, only H4H581P blocked trypsin cleavage at the activating PAR-2 protease cleavage site. Without being bound by any mechanistic theory, it therefore appears that H4H588N may exert its inhibitory effect(s) by interfering with the interaction between the tethered ligand and one or more extracellular loops (*e.g.*, loop 1, loop 2 and/or loop 3) of PAR-2. On the other hand, H4H581P may inhibit PAR-2 activity primarily by blocking protease cleavage but may also interfere with tethered ligand interactions as well.

[0149] To further investigate the protease cleavage-blocking properties of anti-PAR-2 antibodies, additional MALDI-TOF experiments were conducted using C-terminal biotinylated mouse, rat and human PAR-2 peptides. (See Fig. 4). The antibodies tested in these experiments were H4H581P, H4H588N, a comparator antibody having the heavy and light chain variable regions of the antibody referred to as "1A1" in WO 2009/005726 (referred to in Fig. 5 as "Comp. Ab"), and a negative control antibody (referred to in Fig. 4 as "Neg Ctrl"). The same experimental procedures that were used in the previous MALD-TOF experiment (described above) were used in this experiment as well.

[0150] The peptides used in these experiments each possess multiple sites capable of being cleaved by trypsin (designated "(1)," "(2)," and "(3)" in Fig. 5.) Site (3) for each peptide is the activating protease cleavage site. The sizes of the peptides produced following cleavage at the different sites are shown in the top portion (panel A) of Fig. 4.

[0151] As summarized in Fig. 4, the biotinylated human PAR-2 peptide, after being treated with H4H581P, and following trypsin incubation, produced a 2074 kDa peptide which corresponds to cleavage at site (1) only. Thus, H4H581P blocks cleavage at both site (2) and at site (3). By contrast, the human PAR-2 peptide, after being treated with the comparator antibody, and following trypsin incubation, remained at 2502 kDa which signifies no cleavage. Thus, the comparator antibody blocks all three protease cleavage sites in this assay, including the N-terminal-most site (1). When pre-treated with antibody H4H588N, the human PAR-2 peptide produces both a 1772 kDa and a 1558 kDa fragment following trypsin cleavage. This cleavage pattern suggests that H4H588N partially blocks cleavage at the activating site (3) but completely blocks the middle site (2).

[0152] This experiment was also conducted using a comparator antibody having the heavy and light chain variable regions of the antibody referred to as Sam-11 (Molino *et al.*, *Arterioscler. Thromb. Vasc. Biol.* 18:825-832 (1998)). As expected, this particular comparator antibody did not block cleavage at any of the protease cleavage sites (data not shown).

Example 9. Epitope Mapping by Alanine Scanning Mutagenesis of PAR-2 Peptide

[0153] In order to more particularly identify the amino acids of PAR-2 with which the PAR-2 antibodies interact, an alanine scanning study was carried out using peptides comprising the activating PAR-2 protease cleavage site. For these experiments, 11 separate C-terminal biotinylated peptides were synthesized in which each amino acid from position 35 through 45 of human PAR-2 (SEQ ID NO:851) was individually replaced with an alanine (SEQ ID NOs: 871-882). An additional set of C-terminal biotinylated peptides was also used which comprise the 14 amino acids located immediately C-terminal to the activating PAR-2 protease cleavage site, with Val-42 and/or Asp-43 changed to alanine (SEQ ID NOs: 884-887).

[0154] The ability of each peptide mutant to bind to PAR-2 antibodies was measured using biolayer interferometry (Octet Red; ForteBio). Each peptide (2.5µg/ml) was captured on streptavidin coated biosensor tips (Octet SA sensor) for 10 seconds. To measure binding and

dissociation between each peptide and PAR-2 antibody, the peptide-coated biosensors were contacted with 200nM solutions of PAR-2 antibodies for 5 minutes (binding) followed by transfer to buffer with no antibody for 10 min (dissociation). The binding of PAR-2 antibody to each peptide was expressed as percent native signal after dividing individual antibody binding signals by the original peptide loading signal observed for that peptide, to correct for slight variations in peptide loading on the individual biosensors. Dissociation half-lives ($T_{1/2}$) were calculated from the dissociation curves using the Scrubber version 2.0a curve-fitting software, and relative half-lives were calculated by dividing observed half-lives for an individual peptide by the half-life of the native peptide. The results are expressed as percent binding and percent $T_{1/2}$ relative to WT peptide (Tables 24-28). [Comparator 1 = an antibody having the heavy and light chain variable regions of the antibody referred to as "1A1" in WO 2009/005726; Comparator 2 = an antibody having the heavy and light chain variable regions of the antibody referred to as Sam-11 (Molino *et al.*, Arterioscler. Thromb. Vasc. Biol. 18:825-832 (1998)); and Comparator 3 = an antibody having the heavy and light chain variable regions of the antibody referred to as "PAR-B" in US 2010/0119506]. In certain cases, the binding experiments were repeated (indicated under the column headings Exp1 and Exp2). NB = no binding observed.

Table 24: H4H581P

SEQ ID NO:	SEQUENCE	% Rel Binding		% Rel $T_{1/2}$	
		Exp1	Exp2	Exp1	Exp2
871	GTNRSSKGRSLIGKVDGT-----GGGGSK-B	100	100	100	100
872	GTNRSSK <u>A</u> RSKSLIGKVDGT-----GGGGSK-B	78	97	118	117
873	GTNRSSK <u>G</u> ASLIGKVDGT-----GGGGSK-B	87	105	122	90
874	GTNRSSKGR <u>A</u> LIGKVDGT-----GGGGSK-B	45	56	7	3
875	GTNRSSKGRS <u>A</u> IGKVDGT-----GGGGSK-B	9	19	0.4	0
876	GTNRSSKGRSL <u>A</u> GKVDGT-----GGGGSK-B	8	14	0.2	0
877	GTNRSSKGRSLI <u>A</u> KVDGT-----GGGGSK-B	101	92	33	15
878	GTNRSSKGRSLIG <u>A</u> VDGT-----GGGGSK-B	113	109	63	49
879	GTNRSSKGRSLIGK <u>A</u> DGT-----GGGGSK-B	36	46	1	1
880	GTNRSSKGRSLIGKV <u>A</u> GT-----GGGGSK-B	18	5	36	4
881	GTNRSSKGRSLIGKVD <u>A</u> T-----GGGGSK-B	67	102	117	124
882	GTNRSSKGRSLIGKVDG <u>A</u> -----GGGGSK-B	65	91	129	94

884	SLIGKVDGTSHVTG-GGGGSK-B	---	100	---	100
885	SLIGK <u>A</u> DGTSHVTG-GGGGSK-B	---	19	---	0
886	SLIGKV <u>A</u> GTSHVTG-GGGGSK-B	---	NB	---	NB
887	SLIGK <u>AA</u> GTSHVTG-GGGGSK-B	---	NB	---	NB

Table 25: H4H588N

SEQ ID NO:	SEQUENCE	% Rel Binding		% Rel T _½	
		Exp1	Exp2	Exp1	Exp2
871	GTNRSSKGRSLIGKVDGT-----GGGGSK-B	100	100	100	100
872	GTNRSSK <u>A</u> RSKSLIGKVDGT-----GGGGSK-B	122	99	100	253
873	GTNRSSK <u>G</u> ASLIGKVDGT-----GGGGSK-B	208	115	100	180
874	GTNRSSKGR <u>A</u> LIGKVDGT-----GGGGSK-B	119	93	100	70
875	GTNRSSKGRS <u>A</u> IGKVDGT-----GGGGSK-B	127	105	100	42
876	GTNRSSKGRSL <u>A</u> GKVDGT-----GGGGSK-B	92	85	36	8
877	GTNRSSKGRSLI <u>A</u> KVDGT-----GGGGSK-B	30	30	1	0
878	GTNRSSKGRSLIG <u>A</u> VDGT-----GGGGSK-B	217	121	108	60
879	GTNRSSKGRSLIGK <u>A</u> DGT-----GGGGSK-B	74	52	1	0
880	GTNRSSKGRSLIGKV <u>A</u> GT-----GGGGSK-B	35	8	4	5
881	GTNRSSKGRSLIGKVD <u>A</u> T-----GGGGSK-B	81	67	1	1
882	GTNRSSKGRSLIGKVDG <u>A</u> -----GGGGSK-B	125	121	94	33
884	SLIGKVDGTSHVTG-GGGGSK-B	---	100	---	100
885	SLIGK <u>A</u> DGTSHVTG-GGGGSK-B	---	83	---	0
886	SLIGKV <u>A</u> GTSHVTG-GGGGSK-B	---	NB	---	NB
887	SLIGK <u>AA</u> GTSHVTG-GGGGSK-B	---	NB	---	NB

Table 26: Comparator 1

SEQ ID NO:	SEQUENCE	% Rel Binding		% Rel T _½	
		Exp1	Exp2	Exp1	Exp2
871	GTNRSSKGRSLIGKVDGT-----GGGGSK-B	100	100	100	100
872	GTNRSSK <u>A</u> RSKSLIGKVDGT-----GGGGSK-B	111	111	29	27

873	GTNRSSKGA <u>SL</u> IGKVDGT-----GGGGSK-B	135	87	0.2	0
874	GTNRSSKGR <u>AL</u> IGKVDGT-----GGGGSK-B	126	102	223	148
875	GTNRSSKGRS <u>A</u> IGKVDGT-----GGGGSK-B	147	105	2	1
876	GTNRSSKGRSL <u>A</u> GKVDGT-----GGGGSK-B	156	108	47	41
877	GTNRSSKGRSLI <u>A</u> KVDGT-----GGGGSK-B	139	108	31	24
878	GTNRSSKGRSLIG <u>A</u> VDGT-----GGGGSK-B	118	84	3	2
879	GTNRSSKGRSLIGK <u>A</u> DGT-----GGGGSK-B	148	104	173	100
880	GTNRSSKGRSLIGKV <u>A</u> GT-----GGGGSK-B	124	102	192	111
881	GTNRSSKGRSLIGKVD <u>A</u> T-----GGGGSK-B	119	97	130	121
882	GTNRSSKGRSLIGKVDG <u>A</u> -----GGGGSK-B	132	119	154	116
884	SLIGKVDGTSHVTG-GGGGSK-B	---	NB	---	NB
885	SLIGK <u>A</u> DGTSHVTG-GGGGSK-B	---	NB	---	NB
886	SLIGKV <u>A</u> GTSHVTG-GGGGSK-B	---	NB	---	NB
887	SLIGK <u>AA</u> GTSHVTG-GGGGSK-B	---	NB	---	NB

Table 27: Comparator 2

SEQ ID NO:	SEQUENCE	% Rel Binding		% Rel T _{1/2}	
		Exp1	Exp2	Exp1	Exp2
871	GTNRSSKGRSLIGKVDGT-----GGGGSK-B	---	NB	---	NB
872	GTNRSSK <u>A</u> RSIGKVDGT-----GGGGSK-B	---	NB	---	NB
873	GTNRSSKGA <u>SL</u> IGKVDGT-----GGGGSK-B	---	NB	---	NB
874	GTNRSSKGR <u>AL</u> IGKVDGT-----GGGGSK-B	---	NB	---	NB
875	GTNRSSKGRS <u>A</u> IGKVDGT-----GGGGSK-B	---	NB	---	NB
876	GTNRSSKGRSL <u>A</u> GKVDGT-----GGGGSK-B	---	NB	---	NB
877	GTNRSSKGRSLI <u>A</u> KVDGT-----GGGGSK-B	---	NB	---	NB
878	GTNRSSKGRSLIG <u>A</u> VDGT-----GGGGSK-B	---	NB	---	NB
879	GTNRSSKGRSLIGK <u>A</u> DGT-----GGGGSK-B	---	NB	---	NB
880	GTNRSSKGRSLIGKV <u>A</u> GT-----GGGGSK-B	---	NB	---	NB

881	GTNRSSKGRSLIGKVD <u>A</u> T-----GGGGSK-B	---	NB	---	NB
882	GTNRSSKGRSLIGKVD <u>C</u> A-----GGGGSK-B	---	NB	---	NB
884	SLIGKVDGTSHVTG-GGGGSK-B	---	100	---	100
885	SLIGK <u>A</u> DGTSHVTG-GGGGSK-B	---	120	---	159
886	SLIGKV <u>A</u> GTSHVTG-GGGGSK-B	---	88	---	27
887	SLIGK <u>AA</u> GTSHVTG-GGGGSK-B	---	87	---	27

Table 28: Comparator 3

SEQ ID NO:	SEQUENCE	% Rel Binding		% Rel T _{1/2}	
		Exp1	Exp2	Exp1	Exp2
871	GTNRSSKGRSLIGKVDGT-----GGGGSK-B	---	100	---	100
872	GTNRSSK <u>A</u> RSLIGKVDGT-----GGGGSK-B	---	101	---	109
873	GTNRSSK <u>G</u> ASLIGKVDGT-----GGGGSK-B	---	98	---	7
874	GTNRSSKGR <u>A</u> LIGKVDGT-----GGGGSK-B	---	106	---	21
875	GTNRSSKGRS <u>A</u> IGKVDGT-----GGGGSK-B	---	115	---	79
876	GTNRSSKGRSL <u>A</u> GKVDGT-----GGGGSK-B	---	92	---	7
877	GTNRSSKGRSLI <u>A</u> KVDGT-----GGGGSK-B	---	101	---	8
878	GTNRSSKGRSLIG <u>A</u> VDGT-----GGGGSK-B	---	109	---	95
879	GTNRSSKGRSLIGK <u>A</u> DGT-----GGGGSK-B	---	96	---	98
880	GTNRSSKGRSLIGKV <u>A</u> CT-----GGGGSK-B	---	99	---	120
881	GTNRSSKGRSLIGKVD <u>A</u> T-----GGGGSK-B	---	93	---	128
882	GTNRSSKGRSLIGKVD <u>C</u> A-----GGGGSK-B	---	117	---	118
884	SLIGKVDGTSHVTG-GGGGSK-B	---	NB	---	NB
885	SLIGK <u>A</u> DGTSHVTG-GGGGSK-B	---	NB	---	NB
886	SLIGKV <u>A</u> GTSHVTG-GGGGSK-B	---	NB	---	NB
887	SLIGK <u>AA</u> GTSHVTG-GGGGSK-B	---	NB	---	NB

[0155] The results from the alanine scanning experiments are summarized in Fig. 5, where the black circles indicate amino acids of PAR-2 which, when changed to alanine, substantially reduce binding by the corresponding antibody (*i.e.*, the T_{1/2} of antibody binding to the mutated peptide is less than 30% of the T_{1/2} of antibody binding to the wild-type peptide). (Open

triangles in Fig. 5 indicate non-activating upstream protease cleavage sites, and the black triangle indicates the activating protease cleavage site). As illustrated in Fig. 5, Comparators 1 and 3 were sensitive to mutations at residues on both sides of the activating protease cleavage site. By contrast, antibodies H4H581P and H4H588N are only sensitive to mutations at residues which are found C-terminal to the activating protease cleavage site. Thus, the H4H581P binding site on PAR-2 appears to be shifted by about 2-4 amino acids in the C-terminal direction relative to binding site of the Comparator 1 and 3 antibodies, and the H4H588N binding site is shifted by about 2-4 amino acids in the C-terminal direction from the H4H581P binding site. The Comparator 2 antibody only bound to the peptides comprising the 14 amino acids downstream from the activating PAR-2 protease cleavage site, *i.e.*, SLIGKVDGTSHVTG (residues 1-14 of SEQ ID NO:884), and was sensitive to mutations at the aspartic acid residue (Asp-43 of SEQ ID NO:851), but not to mutations at the valine residue (Val-42 of SEQ ID NO:851).

[0156] Significantly, this experiment indicates that antibodies H4H581P and H4H588N both interact with the first V and D residues located C-terminal to the activating PAR-2 protease cleavage site (*i.e.*, Val-42 and Asp-43 of SEQ ID NO:851), whereas the Comparator 1 and 3 antibodies do not interact with either of these residues, and the Comparator 2 antibody interacts with Asp-43 but not Val-42. The shifted binding of H4H581P on PAR-2 as compared to the comparator antibodies may explain the functional superiority of H4H581P over the comparator as demonstrated in the following *in vivo* examples.

Example 10. Dose Response of Anti-PAR-2 Antibody in Pruritus Models

[0157] In this Example, the ability of the anti-PAR-2 antibody H4H581P to attenuate itch in two different protease-induced pruritus models was assessed. Transgenic mice expressing human PAR-2 (hPAR2^{+/+}) were used for all cohorts in these experiments. Separate cohorts of mice received 150 mg/kg (s.c.) of an isotype control mAb or 10, 25, 50, 75, 100, and 150 mg/kg (s.c.) of H4H581P. Twenty-four hours after antibody dosing all cohorts received 150 µg of porcine trypsin, or 10 µg recombinant human beta tryptase, (s.c., interscapular), which produced bouts of scratching behavior for 30 to 60 minutes. A dose-response relationship was observed in mice receiving H4H581P prior to trypsin injection, with an estimated ED₅₀ of 25 mg/kg. The results of these experiments, expressed in terms of the percent change in the total number of scratching bouts recorded over a 30 minute period following trypsin administration, or over a 60 minute period following tryptase administration, are shown in Table 29 (all data are represented as mean ± SEM; ND = not determined; * = p<0.05 compared to the isotype control group).

Table 29

Dose of mAb H4H581P (mg/kg)	Percent Change in Scratching Bouts Relative to Control	
	Trypsin	Tryptase
10	9.9 ± 23.1	-40.7 ± 23.4

25	-26.6 ± 11.3	-38.5 ± 11.1
50	-31.3 ± 13.5	-47.7 ± 8.0*
75	-34.9 ± 4.7*	ND
100	-55.2 ± 8.0*	-39.6 ± 6.9*
150	-42.9 ± 9.7*	ND

[0158] As shown in this Example, mAb H4H581P was able to block protease-induced pruritus behaviors in a dose dependent manner using two different protease-induced itch models.

Example 11. Reduction of Pruritus Behaviors by Administration of an Anti-PAR-2 Antibody in a Hapten-Induced Chronic Dermatitis Model

[0159] To further assess the ability of the anti-PAR-2 antibody H4H581P to reduce pruritus behaviors in a physiologically relevant disease state, a mouse model of chronic dermatitis was used. In this model, mice received repeated cutaneous applications of the haptenizing agent, oxazolone. This chronic oxazolone-induced dermatitis model has been shown to recapitulate many of the clinical, histological, and immunological hallmarks of atopic dermatitis in humans (Man *et al.*, 2008, *J. Invest. Dermatol.* 128(1):79-86).

[0160] Mice were sensitized with a single cutaneous application of 1% oxazolone on the left ear or vehicle (100 mg/kg, s.c.). The mice then received nine total cutaneous applications (challenges) of 0.6% oxazolone between the scapulae beginning seven days after the sensitization application. Weekly dosing (3 total) of the H4H581P anti-PAR2 antibody was initiated 24 hours prior to the first oxazolone challenge (100 mg/kg, s.c.). This dosing paradigm significantly reduced pruritus behaviors as measured by reduced numbers of scratching bouts elicited by the final oxazolone challenge. All data are represented as mean number of scratching bouts ± SEM for n=6 mice/group; * = p<0.05 by Tukey post-hoc test as compared to the Oxazolone + IgG control group; # = p<0.05 by Tukey post-hoc test compared to the Vehicle + IgG control group).

Table 30

Treatment	Time (minutes)						Total
	0-10	10-20	20-30	30-40	40-50	50-60	
Vehicle + IgG control	0.0±0.0	0.8±0.6	2.2±1.4	3.4±1.3	4.8±2.0	2.4±1.0	13.6±4.2
Oxazolone + IgG control	0.5±0.5	11.3±3.9	24.8±9.7	28.0±7.3	21.0±7.9	21.3±7.3	#106.8±33.2
Oxazolone + H4H581P	0.2±0.2	1.6±1.2	*6.0±2.4	16.6±5.1	18.2±4.8	18.0±5.5	60.6±11.6

[0161] Histological analysis showed a significant increase in epidermal hyperplasia and immune cell infiltrate in the oxazolone-challenged animals. (Data not shown). No significant differences were observed in any of these parameters between the H4H581P anti-PAR2 antibody and the isotype control.

Example 12. Comparison of Pruritus Inhibiting Activities of mAb H4H581P

[0100] In this Example, the ability of mAb H4H581P to attenuate itching bouts in a mouse pruritus model was compared to that of a comparator anti-PAR-2 mAb (Comparator "1A1" described in WO 2009/005726.

[0101] Transgenic mice expressing human PAR-2 (hPAR2^{+/+}) were divided into 3 cohorts. Cohort A received 50 mg/kg (s.c.) of an isotype control mAb, cohort B received 50 mg/kg (s.c.) of H4H581P, and Cohort C received 50 mg/kg (s.c.) of the comparator anti-PAR-2 antibody. Twenty-four hours after antibody dosing all cohorts received 150 µg of trypsin (s.c., interscapular), which produced bouts of scratching behavior for 30 minutes. The percent change in the number of scratching bouts observed for the treated mice as compared to control-treated mice is shown in Table 29 (all data are represented as mean ± SEM).

Table 31

Antibody Treatment (50 mg/kg)	(% change in scratching bouts from control)
mAb H4H581P	- 41.1 ± 13.5
Comparator mAb	- 13.9 ± 9.9

[0102] As shown in this Example, mAb H4H581P was substantially more effective than the comparator mAb in reducing pruritus behaviors in the trypsin-induced itch model used herein.

[0103] The present invention is not to be limited in scope by the specific embodiments describe herein. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and the accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

[0104] Throughout the description and claims of the specification, the word "comprise" and variations of the word, such as "comprising" and "comprises", is not intended to exclude other additives, components, integers or steps.

[0105] A reference herein to a patent document or other matter which is given as prior art is not to be taken as an admission or a suggestion that that document was, known or that the information it contains was part of the common general knowledge as at the priority date of any of the claims.

The claims defining the invention are as follows:

1. An isolated human antibody or antigen-binding fragment thereof that specifically binds to human PAR-2 (SEQ ID NO:851), wherein the antibody or antigen-binding fragment thereof:
 - (a) interacts with Ser-37, Leu-38, Ile-39, Gly-40, Val-42 and Asp-43 of human PAR-2;
 - (b) does not interact with Lys-41 of human PAR-2;
 - (c) blocks trypsin cleavage of human PAR-2 at the activating cleavage site located at the junction of residues Arg-36 and Ser-37 of human PAR-2;
 - (d) does not block trypsin cleavage of human PAR-2 at the non-activating cleavage site located at the junction of residues Arg-31 and Ser-32; and
 - (e) competes for binding to human PAR-2 with a reference antibody comprising heavy chain complementary determining regions (HCDR1-HCDR2-HCDR3) having the amino acid sequences of SEQ ID NOs:700-702-704; and the light chain CDRs (LCDR1-LCDR2-LCDR3) having the amino acid sequences of SEQ ID NOs:708-710-712.
2. The isolated human antibody or antigen-binding fragment of claim 1, wherein the antibody or antigen-binding fragment comprises a heavy chain variable region (HCVR) and a light chain variable region (LCVR), wherein the HCVR comprises the heavy chain CDRs (HCDR1-HCDR2-HCDR3) having the amino acid sequences of SEQ ID NOs:700-702-704, and wherein the LCVR comprises the light chain CDRs (LCDR1-LCDR2-LCDR3) having the amino acid sequences of SEQ ID NOs:708-710-712.
3. The isolated human antibody or antigen-binding fragment of claim 2, wherein the antibody or antigen-binding fragment comprises a HCVR having the amino acid sequence of SEQ ID NO:714 and a LCVR having the amino acid sequence of SEQ ID NO:692.
4. A pharmaceutical composition comprising the antibody or antigen-binding fragment of any one of claims 1 to 3 and a pharmaceutically-acceptable carrier.
5. A formulation, comprising:
 - a pharmaceutically acceptable carrier; and
 - an effective amount of an antibody or antigen-binding fragment thereof that specifically binds human protease-activated receptor 2 (PAR2) (SEQ ID NO:851), wherein the antibody or antigen-binding fragment thereof:
 - (a) interacts with Ser-37, Leu-38, Ile-39, Gly-40, Val-42 and Asp-43 of human PAR2;
 - (b) does not interact with Lys-41 of human PAR2;
 - (c) blocks trypsin cleavage of human PAR2 at the activating cleavage site located at the junction of residues Arg-36 and Ser-37 of human PAR2;

(d) does not block trypsin cleavage of human PAR2 at the non-activating cleavage site located at the junction of residues Arg-31 and Ser-32; and

(e) competes for binding to human PAR2 with a reference antibody comprising heavy chain CDRs (HCDR1-HCDR2-HCDR3) having the amino acid sequences of SEQ ID NOs:700-702-704; and the light chain CDRs (LCDR1-LCDR2-LCDR3) having the amino acid sequences of SEQ ID NOs:708-710-712.

6. The formulation of claim 5 for use in the treatment of pruritus associated with atopic dermatitis, psoriasis, burn scarring, hypertrophic scarring, keloids, renal failure or hepatic failure.
7. The formulation of claim 5, wherein the antibody or antigen-binding fragment comprises: a heavy chain variable region (HCVR) and a light chain variable region (LCVR), wherein the HCVR comprises the heavy chain CDRs (HCDR1-HCDR2-HCDR3) having the amino acid sequences of SEQ ID NOs:700-702-704, and wherein the LCVR comprises the light chain CDRs (LCDR1-LCDR2-LCDR3) having the amino acid sequences of SEQ ID NOs:708-710-712.
8. The formulation of claim 5, wherein the antibody or antigen-binding fragment comprises: a HCVR having the amino acid sequence of SEQ ID NO:714; and a LCVR having the amino acid sequence of SEQ ID NO:692.
9. The formulation of claim 5, wherein the antibody or antigen-binding fragment thereof causes a dose-dependent reduction in scratching behaviors when administered at a dose of at least 25 mg/kg to a hPAR2+/+ mouse protease-induced pruritus model.
10. The formulation of claim 5, further comprising:
an additional therapeutic agent selected from the group consisting of:
an IL-1 inhibitor, an IL-18 inhibitor, an IL-4 inhibitor, an IL-4 receptor inhibitor, an IL-6 inhibitor, an IL-6 receptor inhibitor, a nerve growth factor (NGF) inhibitor, a tumor necrosis factor (TNF) inhibitor, a TNF receptor inhibitor, a uric acid synthesis inhibitor and a corticosteroid.
11. A use of a formulation of claim 5 for the manufacture of a medicament for the treatment of pruritus associated with atopic dermatitis, psoriasis, burn scarring, hypertrophic scarring, keloids, renal failure or hepatic failure.
12. A method for treating pruritus, the method comprising administering to a patient in need thereof an effective amount of an antibody or antigen-binding fragment thereof that specifically binds human protease-activated receptor 2 (PAR2) (SEQ ID NO:851),

wherein the antibody or antigen-binding fragment thereof: (a) interacts with Ser-37, Leu-38, Ile-39, Gly-40, Val-42 and Asp-43 of human PAR2; (b) does not interact with Lys-41 of human PAR2; (c) blocks trypsin cleavage of human PAR2 at the activating cleavage site located at the junction of residues Arg-36 and Ser-37 of human PAR2; (d) does not block trypsin cleavage of human PAR2 at the non-activating cleavage site located at the junction of residues Arg-31 and Ser-32; and (e) competes for binding to human PAR2 with a reference antibody comprising heavy chain CDRs (HCDR1-HCDR2-HCDR3) having the amino acid sequences of SEQ ID NOs:700-702-704; and the light chain CDRs (LCDR1-LCDR2-LCDR3) having the amino acid sequences of SEQ ID NOs:708-710-712.

13. The method of claim 12, wherein the pruritus is associated with atopic dermatitis, psoriasis, burn scarring, hypertrophic scarring, keloids, renal failure or hepatic failure.
14. The method of claim 12, wherein the antibody or antigen-binding fragment comprises a heavy chain variable region (HCVR) and a light chain variable region (LCVR)--, wherein the HCVR comprises the heavy chain CDRs (HCDR1-HCDR2-HCDR3) having the amino acid sequences of SEQ ID NOs:700-702-704, and wherein the LCVR comprises the light chain CDRs (LCDR1-LCDR2-LCDR3) having the amino acid sequences of SEQ ID NOs:708-710-712.
15. The method of claim 12, wherein the antibody or antigen-binding fragment comprises a HCVR having the amino acid sequence of SEQ ID NO:714 and a LCVR having the amino acid sequence of SEQ ID NO:692.
16. The method of claim 12, wherein the antibody or antigen-binding fragment thereof causes a dose-dependent reduction in scratching behaviors when administered at a dose of at least 25 mg/kg to a hPAR2+/+ mouse protease-induced pruritus model.
17. The method of claim 12, further comprising administering to the patient one or more additional therapeutic agent(s) selected from the group consisting of an IL-1 inhibitor, an IL-18 inhibitor, an IL-4 inhibitor, an IL-4 receptor inhibitor, an IL-6 inhibitor, an IL-6 receptor inhibitor, a nerve growth factor (NGF) inhibitor, a tumor necrosis factor (TNF) inhibitor, a TNF receptor inhibitor, a uric acid synthesis inhibitor and a corticosteroid.
18. The isolated human antibody or antigen-binding fragment according to claim 1, the formulation according to claim 5 or the method according to claim 12, substantially as hereinbefore described with reference to any of the Examples and/or Figures.

H1H581P HCVR {SEQ ID NO:714}	QVQLVESGGGVVQPPGRSLRLSCVA	SGFTFSRYG	IHWV	RQAPGKGL	EW
H2M588N HCVR {SEQ ID NO:98}	EVQLLESGGGLVQPPGSLRLSCAA	SGFTFS	SSYAMTWV	RQAPGKGL	YW
H2M591N HCVR {SEQ ID NO:146}	EVQLLESGGGLVQPPGSLRLSCAT	SGFTFSRYTMTWV	RQAPGKGL	FW	
H2M618N HCVR {SEQ ID NO:338}	EVQLLESGGGLVQPPGSLRLSCAA	SGFTFSRYTMTWV	RQAPGKGL	DW	
		CDR1			
H1H581P HCVR {SEQ ID NO:714}	VIVISYDGINKYYADSVKGRFTISRDN	SKNTVYLQMN	SLRAED	TA	VY
H2M588N HCVR {SEQ ID NO:98}	VSAISGGRGSAYYADSVKGRFTISRDN	SKNTVYLQMN	SLRAED	TA	VY
H2M591N HCVR {SEQ ID NO:146}	VSGIGSGGGRAYYADSVKGRFTLSRDN	SKNTVYLQMN	SLRAED	TA	VY
H2M618N HCVR {SEQ ID NO:338}	VSGITDSGAGTYYGDSVKGRFTISRDN	SKNTVYLQMN	SLRAED	TA	VY
		CDR2			
H1H581P HCVR {SEQ ID NO:714}	YCAKGD	FWSGYFDYWGQG	TLVTV	SS	
H2M588N HCVR {SEQ ID NO:98}	YCAKEG	DSGYDLAYWGRG	TLVTV	SS	
H2M591N HCVR {SEQ ID NO:146}	YCAKEG	DSGYDLDYWGRG	TLVTV	SS	
H2M618N HCVR {SEQ ID NO:338}	YCVKEG	DSGYDLDYWQG	TLVTV	SS	
		CDR3			

Fig. 1

H1H581P LCVR (SEQ ID NO:692)	D I V M T Q T P L S S P V T L G Q P A S I S C R S S	30	Q S L V H S D G N T Y	40	L S W L H Q
H2M588N LCVR (SEQ ID NO:106)	D I Q M T Q S P S S L S A S V G D R V T I T C R A R	20	Q G I S N N - - - -	-	L A W L Q Q
H2M591N LCVR (SEQ ID NO:154)	D I Q M T Q Y P S S L S A S V G D R V T I T C R A R	-	Q G I S N Y - - - -	-	L A W L Q Q
H2M618N LCVR (SEQ ID NO:346)	D I Q M T Q S P S S L S A S V G D R V T I T C R A S	-	Q G I S T Y - - - -	-	L A W L Q Q
			CDR1		
H1H581P LCVR (SEQ ID NO:692)	R P G Q P P R L L I Y K I S N R F S G V P D R F S G S G A G T D F T L Q I S R V E A E	50	70	80	
H2M588N LCVR (SEQ ID NO:106)	K P G K A P K S L I Y A A S S L Q S G I P S K F S G S G S G T Y F T L T I S S L Q P E	-	-	-	-
H2M591N LCVR (SEQ ID NO:154)	K P G K A P K S L I Y A A S S L Q R G V P S K F S G S G S G T D F T L T I S S L Q P E	-	-	-	-
H2M618N LCVR (SEQ ID NO:346)	K P G K A P K S L I Y A T S S L Q S G V P S K F S G S R S G T D F T L T I S S L Q P E	-	-	-	-
			CDR2		
H1H581P LCVR (SEQ ID NO:692)	D V G I Y Y C M Q A T Q F P - T F G G G T K V E I K	90	100	110	120
H2M588N LCVR (SEQ ID NO:106)	D F A T Y Y C Q Q Y K S S P L T F G G G T K V E I K	-	-	-	-
H2M591N LCVR (SEQ ID NO:154)	D S A T Y Y C Q Q Y K I S P L T F G G G T K V E I K	-	-	-	-
H2M618N LCVR (SEQ ID NO:346)	D F A T Y Y C Q Q Y K S S P L T F G G G T K V E I K	-	-	-	-
				CDR3	

(A)

	C-terminal Biotin	N-terminal Biotin
	① ② GTNRSSKGRSLIGKVDGT-B	① ② B-GTNRSSKGRSLIGKVDGT
No Cleavage	2501 kDa	2373 kDa
Cleavage @ ①	2073 kDa	988 kDa
Cleavage @ ②	1558 kDa	N/A

(B)

Antibody	Time	2501 kDa	2073 kDa	1558 kDa	2373 kDa	988 kDa
Neg Ctrl	0	X			X	
Neg Ctrl	5			X		X
Neg Ctrl	15			X		N/D
H4H581P	0	X			X	
H4H581P	5		X			X
H4H581P	15		X			N/D
H4H588N	0	X			X	
H4H588N	5			X		X
H4H588N	15			X		N/D

Fig. 3

(A)	Mouse			Rat	Human		
	①	②	③		①	②	③
	GRNNSKGRSLIGRLLETQPPI			GPNSKGRSLIGRLDTP			GTNRSSKGRSLIGKVDGT
No Cleavage	2556 kDa	2342 kDa	1898 kDa	1686 kDa	2502 kDa	2074 kDa	1772 kDa
Cleavage @ ①							
Cleavage @ ②							
Cleavage @ ③							

(B)	Antibody	Time	2556 kDa	2342 kDa	1898 kDa	1686 kDa	2337 kDa	1853 kDa	1640 kDa	2502 kDa	2074 kDa	1772 kDa	1558 kDa
			X				X			X			X
	Neg Ctrl	0	X										
	Neg Ctrl	5				X			X				X
	H4H581P	0	X				X			X			
	H4H581P	5				X	X		X		X		
	H4H588N	0	X				X			X			
	H4H588N	5				X			X			X	X
	Comp. Ab	0	X				X			X			
	Comp. Ab	5				X			X	X			

Fig. 4

		(28)(29)(30)(31)(32)(33)(34)(35)(36)(37)(38)(39)(40)(41)(42)(43)(44)(45)	GTNRSSKGRSLIGKVDGT
Comparator 1:		280.11861.544282.5137152126135	
Comparator 3:		10972179789598120128118	
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Fig. 5

SEQUENCE LISTING

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<120> High Affinity Human Antibodies to Human Protease Activated Receptor-2

<130> 6110A-WO

<140> To be assigned

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<150> 61/240,783

<151> 2009-09-09

<150> 61/242,821

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 50             55             60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

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 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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<220>

<223> Synthetic

<400> 26

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Glu Val 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 Asp Asp Tyr
      20             25             30
Thr Met His Trp Val Arg Gln Val Pro Gly Lys Asp Leu Lys Trp Val
      35             40             45
Ser Gly Ile Thr Trp Asn Gly Gly Arg Lys Ala Tyr Ala Asp Ser Val
 50             55             60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Phe
65             70             75             80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Phe Tyr Tyr Cys
      85             90             95
Ala Lys Glu Asp Glu Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
      100            105            110
Thr Val Ser Ser
      115

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<210> 27

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 27

ggattcacct ttgatgatta tacc

24

<210> 28

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 28

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Gly Phe Thr Phe Asp Asp Tyr Thr
 1             5

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<210> 29
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 29
 attacttgga atggtggtag aaaa 24

<210> 30
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 30
 Ile Thr Trp Asn Gly Gly Arg Lys
 1 5

<210> 31
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 31
 gcaaaagaag atgaggcttt tgactac 27

<210> 32
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 32
 Ala Lys Glu Asp Glu Ala Phe Asp Tyr
 1 5

<210> 33
 <211> 336
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 33
 gatattgtga tgaccagac tccactctcc tcacctgtca cccttgga ggcggcctcc 60
 atctcctgca ggtctagtca aagcctcgta cacagtgatg gcaacaccta cttgagttgg 120


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cttcagcaga ggccaggcca gcctccaaga ctcttaattt ataagatttc taaccgggtt 180
tttgggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgaaaatc 240
agcaggggtgg aggctgagga tgtcggcggtt tattactgca tgcaagcaac acaatttcgc 300
tacacttttg gccaggggac caagctggag atcaaa 336

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<210> 34
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 34
 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
 20 25 30
 Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
 35 40 45
 Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Phe Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
 85 90 95
 Thr Gln Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 35
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 35
 caaagcctcg tacacagtga tggcaacacc tac 33

<210> 36
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 36
 Gln Ser Leu Val His Ser Asp Gly Asn Thr Tyr
 1 5 10

<210> 37
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 37
aagatttct

9

<210> 38
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 38
Lys Ile Ser
1

<210> 39
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 39
atgcaagcaa cacaatttcc gtacact

27

<210> 40
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 40
Met Gln Ala Thr Gln Phe Pro Tyr Thr
1 5

<210> 41
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 41
gaagtgcagc tgggtggagtc tgggggaggc gtggtccagc ctggcaggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttgat gattatacca tgcactgggt ccggcaagtt 120
ccagggaagg acctgaagtg ggtctcaggt attacttgga atggtggtag aaaagcctat 180
gcggaactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctcttt 240
ctgcaaattga acagtctgag agctgaggac acggccttct attactgtgc aaaagaagat 300
gaggcttttg actactgggg ccagggaacc ctggtcaccg tctcctca 348

<210> 42
<211> 116
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 42

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Glu Val 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 Asp Asp Tyr
      20           25           30
Thr Met His Trp Val Arg Gln Val Pro Gly Lys Asp Leu Lys Trp Val
      35           40           45
Ser Gly Ile Thr Trp Asn Gly Gly Arg Lys Ala Tyr Ala Asp Ser Val
      50           55           60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Phe
65           70           75           80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Phe Tyr Tyr Cys
      85           90           95
Ala Lys Glu Asp Glu Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
      100          105          110
Thr Val Ser Ser
      115

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<210> 43

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 43

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gatattgtga tgaccagac tccactctcc tcacctgtca cccttggaca gccggcctcc 60
atctcctgca ggtctagtca aagcctcgta cacagtgatg gcaacaccta cttgagttgg 120
cttcagcaga ggccaggcca gcctccaaga ctcttaattt ataagatttc taaccggttt 180
tttgggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgaaaatc 240
agcaggggtgg aggctgagga tgtcggcggtt tattactgca tgcaagcaac acaatttccg 300
tacacttttg gccaggggac caagctggag atcaaaa 336

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<210> 44

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 44

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Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1           5           10           15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
      20           25           30
Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
      35           40           45
Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Phe Gly Val Pro
      50           55           60
Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65           70           75           80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
      85           90           95
Thr Gln Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys

```

100

105

110

<210> 45
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 45
 gaagtgcagc tgggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttgat gattatacca tgcactgggt ccggcaagct 120
 ccagggaagg gcctggagtg ggtctcaggt attacttgga atggtggtag aaaaggctat 180
 gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
 ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgc aaaagaagat 300
 gaggccttttg actactgggg ccagggaacc ctggtcaccg tctcctca 348

<210> 46
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 46
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Thr Trp Asn Gly Gly Arg Lys Gly Tyr Ala Asp 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 Lys Glu Asp Glu Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115

<210> 47
 <211> 337
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 47
 gatattgtga tgaccagac tccactctcc tcacctgtca cccttgga gcccgcctcc 60
 atctcctgca ggtctagtca aagcctcgta cacagtgatg gcaacaccta cttgagttgg 120
 cttcagcaga ggccaggcca gcctccaaga ctcctaattt ataagatttc taaccgggtc 180
 tctgggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgaaaatc 240
 agcagggtgg aagctgagga tgtcgggggtt tattactgca tgcaagcaac acaatttccg 300
 tacacttttg gccaggggac caagctggag atcaaac 337

<210> 48
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 48
 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
 20 25 30
 Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
 35 40 45
 Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
 85 90 95
 Thr Gln Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 49
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 49
 gaagtgcagt tgggtggagtc tggggggaggc ttggcacagc ctggcaggtc cctgagagtc 60
 tctgttccag cctctggatt caattttgat gattatgcca tgcactgggt ccggcaagct 120
 ccggggaagg gcctggagtg ggtctcaggt attagttaga atagtggtag cagaggctat 180
 gcggactctg tgaagggccg cttcaccatc tccagagaca acgccaagaa ctccctgtat 240
 ctgcaaataa acagtctgag agctgaggac acggccttgt attactgtgt aaaagagaa 300
 tgggcctttg aatactgggg ccagggaacc ctggtcaccg tctcctca 348

<210> 50
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 50
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ala Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Val Ser Cys Ser Ala Ser Gly Phe Asn Phe Asp Asp Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Ser Trp Asn Ser Gly Ser Arg Gly Tyr Ala Asp 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

[illegible]

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<210> 51
<211> 24
<212> DNA
<213> Artificial Sequence
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<220>
<223> Synthetic

<400> 51
ggattcaatt ttgatgatta tgcc 24

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<210> 52
<211> 8
<212> PRT
<213> Artificial Sequence
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<220>
<223> Synthetic

```
<400> 52
Gly Phe Asn Phe Asp Asp Tyr Ala
 1             5
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```
<210> 53
<211> 24
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Synthetic

<400> 53
attagtgtgga atagtggtag caga 24

```
<210> 54
<211> 8
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Synthetic

```
<400> 54
Ile Ser Trp Asn Ser Gly Ser Arg
  1                      5
```

```
<210> 55
<211> 27
<212> DNA
<213> Artificial Sequence
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<220>

<223> Synthetic

<400> 55

gtaaaagaga actgggcctt tgaatac

27

<210> 56

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 56

Val Lys Glu Asn Trp Ala Phe Glu Tyr

1

5

<210> 57

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 57

gatattgtga tgaccagac tccactctcc tcacctgtca cccttggaca gccggcctcc 60
atctcctgca ggtctagtc tagcctcgta cacagtgatg gaagcaccta cttgagttgg 120
cttcagcaga ggccaggcca gcctccaaga ctcctaattt ataaaatttc taaccgattc 180
tctgggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgaaaatc 240
agcagggtgg aagctgagga tgtcgggctt tattactgca tgcaggctac acaatttccg 300
tacacttttg gccaggggac caagctggag atcaaa 336

<210> 58

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 58

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
1 5 10 15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser His Ser Leu Val His Ser
20 25 30
Asp Gly Ser Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
35 40 45
Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Leu Tyr Tyr Cys Met Gln Ala
85 90 95
Thr Gln Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 59

<211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 59
 catagcctcg tacacagtga tggaagcacc tac 33

 <210> 60
 <211> 11
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 60
 His Ser Leu Val His Ser Asp Gly Ser Thr Tyr
 1 5 10

 <210> 61
 <211> 9
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 61
 aaaatttct 9

 <210> 62
 <211> 3
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 62
 Lys Ile Ser
 1

 <210> 63
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 63
 atgcaggcta cacaatttcc gtacact 27

 <210> 64
 <211> 9
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 64

Met Gln Ala Thr Gln Phe Pro Tyr Thr
1 5

<210> 65

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 65

gaagtgcagc tgggtggagtc tggggggaggc ttggcacagc ctggcaggtc cctgagagtc 60
tcctgttcag cctctggatt caattttgat gattatgcca tgcactgggt ccggcaagct 120
ccggggaagg gcctggagtg ggtctcaggt attagttgga atagtggtag cagaggctat 180
gcggactctg tgaagggccg cttcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgt aaaagagaac 300
tgggcctttg aatactgggg ccaggggaacc ctggtcaccg tctcctca 348

<210> 66

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 66

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ala Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Val Ser Cys Ser Ala Ser Gly Phe Asn Phe Asp Asp Tyr
20 25 30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Gly Ile Ser Trp Asn Ser Gly Ser Arg Gly Tyr Ala Asp 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
Val Lys Glu Asn Trp Ala Phe Glu Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110
Thr Val Ser Ser
115

<210> 67

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 67
 gatattgtga tgaccagac tccactctcc tcacctgtca cccttgga gcccgcctcc 60
 atctcctgca ggtctagtc tagcctcgta cacagtgatg gaagcaccta cttgagttgg 120
 cttcagcaga ggccaggcca gcctccaaga ctcctaattt ataaaatttc taaccgattc 180
 tctgggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgaaaatc 240
 agcagggtgg aagctgagga tgtcgggctt tattactgca tgcaggctac acaatttccg 300
 tacacttttg gccaggggac caagctggag atcaaa 336

<210> 68
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 68
 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser His Ser Leu Val His Ser
 20 25 30
 Asp Gly Ser Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
 35 40 45
 Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Val Gly Leu Tyr Tyr Cys Met Gln Ala
 85 90 95
 Thr Gln Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 69
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 69
 gaagtgcagc tgggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60
 tcctgtgcag cctctggatt caattttgat gattatgcca tgcactgggt ccggcaagct 120
 ccagggaagg gcctggagtg ggtctcaggt attagttgga atagtggtag cagaggctat 180
 gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
 ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgt aaaagagaac 300
 tgggcctttg aatactgggg ccagggaacc ctggtcaccg tctcctca 348

<210> 70
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 70
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Phe Asp Asp Tyr

20							25					30			
Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
35			40				45								
Ser	Gly	Ile	Ser	Trp	Asn	Ser	Gly	Ser	Arg	Gly	Tyr	Ala	Asp	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								
Val	Lys	Glu	Asn	Trp	Ala	Phe	Glu	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val
100			105				110								
Thr	Val	Ser	Ser												
115															

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<210> 71
<211> 337
<212> DNA
<213> Artificial Sequence
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<220>
<223> Synthetic

<400>	71						
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atctctgtga	ggtctagtca	tagcctctga	cacagtgatg	gaagcaccta	cttgagttgg	120	
cttcagcaga	ggccaggcca	gcctccaaga	ctcctaattt	ataaaatttc	taaccggttc	180	
tctgggggtcc	cagacagatt	cagtggcagt	ggggcaggga	cagatttcac	actgaaaatc	240	
agcagggttg	aagctgagga	tgtcgggggt	tattactgca	tgcaggctac	acaattttccg	300	
tacacttttg	gccaggggac	caagctggag	atcaaac			337	

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<210> 72
<211> 112
<212> PRT
<213> Artificial Sequence
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<220>
<223> Synthetic

<400> 72															
Asp	Ile	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Ser	Pro	Val	Thr	Leu	Gly
1				5					10					15	
Gln	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	His	Ser	Leu	Val	His	Ser
			20					25					30		
Asp	Gly	Ser	Thr	Tyr	Leu	Ser	Trp	Leu	Gln	Gln	Arg	Pro	Gly	Gln	Pro
		35					40					45			
Pro	Arg	Leu	Leu	Ile	Tyr	Lys	Ile	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro
	50					55					60				
Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ala	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile
65					70					75				80	
Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys	Met	Gln	Ala
				85					90					95	
Thr	Gln	Phe	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys
			100					105					110		

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<210> 73
<211> 348
<212> DNA
<213> Artificial Sequence
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<220>

<223> Synthetic

<400> 73

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gaagtgcagc tgggtggagtc tgggggaggc ttggtacagg ctggcaggtc cctgcgactc 60
tcctgtgcag cctctggatt cacctttgat gattatgcc a tgactgggt ccggcaagct 120
ccagggaagg gcctggagtg ggtctcaggt attagttaga atagtggtag cagaggctat 180
gcggactctg tgaagggccg attcaccatc tccagagaca acgcaaaaaa ctccctgcat 240
ctgcaaattg acagtctgag agctgaggac acggccttgt attactgtgc aaaagagaac 300
tggtcctttg actactgggg ccagggaacc ctggtcaccg tctcctca 348

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<210> 74

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 74

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Arg
 1             5             10             15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
          20             25             30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35             40             45
Ser Gly Ile Ser Trp Asn Ser Gly Ser Arg Gly Tyr Ala Asp Ser Val
 50             55             60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu His
65             70             75             80
Leu Gln Met Tyr Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
          85             90             95
Ala Lys Glu Asn Trp Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
          100             105             110
Thr Val Ser Ser
          115

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<210> 75

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 75

ggattcacct ttgatgatta tgcc

24

<210> 76

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 76

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Gly Phe Thr Phe Asp Asp Tyr Ala
 1             5

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<210> 77
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 77
 attagttgga atagtggtag caga

24

<210> 78
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 78
 Ile Ser Trp Asn Ser Gly Ser Arg
 1 5

<210> 79
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 79
 gcaaaagaga actggtcctt tgactac

27

<210> 80
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 80
 Ala Lys Glu Asn Trp Ser Phe Asp Tyr
 1 5

<210> 81
 <211> 336
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 81
 gatattgtga tgacccagac tccactctcc tcacctgtca cccttgga gacggcctcc 60
 atctcctgca ggtctagtca aagcctcgta cacagtgatg gaaacaccta cttgagttgg 120
 cttcagcaga ggccaggcca gctccaaga ctctaattt ataagatttc ttaccggttc 180

tctgggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgaaaatc 240
 agcagggtgg caactgagga tgtcgggggtt tattactgca tgcaagctac acaattgccg 300
 tacacttttg gccaggggac caagctggag atcaaa 336

<210> 82
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 82
 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
 20 25 30
 Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
 35 40 45
 Pro Arg Leu Leu Ile Tyr Lys Ile Ser Tyr Arg Phe Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Ala Thr Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
 85 90 95
 Thr Gln Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 83
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 83
 caaagcctcg tacacagtga tggaaacacc tac 33

<210> 84
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 84
 Gln Ser Leu Val His Ser Asp Gly Asn Thr Tyr
 1 5 10

<210> 85
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 85
aagatttct

9

<210> 86
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 86
Lys Ile Ser
1

<210> 87
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 87
atgcaagcta cacaattgcc gtacact

27

<210> 88
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 88
Met Gln Ala Thr Gln Leu Pro Tyr Thr
1 5

<210> 89
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 89
gaagtgcagc tgggtggagtc tggggggaggc ttggtacagg ctggcaggtc cctgcgactc 60
tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccggcaagct 120
ccagggaagg gcctggagtg ggtctcaggt attagttgga atagtggtag cagaggctat 180
gcggactctg tgaagggccg attcaccatc tccagagaca acgccaaaaa ctccctgcat 240
ctgcaaattgt acagtctgag agctgaggac acggccttgt attactgtgc aaaagagaac 300
tggtcctttg actactgggg ccagggaacc ctggtcaccg tctcctca 348

<210> 90
<211> 116
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 90

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Arg
 1           5           10           15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
          20           25           30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35           40           45
Ser Gly Ile Ser Trp Asn Ser Gly Ser Arg Gly Tyr Ala Asp Ser Val
 50           55           60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu His
65           70           75           80
Leu Gln Met Tyr Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
          85           90           95
Ala Lys Glu Asn Trp Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
          100          105          110
Thr Val Ser Ser
          115

```

<210> 91

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 91

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gatattgtga tgaccagac tccactctcc tcacctgtca cccttgaca gccggcctcc 60
atctcctgca ggtctagtca aagcctcgta cacagtgatg gaaacaccta cttgagttgg 120
cttcagcaga ggccaggcca gctccaaga ctctaattt ataagatttc ttaccggttc 180
tctgggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgaaaatc 240
agcagggtgg caactgagga tgtcgggggtt tattactgca tgcaagctac acaattgccg 300
tacacttttg gccaggggac caagctggag atcaaaa 336

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<210> 92

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 92

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Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1           5           10           15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
          20           25           30
Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
          35           40           45
Pro Arg Leu Leu Ile Tyr Lys Ile Ser Tyr Arg Phe Ser Gly Val Pro
 50           55           60
Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65           70           75           80
Ser Arg Val Ala Thr Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
          85           90           95
Thr Gln Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
          100          105          110

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<210> 93
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 93
 gaagtgcagc tgggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttgat gattatgccca tgcactgggt ccggcaagct 120
 ccagggaagg gcctggagtg ggtctcaggt attagttgga atagtggtag cagaggctat 180
 gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
 ctgcaaataga acagtctgag agctgaggac acggccttgt attactgtgc aaaagagaac 300
 tggtcctttg actactgggg ccagggaacc ctggtcaccg tctcctca 348

<210> 94
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 94
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Ser Trp Asn Ser Gly Ser Arg Gly Tyr Ala Asp 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 Lys Glu Asn Trp Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115

<210> 95
 <211> 337
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 95
 gatattgtga tgaccagac tccactctcc tcacctgtca cccttggaca gccggcctcc 60
 atctcctgca ggtctagtca aagcctcgta cacagtgatg gaaacaccta cttgagttgg 120
 cttcagcaga ggccaggcca gcctccaaga ctcctaattt ataagatttc taaccgggtc 180
 tctggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgaaaatc 240
 agcaggggtg aagctgagga tgtcggggtt tattactgca tgcaagctac acaattgccg 300
 tacacttttg gccaggggac caagctggag atcaaac 337

<210> 96
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 96
 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
 20 25 30
 Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
 35 40 45
 Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
 85 90 95
 Thr Gln Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 97
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 97
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc cggggggggtc cctgagactc 60
 tctgtgcag cctctggatt caccttttagc agctatgcca tgacctgggt ccgccaggct 120
 ccggggaagg ggctgtattg ggtctcagct attagtgggtg gtcgtggtag cgcatactac 180
 gcagactccg tgaagggccg gtccaccatc tccagagaca attccaagaa cgcgtgtat 240
 ctgcaaatga acagcctgcg agccgaggac acggccgtat attactgtgc gaaagagggg 300
 gatagtggct acgatttggc ctactggggc cggggaaccc tggtcaccgt ctcgtca 357

<210> 98
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 98
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Tyr Trp Val
 35 40 45
 Ser Ala Ile Ser Gly Gly Arg Gly Ser Ala Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile 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	Lys	Glu	Gly	Asp	Ser	Gly	Tyr	Asp	Leu	Ala	Tyr	Trp	Gly	Arg	Gly
			100					105					110		
Thr	Leu	Val	Thr	Val	Ser	Ser									
			115												

<210> 99
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 99
 ggattcacct ttagcagcta tgcc 24

<210> 100
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 100
 Gly Phe Thr Phe Ser Ser Tyr Ala
 1 5

<210> 101
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 101
 attagtggtag gtcgtggtag cgca 24

<210> 102
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 102
 Ile Ser Gly Gly Arg Gly Ser Ala
 1 5

<210> 103
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 103

gcgaaagagg gggatagtg ctacgatttg gcctac

36

<210> 104

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 104

Ala Lys Glu Gly Asp Ser Gly Tyr Asp Leu Ala Tyr

1

5

10

<210> 105

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 105

gacatccaga tgaccagtc tccatcctca ctgtccgcat ctgtaggaga cagagtcacc 60
atcacttgtc gggcgaggca gggcattagt aataatttag cctggcttca gcagaaacca 120
gggaaagccc ctaagtccct gatctatgct gcatccagtt tgcaaagtgg gatcccatca 180
aagttcagcg gcagtggatc tgggacatat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg cgacttatta ctgccaacaa tataaaagtt ccccgctcac tttcggcgga 300
gggaccaagg tggagatcaa a 321

<210> 106

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 106

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Arg Gln Gly Ile Ser Asn Asn
20 25 30
Leu Ala Trp Leu Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
35 40 45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Ile Pro Ser Lys Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Tyr Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Lys Ser Ser Pro Leu
85 90 95
Thr Phe Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 107

<211> 18

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 107
cagggcatta gtaataat

18

<210> 108
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 108
Gln Gly Ile Ser Asn Asn
1 5

<210> 109
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 109
gctgcatcc

9

<210> 110
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 110
Ala Ala Ser
1

<210> 111
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 111
caacaatata aaagttcccc gctcact

27

<210> 112
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 112

Gln Gln Tyr Lys Ser Ser Pro Leu Thr
 1 5

<210> 113

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 113

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc cggggggggtc cctgagactc 60
 tcctgtgcag cctctggatt caccttttagc agctatgccg tgacctgggt ccgccaggct 120
 ccggggaagg ggctgtattg ggtctcagct attagtgggtg gtcgtggtag cgcatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcaaatac acagcctgcg agccgaggac acggccgtat attactgtgc gaaagagggg 300
 gatagtggct acgatttggc ctactggggc cggggaaccc tggtcaccgt ctctca 357

<210> 114

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 114

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Tyr Trp Val
 35 40 45
 Ser Ala Ile Ser Gly Gly Arg Gly Ser Ala Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile 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 Lys Glu Gly Asp Ser Gly Tyr Asp Leu Ala Tyr Trp Gly Arg Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 115

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 115

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gacatccaga tgaccagtc tccatcctca ctgtccgcat ctgtaggaga cagagtcacc 60
atcacttgtc gggcgaggca gggcattagt aataatttag cctggcttca gcagaaacca 120
gggaaagccc ctaagtcctt gatctatgct gcatccagtt tgcaaagtgg gatcccatca 180
aagttcagcg gcagtggatc tgggacatat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg cgacttatta ctgccaacaa tataaaagtt ccccgctcac tttcggcgga 300
gggaccaagg tggagatcaa a                                     321

```

<210> 116

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 116

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1             5             10             15
Asp Arg Val Thr Ile Thr Cys Arg Ala Arg Gln Gly Ile Ser Asn Asn
          20          25          30
Leu Ala Trp Leu Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
          35          40          45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Ile Pro Ser Lys Phe Ser Gly
          50          55          60
Ser Gly Ser Gly Thr Tyr Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65          70          75          80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Lys Ser Ser Pro Leu
          85          90          95
Thr Phe Gly Gly Thr Lys Val Glu Ile Lys
          100          105

```

<210> 117

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 117

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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt caccttttagc agctatgcca tgagctgggt ccgccaggct 120
ccaggggaagg ggcctggagt ggtctcagct attagtgggt gtcgtggtag cgcatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaataga acagcctgag agccgaggac acggccgtat attactgtgc gaaagagggg 300
gatagtggct acgatttggc ctactggggc caggggaacc tggtcaccgt ctccctca 357

```

<210> 118

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 118

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1             5             10             15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
          20          25          30

```

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ala Ile Ser Gly Gly Arg Gly Ser Ala Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile 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 Lys Glu Gly Asp Ser Gly Tyr Asp Leu Ala Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 119
 <211> 322
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 119
 gacatccaga tgacccagtc tccatcctca ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgctc gggcgagtc gggcattagt aataatttag cctggtttca gcagaaacca 120
 gggaaagccc ctaagtcctt gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
 aggttcagcg gcagtggtatc tgggacagat ttcactctca ccatacagcag cctgcagcct 240
 gaagattttg caacttatta ctgccaacaa tataaaagt ccccgctcac tttcggcgga 300
 gggaccaagg tggagatcaa ac 322

<210> 120
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 120
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Asn
 20 25 30
 Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
 35 40 45
 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Lys Ser Ser Pro Leu
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 121
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 121

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gaggtgcagc tgttgagtc ggggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcaa cctctggatt caccttttagc agatatacca tgacctgggt ccgccaggct 120
ccagggaagg ggcgtgttttg ggtctcaggt attgggtggta gtgggtggtcg cgcatactac 180
gcagactccg tgaagggccg gttcaccctc tccagagaca attccaagaa cacgctgtat 240
ctgcaaataga acagcctgag agccgaggac acggccgtat attactgtgc gaaagagggg 300
gatagtggct acgatttgga ctactggggc cggggaaccc tggtcaccgt ctcgtca 357
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<210> 122

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 122

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1          5          10          15
Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Arg Tyr
 20          25          30
Thr Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Phe Trp Val
 35          40          45
Ser Gly Ile Gly Gly Ser Gly Gly Arg Ala Tyr Tyr Ala Asp Ser Val
 50          55          60
Lys Gly Arg Phe Thr Leu 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 Lys Glu Gly Asp Ser Gly Tyr Asp Leu Asp Tyr Trp Gly Arg Gly
100          105          110
Thr Leu Val Thr Val Ser Ser
115
```

<210> 123

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 123

ggattcacct ttagcagata tacc

24

<210> 124

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 124

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Gly Phe Thr Phe Ser Arg Tyr Thr
 1          5
```

<210> 125
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 125
 attggtggta gtggtggtcg cgca 24

<210> 126
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 126
 Ile Gly Gly Ser Gly Gly Arg Ala
 1 5

<210> 127
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 127
 gcgaaagagg gggatagtgg ctacgatttg gactac 36

<210> 128
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 128
 Ala Lys Glu Gly Asp Ser Gly Tyr Asp Leu Asp Tyr
 1 5 10

<210> 129
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 129
 gacatccaga tgaccagta tccatcctca ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgtc gggcgaggca gggcataagt aattatttag cctggcttca gcagaaacca 120
 gggaaagccc ctaagtcctt gatctatgct gcatccagtt tgcaaagggg ggtcccatca 180
 aagttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagattctg caacttatta ctgccaaaca tataaaattt ccccgctcac tttcggcgga 300
 gggaccaagg tggagatcaa g 321

<210> 130
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 130
 Asp Ile Gln Met Thr Gln Tyr Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Arg Gln Gly Ile Ser Asn Tyr
 20 25 30
 Leu Ala Trp Leu Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
 35 40 45
 Tyr Ala Ala Ser Ser Leu Gln Arg Gly Val Pro Ser Lys Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Tyr Lys Ile Ser Pro Leu
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 131
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 131
 cagggcataa gtaattat 18

<210> 132
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 132
 Gln Gly Ile Ser Asn Tyr
 1 5

<210> 133
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 133

gctgcatcc

9

<210> 134

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 134

Ala Ala Ser

1

<210> 135

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 135

caacaatata aaatttcccc gctcact

27

<210> 136

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 136

Gln Gln Tyr Lys Ile Ser Pro Leu Thr

1

5

<210> 137

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 137

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tctgtgcaa cctctggatt cacctttagc agatatacca tgacctgggt ccgccaggct 120
ccaggggaagg ggctgttttg ggtctcaggt attggtggta gtggtggtcg cgcatactac 180
gcagactccg tgaagggccg gtccaccctc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatac acagcctgag agccgaggac acggccgtat attactgtgc gaaagagggg 300
gatagtggct acgatttgga ctactggggc cggggaaccc tggtcaccgt ctcctca 357

<210> 138

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 138

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1          5          10          15
Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Arg Tyr
          20          25          30
Thr Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Phe Trp Val
          35          40          45
Ser Gly Ile Gly Gly Ser Gly Gly Arg Ala Tyr Tyr Ala Asp Ser Val
 50          55          60
Lys Gly Arg Phe Thr Leu 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 Lys Glu Gly Asp Ser Gly Tyr Asp Leu Asp Tyr Trp Gly Arg Gly
          100          105          110
Thr Leu Val Thr Val Ser Ser
          115

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<210> 139

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 139

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gacatccaga tgacccagtc tccatcctca ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgtc gggcgaggca gggcataagt aattatttag cctggcttca gcagaaacca 120
gggaaagccc ctaagtcctt gatctatgct gcatccagtt tgcaaagggg ggtcccatca 180
aagttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattctg caacttatta ctgccaacaa tataaaattt ccccgctcac tttcggcgga 300
gggaccaagg tggagatcaa a                                     321

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<210> 140

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 140

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1          5          10          15
Asp Arg Val Thr Ile Thr Cys Arg Ala Arg Gln Gly Ile Ser Asn Tyr
          20          25          30
Leu Ala Trp Leu Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
          35          40          45
Tyr Ala Ala Ser Ser Leu Gln Arg Gly Val Pro Ser Lys Phe Ser Gly
 50          55          60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65          70          75          80
Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Tyr Lys Ile Ser Pro Leu
          85          90          95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
          100          105

```

<210> 141
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 141
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttagc agatatacca tgagctgggt ccgccaggct 120
 ccagggaagg ggcctggagtg ggtctcagct attggtggta gtggtggtcg cgcatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcaaataga acagcctgag agccgaggac acggccgtat attactgtgc gaaagagggg 300
 gatagtggct acgatttggg ctactggggc cagggaacc tggtcaccgt ctctca 357

<210> 142
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 142
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
 20 25 30
 Thr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ala Ile Gly Gly Ser Gly Gly Arg Ala Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile 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 Lys Glu Gly Asp Ser Gly Tyr Asp Leu Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 143
 <211> 322
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 143
 gacatccaga tgaccagtc tccatcctca ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgctc gggcgagtca gggcataagt aattatttag cctggtttca gcagaaacca 120
 gggaaagccc ctaagtcctt gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
 aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
 gaagattttg caacttatta ctgccaacaa tataaaattt ccccgctcac tttcggcgga 300
 gggaccaagg tggagatcaa ac 322

<210> 144

<211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 144
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr
 20 25 30
 Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
 35 40 45
 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Lys Ile Ser Pro Leu
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 145
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 145
 gaggtgcagc tgttggagtc ggggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcaa cctctggatt caccttttagc agatatacca tgacctgggt ccgccaggct 120
 ccagggaagg ggctgttttg ggtctcaggt attggtggta gtggtggtcg cgcatactac 180
 gcagactccg tgaagggccg gttcaccctc tccagagaca attccaagaa cagctgtat 240
 ctgcaaataga acagcctgag agccgaggac acggccgtat attactgtgc gaaagagggg 300
 gatagtggct acgatttggga ctactggggc cggggaaccc tggtcaccgt ctcgtca 357

<210> 146
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 146
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Arg Tyr
 20 25 30
 Thr Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Phe Trp Val
 35 40 45
 Ser Gly Ile Gly Gly Ser Gly Gly Arg Ala Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Leu 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 Lys Glu Gly Asp Ser Gly Tyr Asp Leu Asp Tyr Trp Gly Arg Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 147
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 147
 ggattcacct ttagcagata tacc

24

<210> 148
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 148
 Gly Phe Thr Phe Ser Arg Tyr Thr
 1 5

<210> 149
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 149
 attggtggtg gtggtggtcg cgca

24

<210> 150
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 150
 Ile Gly Gly Ser Gly Gly Arg Ala
 1 5

<210> 151
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 151
gcgaaagagg gggatagtggt ctacgatttg gactac 36

<210> 152
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 152
Ala Lys Glu Gly Asp Ser Gly Tyr Asp Leu Asp Tyr
1 5 10

<210> 153
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 153
gacatccaga tgacccagta tccatcctca ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgctc gggcgaggca gggcataagt aattatttag cctggcttca gcagaaacca 120
gggaaagccc ctaagtcctt gatctatgct gcatccagtt tgcaaagggg ggtcccatca 180
aagttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattctg caacttatta ctgccaacaa tataaaattt ccccgctcac ttctggcgga 300
gggaccaagg tggagatcaa g 321

<210> 154
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 154
Asp Ile Gln Met Thr Gln Tyr Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Arg Gln Gly Ile Ser Asn Tyr
20 25 30
Leu Ala Trp Leu Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
35 40 45
Tyr Ala Ala Ser Ser Leu Gln Arg Gly Val Pro Ser Lys Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Tyr Lys Ile Ser Pro Leu
85 90 95
Thr Phe Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 155
<211> 18
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 155

cagggcataa gtaattat

18

<210> 156

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 156

Gln Gly Ile Ser Asn Tyr

1

5

<210> 157

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 157

gctgcatcc

9

<210> 158

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 158

Ala Ala Ser

1

<210> 159

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 159

caacaatata aaatttcccc gtcact

27

<210> 160

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 160

Gln Gln Tyr Lys Ile Ser Pro Leu Thr
 1 5

<210> 161

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 161

gagggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcaa cctctggatt caccttttagc agatatacca tgacctgggt ccgccaggct 120
 ccagggaagg ggtctgtttg ggtctcaggt attggtggta gtggtggtcg cgcatactac 180
 gcagactccg tgaagggccg gttcaccctc tccagagaca attccaagaa cacgctgtat 240
 ctgcaaataga acagcctgag agccgaggac acggccgtat attactgtgc gaaagagggg 300
 gatagtggct acgatttggg ctactggggc cggggaacc tggtcaccgt ctctca 357

<210> 162

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 162

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Arg Tyr
 20 25 30
 Thr Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Phe Trp Val
 35 40 45
 Ser Gly Ile Gly Gly Ser Gly Gly Arg Ala Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Leu 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 Lys Glu Gly Asp Ser Gly Tyr Asp Leu Asp Tyr Trp Gly Arg Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 163

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 163

gacatccaga tgaccagtc tccatcctca ctgtctgcat ctgtaggaga cagagtcacc 60

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atcacttgtc gggcgaggca gggcataagt aattatttag cctgggttca gcagaaacca 120
gggaaagccc ctaagtccct gatctatgct gcatccagtt tgcaaagggg ggtcccatca 180
aagttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattctg caacttatta ctgccaacaa tataaaattt ccccgctcac tttcggcgga 300
gggaccaagg tggagatcaa a                                     321

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<210> 164

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 164

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1           5           10           15
Asp Arg Val Thr Ile Thr Cys Arg Ala Arg Gln Gly Ile Ser Asn Tyr
          20          25          30
Leu Ala Trp Leu Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
          35          40          45
Tyr Ala Ala Ser Ser Leu Gln Arg Gly Val Pro Ser Lys Phe Ser Gly
          50          55          60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65          70          75          80
Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Tyr Lys Ile Ser Pro Leu
          85          90          95
Thr Phe Gly Gly Thr Lys Val Glu Ile Lys
          100          105

```

<210> 165

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 165

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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt caccttttagc agatatacca tgagctgggt ccgccaggct 120
ccaggggaagg ggcctggagtg ggtctcagct attggtggta gtggtggtcg cgcatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaataga acagcctgag agccgaggac acggccgtat attactgtgc gaaagagggg 300
gatagtggct acgatttggg ctactggggc caggggaacc tggtcaccgt ctccctca 357

```

<210> 166

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 166

```

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1           5           10           15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
          20          25          30
Thr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

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[illegible]

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<210> 167
<211> 322
<212> DNA
<213> Artificial Sequence
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<220>
<223> Synthetic

<400>	167						
gacatccaga	tgaccagctc	tccatcctca	ctgtctgcat	ctgtaggaga	cagagtcacc	60	
atcacttgtc	gggcgagtc	gggcataagt	aattatttag	cctggtttca	gcagaaacca	120	
gggaaagccc	ctaagtccct	gatctatgct	gcacccagtt	tgcaaagtgg	ggtcccatca	180	
aggttcagcg	gcagtggtatc	tgggacagat	ttcactctca	ccatcagcag	cctgcagcct	240	
gaagattttg	caacttatta	ctgccaaaca	tataaaattt	ccccgctcac	tttcggcgga	300	
gggaccaagg	tggagatcaa	ac				322	

```
<210> 168
<211> 107
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Synthetic

<400> 168															
Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5					10					15	
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Gly	Ile	Ser	Asn	Tyr
			20					25					30		
Leu	Ala	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Ser	Leu	Ile
		35				40						45			
Tyr	Ala	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75				80	
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Tyr	Lys	Ile	Ser	Pro	Leu
				85					90					95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys					
			100					105							

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<210> 169
<211> 348
<212> DNA
<213> Artificial Sequence
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<220>
<223> Synthetic

<400> 169
gaagtgcagt tgggtggagtc tgggggaggc ttagtacagc ctggcaggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccggcaagct 120
ccagggaagg gcctggaatg ggtctcaggt attagttgga atagcggtag caaaggcttt 180
gcggactctg tgaagggccg gttcaccatc tccagagaca acgccaagaa ctccctctat 240
ctgcaaatac acagtctgag agttgaagac acggccttgt attactgtgc aaaagagAAC 300
tggtcctttg actactgggg ccagggaacc ctggtcaccg tctcctca 348

<210> 170

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 170

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Arg
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Asp	Asp	Tyr
			20					25					30		
Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
			35				40					45			
Ser	Gly	Ile	Ser	Trp	Asn	Ser	Gly	Ser	Lys	Gly	Phe	Ala	Asp	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	Val	Glu	Asp	Thr	Ala	Leu	Tyr	Tyr	Cys
			85						90				95		
Ala	Lys	Glu	Asn	Trp	Ser	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val
			100					105					110		
Thr	Val	Ser	Ser												
			115												

<210> 171

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 171

ggattcacct ttgatgatta tgcc

24

<210> 172

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 172

Gly	Phe	Thr	Phe	Asp	Asp	Tyr	Ala
1				5			

<210> 173

<211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 173
 attagttgga atagcggtag caaa

24

<210> 174
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 174
 Ile Ser Trp Asn Ser Gly Ser Lys
 1 5

<210> 175
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 175
 gcaaaagaga actgggtcctt tgactac

27

<210> 176
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 176
 Ala Lys Glu Asn Trp Ser Phe Asp Tyr
 1 5

<210> 177
 <211> 336
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 177
 gatattgtga tgaccagac tccactctcc tcgcctgtca cccttgga gcccgcctcc 60
 atctcctgca ggtctagtca aagcctcgta cacagtgatg gaaatatcta cttgagttgg 120
 cttcagcaga ggccaggcca gcctccaaga ctcctaattt ataagatttc taaccgggttc 180
 tctgggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgaaaatc 240
 agcagggtgg aagctgaaga tgtcggaatt tattattgca tgcaagcttc gcattttccg 300

tacacttttg gccaggggac caagctggag atcaaa

336

<210> 178

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 178

Asp	Ile	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Ser	Pro	Val	Thr	Leu	Gly
1				5					10					15	
Gln	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	His	Ser
			20					25					30		
Asp	Gly	Asn	Ile	Tyr	Leu	Ser	Trp	Leu	Gln	Gln	Arg	Pro	Gly	Gln	Pro
		35					40					45			
Pro	Arg	Leu	Leu	Ile	Tyr	Lys	Ile	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro
		50				55					60				
Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ala	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile
65					70					75				80	
Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Ile	Tyr	Tyr	Cys	Met	Gln	Ala
				85					90					95	
Ser	His	Phe	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys
			100					105					110		

<210> 179

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 179

caaagcctcg tacacagtga tggaaatatac tac

33

<210> 180

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 180

Gln	Ser	Leu	Val	His	Ser	Asp	Gly	Asn	Ile	Tyr
1				5					10	

<210> 181

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 181

aagatttct

9

<210> 182
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 182
 Lys Ile Ser
 1

<210> 183
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 183
 atgcaagctt cgcattttcc gtacact

27

<210> 184
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 184
 Met Gln Ala Ser His Phe Pro Tyr Thr
 1 5

<210> 185
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 185
 gaagtgcagc tgggtggagtc tggggggaggc ttagtacagc ctggcaggtc cctgagactc 60
 tctgtgacag cctctggatt cacctttgat gattatgcca tgcactgggt ccggcaagct 120
 ccaggggaagg gcctggaatg ggtctcaggt attagttaga atagcggtag caaaggcttt 180
 gcggactctg tgaagggccg gttcaccatc tccagagaca acgccaagaa ctccctctat 240
 ctgcaaataga acagtctgag agttgaagac acggccttgt attactgtgc aaaagagaac 300
 tggtcctttg actactgggg ccaggggaacc ctggtcaccg tctcctca 348

<210> 186
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 186

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1          5          10          15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
      20          25          30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
      35          40          45
Ser Gly Ile Ser Trp Asn Ser Gly Ser Lys Gly Phe Ala Asp 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 Val Glu Asp Thr Ala Leu Tyr Tyr Cys
      85          90          95
Ala Lys Glu Asn Trp Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
      100          105          110
Thr Val Ser Ser
      115

```

<210> 187

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 187

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gatattgtga tgaccagac tccactctcc tcgcctgtca cccttgagaca gccggcctcc 60
atctcctgca ggtctagtca aagcctcgta cacagtgatg gaaatatcta cttgagttgg 120
cttcagcaga ggccaggcca gcctccaaga ctcttaattt ataagatttc taaccgggttc 180
tctgggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgaaaatc 240
agcagggtgg aagctgaaga tgtcggaatt tattattgca tgcaagcttc gcattttccg 300
tacacttttg gccaggggac caagctggag atcaaaa 336

```

<210> 188

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 188

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Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1          5          10          15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
      20          25          30
Asp Gly Asn Ile Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
      35          40          45
Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
      50          55          60
Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
      65          70          75          80
Ser Arg Val Glu Ala Glu Asp Val Gly Ile Tyr Tyr Cys Met Gln Ala
      85          90          95
Ser His Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
      100          105          110

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<210> 189
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 189
 gaagtgcagc tgggtggagtc tggggggaggc ttggtacagc ctggcaggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttgat gattatgccca tgcactgggt ccggcaagct 120
 ccagggaagg gcctggagtg ggtctcaggt attagttgga atagcggtag caaaggctat 180
 gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
 ctgcaaataga acagtctgag agctgaggac acggccttgt attactgtgc aaaagagaa 300
 tggtcctttg actactgggg ccagggaacc ctggtcaccg tctcctca 348

<210> 190
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 190
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Ser Trp Asn Ser Gly Ser Lys Gly Tyr Ala Asp 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 Lys Glu Asn Trp Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115

<210> 191
 <211> 337
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 191
 gatattgtga tgaccagac tccactctcc tcacctgtca cccttggaca gccggcctcc 60
 atctcctgca ggtctagtca aagcctcgta cacagtgatg gaaatatcta cttgagttgg 120
 cttcagcaga ggccaggcca gcctccaaga ctccctaattt ataagatttc taaccggttc 180
 tctgggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgaaaatc 240
 agcaggggtgg aagctgagga tgtcgggggtt tattactgca tgcaagcttc gcattttccg 300
 tacacttttg gccaggggac caagctggag atcaaac 337

<210> 192
 <211> 112

<212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 192
 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
 20 25 30
 Asp Gly Asn Ile Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
 35 40 45
 Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
 85 90 95
 Ser His Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 193
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 193
 gaagtgcaat tgggtggagtc tgggggaaac ttggtacagc ctggcaggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccggcaagct 120
 ccagggaagg gcctggagtg ggtctcaggt atcagttgga atagtggtag tagaggctat 180
 gcggactctg tgaagggccg attcaccatt tccagagaca acgccaacaaa ctccctgtat 240
 ctgcaaatga acagtctgag aactgaggac acggcctttt attattgtac aaaagaagac 300
 gaggccttttg actactgggg ccagggaacc ctggtcacccg tctcctca 348

<210> 194
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 194
 Glu Val Gln Leu Val Glu Ser Gly Gly Asn Leu Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Ser Trp Asn Ser Gly Ser Arg Gly Tyr Ala Asp 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 Thr Glu Asp Thr Ala Phe Tyr Tyr Cys
 85 90 95
 Thr Lys Glu Asp Glu Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

	100	105	110
Thr Val Ser Ser			
115			
<210> 195			
<211> 24			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Synthetic			
<400> 195			
ggattcacct ttgatgatta tgcc			24
<210> 196			
<211> 8			
<212> PRT			
<213> Artificial Sequence			
<220>			
<223> Synthetic			
<400> 196			
Gly Phe Thr Phe Asp Asp Tyr Ala			
1 5			
<210> 197			
<211> 24			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Synthetic			
<400> 197			
atcagttgga atagtggtag taga			24
<210> 198			
<211> 8			
<212> PRT			
<213> Artificial Sequence			
<220>			
<223> Synthetic			
<400> 198			
Ile Ser Trp Asn Ser Gly Ser Arg			
1 5			
<210> 199			
<211> 27			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Synthetic			

<400> 199
acaaaagaag acgaggcttt tgactac

27

<210> 200
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 200
Thr Lys Glu Asp Glu Ala Phe Asp Tyr
1 5

<210> 201
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 201
gatattgtga tgaccagac tccactctcc tcacctgtca cccttggaca gccggcctcc 60
atctcctgca ggtctagtca aagcctcgta cacagtgatc gaaacaccta cttgagttgg 120
cttcagcaga ggccaggcca gcctccaaga ctcttattt ataagatttc taaccggttc 180
tctggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgaaaatc 240
agcaggggtgg aagctgagga tgtcgggttt tattactgca tgcaggccac acaatttcgc 300
tacacttttg gccaggggac caaactgcag atcaat 336

<210> 202
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 202
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
1 5 10 15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30
Asp Arg Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
35 40 45
Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Phe Tyr Tyr Cys Met Gln Ala
85 90 95
Thr Gln Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Gln Ile Asn
100 105 110

<210> 203
<211> 33
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 203

caaagcctcg tacacagtga tcgaaacacc tac

33

<210> 204

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 204

Gln Ser Leu Val His Ser Asp Arg Asn Thr Tyr

1

5

10

<210> 205

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 205

aagatttct

9

<210> 206

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 206

Lys Ile Ser

1

<210> 207

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 207

atgcaggcca cacaatttcc gtacact

27

<210> 208

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 208

Met Gln Ala Thr Gln Phe Pro Tyr Thr
1 5

<210> 209

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 209

gaagtgcagc tgggtggagtc tgggggaaac ttggtacagc ctggcaggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttgat gattatgccca tgcactgggt ccggcaagct 120
ccagggaagg gcctggagtg ggtctcaggt atcagttgga atagtggtag tagaggctat 180
gcggactctg tgaagggccg attcaccatt tccagagaca acgcaaaaaa ctccctgtat 240
ctgcaaatga acagtctgag aactgaggac acggcctttt attattgtac aaaagaagac 300
gaggcttttg actactgggg ccagggaacc ctggtcaccg tctcctca 348

<210> 210

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 210

Glu Val Gln Leu Val Glu Ser Gly Gly Asn Leu Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Gly Ile Ser Trp Asn Ser Gly Ser Arg Gly Tyr Ala Asp 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 Thr Glu Asp Thr Ala Phe Tyr Tyr Cys
85 90 95
Thr Lys Glu Asp Glu Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110
Thr Val Ser Ser
115

<210> 211

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 211

gatattgtga tgaccacagac tccactctcc tcacctgtca ccttggaca gccggcctcc 60
atctcctgca ggtctagtca aagcctcgta cacagtgatc gaaacaccta cttgagttgg 120


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cttcagcaga ggccaggcca gcctccaaga ctcttattt ataagatttc taaccggttc 180
tctgggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgaaaatc 240
agcagggtgg aagctgagga tgtcgggttt tattactgca tgcaggccac acaatttcgc 300
tacacttttg gccaggggac caagctggag atcaaa 336

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<210> 212
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 212

Asp	Ile	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Ser	Pro	Val	Thr	Leu	Gly
1				5				10					15		
Gln	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	His	Ser
			20				25					30			
Asp	Arg	Asn	Thr	Tyr	Leu	Ser	Trp	Leu	Gln	Gln	Arg	Pro	Gly	Gln	Pro
		35					40				45				
Pro	Arg	Leu	Leu	Ile	Tyr	Lys	Ile	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro
		50				55					60				
Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ala	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile
65				70					75					80	
Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Phe	Tyr	Tyr	Cys	Met	Gln	Ala
			85					90					95		
Thr	Gln	Phe	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys
			100					105					110		

<210> 213
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 213

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gaagtgcagc tgggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60
tctgtgcag cctctggatt cacccttgat gattatgcca tgcactgggt ccggcaagct 120
ccagggaagg gcctggagtg ggtctcaggt atcagttgga atagtggtag tagaggctat 180
gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtac aaaagaagac 300
gaggcttttg actactgggg ccagggaacc ctggtcaccg tctcctca 348

```

<210> 214
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 214

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Arg
1				5				10					15		
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Asp	Asp	Tyr
			20				25					30			
Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35				40						45			

```

Ser Gly Ile Ser Trp Asn Ser Gly Ser Arg Gly Tyr Ala Asp 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
Thr Lys Glu Asp Glu Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
          100          105          110
Thr Val Ser Ser
          115

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<210> 215
 <211> 337
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

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<400> 215
gatattgtga tgaccagac tccactctcc tcacctgtca cccttggaca gccggcctcc 60
atctcctgca ggtctagtca aagcctcgta cacagtgatc gaaacaccta cttgagttgg 120
cttcagcaga ggccaggcca gcctccaaga ctcctaattt ataagatttc taaccgggtc 180
tctgggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgaaaatc 240
agcaggggtgg aagctgagga tgtcgggggt tattactgca tgcaggccac acaatttccg 300
tacacttttg gccaggggac caagctggag atcaaac 337

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<210> 216
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

```

<400> 216
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1          5          10          15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
          20          25          30
Asp Arg Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
          35          40          45
Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
          50          55          60
Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
 65          70          75          80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
          85          90          95
Thr Gln Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
          100          105          110

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<210> 217
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 217
 gaagtgcagc tgggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60
 tcctgtgcag cctctggctt cacctttgat gattatgcca tgcactgggt cgggcaagct 120
 ccggggaagg gcctagagtg ggtctcaggt attacttggg atagtggtag catggcctat 180
 gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
 ctgcaaatga acagtctgag agctgaggac acggccttat attactgtgc aaaagaaaac 300
 tgggcctttg actactgggg ccaggaacc ctggtcaccg tctcctca 348

<210> 218

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 218

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Arg
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Asp	Asp	Tyr
			20					25					30		
Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			
Ser	Gly	Ile	Thr	Trp	Asn	Ser	Gly	Thr	Met	Ala	Tyr	Ala	Asp	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	Lys	Glu	Asn	Trp	Ala	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val
			100					105						110	
Thr	Val	Ser	Ser												
			115												

<210> 219

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 219

ggcttcacct ttgatgatta tgcc

24

<210> 220

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 220

Gly	Phe	Thr	Phe	Asp	Asp	Tyr	Ala
1					5		

<210> 221

<211> 24

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 221
 attacttgga atagtgggtac catg

24

<210> 222
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 222
 Ile Thr Trp Asn Ser Gly Thr Met
 1 5

<210> 223
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 223
 gcaaaaagaaa actgggcctt tgactac

27

<210> 224
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 224
 Ala Lys Glu Asn Trp Ala Phe Asp Tyr
 1 5

<210> 225
 <211> 336
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 225
 gatattgtga tgaccagac tccactctcc tcacctgtca cccttggaca gccggcctcc 60
 atctcctgca ggtctagtca cagcctcgta cacagtgatg gaaacaccta cttgagttgg 120
 cttcagcaga ggccaggcca gcctccaaga ctccctaattt ataagatttc taaccgggttc 180
 tctgggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgaaaatc 240
 agcagggtgg aagctgagga tgtcgggggtt tatttctgca tgcaagctac acaatttccg 300
 tacacttttg gccaggggac caagctggag atcaaa 336

<210> 226
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 226
 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser His Ser Leu Val His Ser
 20 25 30
 Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
 35 40 45
 Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Phe Cys Met Gln Ala
 85 90 95
 Thr Gln Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 227
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 227
 cacagcctcg tacacagtga tggaaacacc tac

33

<210> 228
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 228
 His Ser Leu Val His Ser Asp Gly Asn Thr Tyr
 1 5 10

<210> 229
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 229
 aagatttct

9

<210> 230
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 230
 Lys Ile Ser
 1

<210> 231
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 231
 atgcaagcta cacaatttcc gtacact

27

<210> 232
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 232
 Met Gln Ala Thr Gln Phe Pro Tyr Thr
 1 5

<210> 233
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 233
 gaagtgcagc tgggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60
 tcctgtgcag cctctggcctt cacctttgat gattatgcca tgcactgggt ccggcaagct 120
 ccggggaagg gcctagagtg ggtctcaggt attacttgga atagtggtag catggcctat 180
 gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
 ctgcaaatga acagtctgag agctgaggac acggccttat attactgtgc aaaagaaaac 300
 tgggcctttg actactgggg ccaggggaacc ctggtcaccg tctcctca 348

<210> 234
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 234

```

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1           5           10           15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
      20           25           30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
      35           40           45
Ser Gly Ile Thr Trp Asn Ser Gly Thr Met Ala Tyr Ala Asp 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 Lys Glu Asn Trp Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
      100          105          110
Thr Val Ser Ser
      115

```

<210> 235

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 235

```

gatattgtga tgaccagac tccactctcc tcacctgtca cccttggaca gccggcctcc 60
atctcctgca ggtctagtca cagcctcgta cacagtgatg gaaacaccta cttgagttgg 120
cttcagcaga ggccaggcca gcctccaaga ctccctaattt ataagatttc taaccgggttc 180
tctgggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgaaaatc 240
agcagggtgg aagctgagga tgtcggggtt tatttctgca tgcaagctac acaatttccg 300
tacacttttg gccaggggac caagctggag atcaaa 336

```

<210> 236

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 236

```

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1           5           10           15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser His Ser Leu Val His Ser
      20           25           30
Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
      35           40           45
Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
      50           55           60
Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
      65           70           75           80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Phe Cys Met Gln Ala
      85           90           95
Thr Gln Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
      100          105          110

```

<210> 237

<211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 237
 gaagtgcagc tgggtggagtc tggggggaggc ttggtacagc ctggcaggtc cctgagactc 60
 tcctgtgcag cctctggctt cacctttgat gattatgcca tgcactgggt ccggcaagct 120
 ccaggggaagg gcctggagtg ggtctcaggt attacttgga atagtgttac catgggctat 180
 gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
 ctgcaaataga acagtctgag agctgaggac acggccttgt attactgtgc aaaagaaaac 300
 tgggcctttg actactgggg ccaggggaacc ctggtcaccg tctcctca 348

<210> 238
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 238
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Thr Trp Asn Ser Gly Thr Met Gly Tyr Ala Asp 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 Lys Glu Asn Trp Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115

<210> 239
 <211> 337
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 239
 gatattgtga tgacccagac tccactctcc tcacctgtca cccttgagaca gccggcctcc 60
 atctcctgca ggtctagtca cagcctcgta cacagtgatg gaaacaccta cttgagttgg 120
 cttcagcaga ggccaggcca gcctccaaga ctccctaattt ataagatttc taaccgggttc 180
 tctgggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgaaaatc 240
 agcagggtgg aagctgagga tgtcgggggt tattactgca tgcaagctac acaatttccg 300
 tacacttttg gccaggggac caagctggag atcaaac 337

<210> 240
 <211> 112
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 240

Asp	Ile	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Ser	Pro	Val	Thr	Leu	Gly
1				5					10					15	
Gln	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	His	Ser	Leu	Val	His	Ser
			20					25					30		
Asp	Gly	Asn	Thr	Tyr	Leu	Ser	Trp	Leu	Gln	Gln	Arg	Pro	Gly	Gln	Pro
		35					40					45			
Pro	Arg	Leu	Leu	Ile	Tyr	Lys	Ile	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro
	50					55					60				
Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ala	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile
65					70					75					80
Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys	Met	Gln	Ala
				85					90					95	
Thr	Gln	Phe	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys
			100					105						110	

<210> 241

<211> 384

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 241

gaagtgcagc	tggtggagtc	tggtggagtc	ttggtacagc	ctggcaggtc	cctgagactc	60
tcctgtgcag	cctctggatt	cacctttgat	gattatgcc	tgcaactggg	ccggcaagct	120
ccagggaagg	gcctggagtg	ggtctcaggt	attagttgga	atagtggtag	cataggctat	180
gcggactctg	tgaagggccg	attcaccatc	tccagagaca	acgccaagaa	ctccctgtat	240
ctgcaaatga	acagtctgag	agctgaggac	acggccttgt	attactgtgc	aaaagataga	300
ttccctccgt	ataagtataa	cagtgggtgt	ttttctgatg	cttttgaaat	ctggggccaa	360
gggacaatgg	tcaccgtctc	ttca				384

<210> 242

<211> 128

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 242

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Arg
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Asp	Asp	Tyr
			20					25					30		
Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			
Ser	Gly	Ile	Ser	Trp	Asn	Ser	Gly	Ser	Ile	Gly	Tyr	Ala	Asp	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	Lys	Asp	Arg	Phe	Pro	Pro	Tyr	Lys	Tyr	Asn	Ser	Gly	Gly	Phe	Ser

	100		105		110										
Asp	Ala	Phe	Glu	Ile	Trp	Gly	Gln	Gly	Thr	Met	Val	Thr	Val	Ser	Ser
	115						120					125			

<210> 243
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 243
 ggattcacct ttgatgatta tgcc 24

<210> 244
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 244
 Gly Phe Thr Phe Asp Asp Tyr Ala
 1 5

<210> 245
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 245
 attagttgga atagtggtag cata 24

<210> 246
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 246
 Ile Ser Trp Asn Ser Gly Ser Ile
 1 5

<210> 247
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 247
gcaaaagata gattccctcc gtataagtat aacagtgggtg gtttttctga tgcttttgaa 60
atc 63

<210> 248
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 248
Ala Lys Asp Arg Phe Pro Pro Tyr Lys Tyr Asn Ser Gly Gly Phe Ser
1 5 10 15
Asp Ala Phe Glu Ile
20

<210> 249
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 249
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtc gagttttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtggt gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtt ttactgtcag cagtatggta gttcacccgat caccttcggc 300
caaggggacac gactggagat tgaa 324

<210> 250
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 250
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Phe Ser Ser Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95
Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Glu
100 105

<210> 251

<211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 251
 cagagtttta gcagcagcta c

21

<210> 252
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 252
 Gln Ser Phe Ser Ser Ser Tyr
 1 5

<210> 253
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 253
 ggtgcatcc

9

<210> 254
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 254
 Gly Ala Ser
 1

<210> 255
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 255
 cagcagtatg gtagttcacc gatcacc

27

<210> 256
 <211> 9
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 256

Gln Gln Tyr Gly Ser Ser Pro Ile Thr
1 5

<210> 257

<211> 384

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 257

```
gaagtgcagc tgggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccggcaagct 120
ccagggaagg gcctggagtg ggtctcaggt attagttgga atagtggtag cataggctat 180
gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgc aaaagataga 300
ttccctccgt ataagtataa cagtgggtgt ttttctgatg cttttgaaat ctggggccaa 360
gggacaatgg tcaccgtctc ttca 384
```

<210> 258

<211> 128

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 258

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp 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 Lys Asp Arg Phe Pro Pro Tyr Lys Tyr Asn Ser Gly Gly Phe Ser
100 105 110
Asp Ala Phe Glu Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120 125
```

<210> 259

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 259
 gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcctgca gggccagtca gagtttttagc agcagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
 gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gttcaccgat caccttcggc 300
 caagggacac gactggagat taaa 324

<210> 260

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 260

Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly
1				5				10						15	
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Phe	Ser	Ser	Ser
			20					25					30		
Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu
		35					40					45			
Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser
	50					55					60				
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu
65					70					75					80
Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Gly	Ser	Ser	Pro
				85					90					95	
Ile	Thr	Phe	Gly	Gln	Gly	Thr	Arg	Leu	Glu	Ile	Lys				
			100					105							

<210> 261

<211> 384

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 261

gaagtgcagc tgggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttgat gattatgccca tgcactgggt ccggcaagct 120
 ccagggaagg gcctggagtg ggtctcaggc attagttgga atagtggtag cataggctat 180
 gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
 ctgcaaataa acagtctgag agctgaggac acggccttgt attactgtgc aaaagataga 300
 ttccctccgt ataagtataa cagtgggtgt ttttctgatg cttttgaaat ctggggccaa 360
 gggacaatgg tcaccgtctc ttca 384

<210> 262

<211> 128

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 262

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg

1	5	10	15
Ser Leu Arg	Leu Ser Cys Ala Ala	Ser Gly Phe Thr Phe	Asp Asp Tyr
	20	25	30
Ala Met His	Trp Val Arg Gln Ala	Pro Gly Lys Gly Leu	Glu Trp Val
	35	40	45
Ser Gly Ile	Ser Trp Asn Ser Gly	Ser Ile Gly Tyr Ala	Asp Ser Val
	50	55	60
Lys Gly Arg	Phe Thr Ile Ser Arg	Asn Ala Lys Asn Ser	Leu Tyr
	65	70	75
Leu Gln Met	Asn Ser Leu Arg Ala	Glu Asp Thr Ala Leu	Tyr Tyr Cys
	85	90	95
Ala Lys Asp	Arg Phe Pro Pro Tyr	Lys Tyr Asn Ser Gly	Gly Phe Ser
	100	105	110
Asp Ala Phe	Glu Ile Trp Gly Gln	Gly Thr Met Val Thr	Val Ser Ser
	115	120	125

<210> 263

<211> 325

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 263

```

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtttttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gattcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gttcaccgat caccttcggc 300
caaggggacac gactggagat taaac                                     325

```

<210> 264

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 264

Glu Ile Val	Leu Thr Gln Ser Pro	Gly Thr Leu Ser Leu	Ser Pro Gly
1	5	10	15
Glu Arg Ala	Thr Leu Ser Cys Arg	Ala Ser Gln Ser Phe	Ser Ser Ser
	20	25	30
Tyr Leu Ala	Trp Tyr Gln Gln Lys	Pro Gly Gln Ala Pro	Arg Leu Leu
	35	40	45
Ile Tyr Gly	Ala Ser Ser Arg Ala	Thr Gly Ile Pro	Asp Arg Phe Ser
	50	55	60
Gly Ser Gly	Ser Gly Thr Asp Phe	Thr Leu Thr Ile Ser	Arg Leu Glu
	65	70	75
Pro Glu Asp	Phe Ala Val Tyr Tyr	Cys Gln Gln Tyr Gly	Ser Ser Pro
	85	90	95
Ile Thr Phe	Gly Gln Gly Thr Arg	Leu Glu Ile Lys	
	100	105	

<210> 265

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 265

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gaggtgcagc tgggtggagtc tggggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt agctacgaca tgcactgggt ccgccaagtt 120
acaggaaaag gtctggaatg ggtctcagtc attggtactg ttggtgacac atactatcca 180
ggctccctga agggccgatt caccatctcc agagaaaatg ccaagaactc cttgtatctt 240
caaatgaaca ccctgagagc cggggacacg gctgtttatt actgtgcaag aactggagca 300
gcagcccact cgtactacta cggtatggac gtctggggcc aaggggacat ggtcaccgtc 360
tcctca 366
```

<210> 266

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 266

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1           5           10           15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
      20           25           30
Asp Met His Trp Val Arg Gln Val Thr Gly Lys Gly Leu Glu Trp Val
      35           40           45
Ser Val Ile Gly Thr Val Gly Asp Thr Tyr Tyr Pro Gly Ser Leu Lys
      50           55           60
Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn Ser Leu Tyr Leu
      65           70           75           80
Gln Met Asn Thr Leu Arg Ala Gly Asp Thr Ala Val Tyr Tyr Cys Ala
      85           90           95
Arg Thr Gly Ala Ala Ala His Ser Tyr Tyr Tyr Gly Met Asp Val Trp
      100          105          110
Gly Gln Gly Thr Met Val Thr Val Ser Ser
      115          120
```

<210> 267

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 267

ggattcacct tcagtagcta cgac

24

<210> 268

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 268

Gly Phe Thr Phe Ser Ser Tyr Asp
 1 5

<210> 269
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 269
 attggtactg ttggtgacac a 21

<210> 270
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 270
 Ile Gly Thr Val Gly Asp Thr
 1 5

<210> 271
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 271
 gcaagaactg gagcagcagc ccactcgtac tactacggta tggacgtc 48

<210> 272
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 272
 Ala Arg Thr Gly Ala Ala Ala His Ser Tyr Tyr Tyr Gly Met Asp Val
 1 5 10 15

<210> 273
 <211> 336
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 273

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gatattgtga tgactcagtc tccactctcc ctgcccgtca cccctggaga gccggcctcc 60
atctcctgca ggtctagtca gagcctcctg tatagtaatg gatacaacta tttggattgg 120
tacctacaga agccagggca gtctccacag ctccctgatct atttgggttc taatcggggc 180
tccgggggtcc ctgacagggtt cagtggcagt ggatcaggca cagattttac actgaaaatc 240
agcagagtgg aggctgagga tgttggaatt tattactgca tgcaagctct acaaaactccg 300
tggaaggttcg gcccaaggac caaggtggaa atcaaa 336

```

<210> 274

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 274

```

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1           5           10           15
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Tyr Ser
20          25          30
Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35          40          45
Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
50          55          60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65          70          75          80
Ser Arg Val Glu Ala Glu Asp Val Gly Ile Tyr Tyr Cys Met Gln Ala
85          90          95
Leu Gln Thr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100         105         110

```

<210> 275

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 275

cagagcctcc tgtatagtaa tggatacaac tat

33

<210> 276

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 276

```

Gln Ser Leu Leu Tyr Ser Asn Gly Tyr Asn Tyr
1           5           10

```

<210> 277

<211> 9

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 277
ttgggttct

9

<210> 278
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 278
Leu Gly Ser
1

<210> 279
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 279
atgcaagctc taaaactcc gtggacg

27

<210> 280
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 280
Met Gln Ala Leu Gln Thr Pro Trp Thr
1 5

<210> 281
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 281
gaggtgcagc tgggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt agctacgaca tgcactgggt ccgccaagtt 120
acaggaaaag gtctggaatg ggtctcagtc atttggtactg ttggtgacac atactatcca 180
ggctccctga agggccgatt caccatctcc agagaaaatg ccaagaactc cttgtatctt 240
caaatgaaca ccctgagagc cggggacacg gctgtttatt actgtgcaag aactggagca 300
gcagccact cgtactacta cggtatggac gtctggggcc aagggaccac ggtcaccgtc 360
tcc 363

<210> 282

<211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 282
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Asp Met His Trp Val Arg Gln Val Thr Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Val Ile Gly Thr Val Gly Asp Thr Tyr Tyr Pro Gly Ser Leu Lys
 50 55 60
 Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80
 Gln Met Asn Thr Leu Arg Ala Gly Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Thr Gly Ala Ala Ala His Ser Tyr Tyr Tyr Gly Met Asp Val Trp
 100 105 110
 Gly Gln Gly Thr Thr Val Thr Val Ser
 115 120

<210> 283
 <211> 336
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 283
 gatattgtga tgactcagtc tccactctcc ctgcccgtca cccctggaga gccggcctcc 60
 atctcctgca ggtctagtca ggcctcctg tatagtaatg gatacaacta ttgggattgg 120
 tacctacaga agccagggca gtctccacag ctccctgatct atttgggttc taatcggggcc 180
 tccgggggtcc ctgacagggt cagtggcagt ggatcaggca cagattttac actgaaaatc 240
 agcagagtgg aggctgagga tgttggaatt tattactgca tgcaagctct acaaaactccg 300
 tggacgttcg gccaaaggac caaggtggaa atcaaa 336

<210> 284
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 284
 Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
 1 5 10 15
 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Tyr Ser
 20 25 30
 Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45
 Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Ile Tyr Tyr Cys Met Gln Ala
 85 90 95
 Leu Gln Thr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105 110

<210> 285
 <211> 364
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 285
 gaggtgcagc tgggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctctggatt caccttcagt agctacgaca tgcaactgggt ccgccaagct 120
 acaggaaaag gtctggagtg ggtctcagct atttggtactg ttggtgacac atactatcca 180
 ggctccgtga agggccgatt caccatctcc agagaaaatg ccaagaactc cttgtatctt 240
 caaatgaaca gcctgagagc cggggacacg gctgtgtatt actgtgcaag aactggagca 300
 gcagcccact cgtactacta cggtatggac gtctggggcc aagggaccac gggtcaccgtc 360
 tcct 364

<210> 286
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 286
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Asp Met His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ala Ile Gly Thr Val Gly Asp Thr Tyr Tyr Pro Gly Ser Val Lys
 50 55 60
 Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80
 Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Thr Gly Ala Ala Ala His Ser Tyr Tyr Tyr Gly Met Asp Val Trp
 100 105 110
 Gly Gln Gly Thr Thr Val Thr Val Ser
 115 120

<210> 287
 <211> 337
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 287
 gatattgtga tgactcagtc tccactctcc ctgcccgtea cccctggaga gccggcctcc 60
 atctcctgca ggtctagtca gagcctcctg tatagtaatg gatacaacta tttggattgg 120

```

tacctgcaga agccagggca gtctccacag ctctgatct atttgggttc taatcgggcc 180
tccgggggtcc ctgacagggt cagtggcagt ggatcaggca cagattttac actgaaaatc 240
agcagagtgg aggctgagga tgttgggggt tattactgca tgcaagctct acaaactccg 300
tggaaggttc gccaaggga caaggtgga atcaaac 337

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<210> 288

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 288

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Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1           5           10           15
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Tyr Ser
20           25           30
Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35           40           45
Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
50           55           60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65           70           75           80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
85           90           95
Leu Gln Thr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100          105          110

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<210> 289

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 289

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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tctgtgcag cctctggatt cacccttagc agctatgcca tgacctgggt ccgccaggct 120
ccagggaagg ggctgtattg ggtctcagct attagtggta gtggtggtag cgcatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagagggg 300
gatagtggct acgatttggga ctactggggc cggggaaccc tggtcaccgt ctcgctca 357

```

<210> 290

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 290

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1           5           10           15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20           25           30
Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Tyr Trp Val
35           40           45

```

```

Ser Ala Ile Ser Gly Ser Gly Gly Ser Ala Tyr Tyr Ala Asp Ser Val
 50          55          60
Lys Gly Arg Phe Thr Ile 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 Lys Glu Gly Asp Ser Gly Tyr Asp Leu Asp Tyr Trp Gly Arg Gly
          100          105          110
Thr Leu Val Thr Val Ser Ser
          115

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<210> 291
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 291
 ggattcacct ttagcagcta tgcc 24

<210> 292
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 292
 Gly Phe Thr Phe Ser Ser Tyr Ala
 1 5

<210> 293
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 293
 attagtggta gtggtggtag cgca 24

<210> 294
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 294
 Ile Ser Gly Ser Gly Gly Ser Ala
 1 5

<210> 295

<211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 295
 gcgaaagagg gggatagtgg ctacgatttg gactac

36

<210> 296
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 296
 Ala Lys Glu Gly Asp Ser Gly Tyr Asp Leu Asp Tyr
 1 5 10

<210> 297
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 297
 gacatccaga tgaccagtc tccatcctca ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgtc gggcgaggca gggcattagt aattatttag cctggcttca gcagaaacca 120
 gggaaagccc ctaagtcctt gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
 aagttcagcg gcagtggatc tgggacagat ttactctca ccatcagcag cctgcagcct 240
 gaagattttg caacttatta ctgccaacaa tataaaagtt ccccgctcac tttcggcgga 300
 gggaccaagg tggagatcaa a 321

<210> 298
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 298
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Arg Gln Gly Ile Ser Asn Tyr
 20 25 30
 Leu Ala Trp Leu Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
 35 40 45
 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Lys Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Lys Ser Ser Pro Leu
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

100	105	
<210> 299		
<211> 18		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Synthetic		
<400> 299		
cagggcatta gtaattat		18
<210> 300		
<211> 6		
<212> PRT		
<213> Artificial Sequence		
<220>		
<223> Synthetic		
<400> 300		
Gln Gly Ile Ser Asn Tyr		
1 5		
<210> 301		
<211> 9		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Synthetic		
<400> 301		
gctgcatcc		9
<210> 302		
<211> 3		
<212> PRT		
<213> Artificial Sequence		
<220>		
<223> Synthetic		
<400> 302		
Ala Ala Ser		
1		
<210> 303		
<211> 27		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Synthetic		
<400> 303		
caacaatata aaagttcccc gctcact		27

<210> 304
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 304
 Gln Gln Tyr Lys Ser Ser Pro Leu Thr
 1 5

<210> 305
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 305
 gaggtgcagc tgttgaggatc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctctggatt caccttttagc agctatgccca tgacctgggt ccgccagggt 120
 ccagggaagg ggcctgtattg ggtctcagct attagtggta gtggtggtag cgcatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcaaatac acagcctgag agccgaggac acggccgtat attactgtgc gaaagagggg 300
 gatagtggct acgatttgga ctactggggc cggggaacc tggtcaccgt ctctca 357

<210> 306
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 306
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Tyr Trp Val
 35 40 45
 Ser Ala Ile Ser Gly Ser Gly Gly Ser Ala Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile 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 Lys Glu Gly Asp Ser Gly Tyr Asp Leu Asp Tyr Trp Gly Arg Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 307
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 307

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gacatccaga tgacccagtc tccatcctca ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgtc gggcgaggca gggcattagt aattatttag cctggcttca gcagaaacca 120
gggaaagccc ctaagtcctt gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aagttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgccaacaa tataaaagtt ccccgctcac ttcggcgga 300
gggaccaagg tggagatcaa a                                     321

```

<210> 308

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 308

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1           5           10           15
Asp Arg Val Thr Ile Thr Cys Arg Ala Arg Gln Gly Ile Ser Asn Tyr
          20           25           30
Leu Ala Trp Leu Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
          35           40           45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Lys Phe Ser Gly
          50           55           60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65           70           75           80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Lys Ser Ser Pro Leu
          85           90           95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
          100          105

```

<210> 309

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 309

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gaggtgcagc tgttgaggtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt caccttttagc agctatgcca tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cgcatactac 180
gcagactccg tgaagggccg gtccaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatac acagcctgag agccgaggac acggccgtat attactgtgc gaaagagggg 300
gatagtggct acgatttgga ctactggggc cagggaaccc tggtcaccgt ctccctca 357

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<210> 310

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 310

```

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1          5          10
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
          20          25          30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35          40          45
Ser Ala Ile Ser Gly Ser Gly Gly Ser Ala Tyr Tyr Ala Asp Ser Val
          50          55          60
Lys Gly Arg Phe Thr Ile 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 Lys Glu Gly Asp Ser Gly Tyr Asp Leu Asp Tyr Trp Gly Gln Gly
          100          105          110
Thr Leu Val Thr Val Ser Ser
          115

```

<210> 311

<211> 322

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 311

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gacatccaga tgacccagtc tccatcctca ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgtc gggcgagtc gggcattagt aattatttag cctgggttca gcagaaacca 120
gggaaagccc ctaagtcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
agggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgccaacaa tataaaagtt ccccgctcac tttcggcgga 300
gggaccaagg tggagatcaa ac                                     322

```

<210> 312

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 312

```

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1          5          10          15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr
          20          25          30
Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
          35          40          45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
          50          55          60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65          70          75          80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Lys Ser Ser Pro Leu
          85          90          95
Thr Phe Gly Gly Thr Lys Val Glu Ile Lys
          100          105

```

<210> 313

<211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 313
 gaagtgcagt tgggtggagtc tggggggaggc ttggtacagc ctggcaggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt cgggcaagtt 120
 ccaggggaagg gcctggagtg ggtctcaggt attacttgga atagtggtag catagactat 180
 gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
 ctgcaaataga acagtctgag agctgaggac acggccttct attattgtgt aaaagaagat 300
 gaggccttttg actactgggg ccaggggaacc ctggtcaccg tctcctca 348

<210> 314
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 314
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Thr Trp Asn Ser Gly Ser Ile Asp Tyr Ala Asp 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 Phe Tyr Tyr Cys
 85 90 95
 Val Lys Glu Asp Glu Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115

<210> 315
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 315
 ggattcacct ttgatgatta tgcc 24

<210> 316
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 316

Gly Phe Thr Phe Asp Asp Tyr Ala
1 5

<210> 317

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 317

attacttgga atagtggtag cata

24

<210> 318

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 318

Ile Thr Trp Asn Ser Gly Ser Ile
1 5

<210> 319

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 319

gtaaaagaag atgaggcttt tgactac

27

<210> 320

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 320

Val Lys Glu Asp Glu Ala Phe Asp Tyr
1 5

<210> 321

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 321
gatattgtga tgacccagac tccactctcc tcacctgtca cccttggaca gccggcctcc 60
atctcctgta ggtctagtca aagcctcgta cacagtgatg gaaacaccta tttgagttgg 120
cttcagcaga ggccaggcca gcctccaaga ctcctaattt ataagatttc taaccgggtc 180
tctgggggtcc cagacagaat cagtggcagt ggggcaggga cagatttcac actgaaaatc 240
agcagggtgg aggetgagga tgtcggcggtt tattattgca tgcaagctac acaatttccg 300
tacacttttg gccaggggac caagctggag atcaaa 336

<210> 322
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 322
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
1 5 10 15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30
Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
35 40 45
Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
50 55 60
Asp Arg Ile Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
85 90 95
Thr Gln Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 323
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 323
caaagcctcg tacacagtga tggaaacacc tat 33

<210> 324
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 324
Gln Ser Leu Val His Ser Asp Gly Asn Thr Tyr
1 5 10

<210> 325
<211> 9
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 325

aagatttct

9

<210> 326

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 326

Lys Ile Ser

1

<210> 327

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 327

atgcaagcta cacaatttcc gtacact

27

<210> 328

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 328

Met Gln Ala Thr Gln Phe Pro Tyr Thr

1

5

<210> 329

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 329

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gaagtgcagc tgggtggagtc tggggggaggc ttggtacagc ctggcaggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccggcaagtt 120
ccagggaagg gcctggagtg ggtctcaggt attacttga atagtggtag catagactat 180
gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaatga acagtctgag agctgaggac acggccttct attattgtgt aaaagaagat 300
gaggcttttg actactgggg ccagggaacc ctggtcaccg tctcctca 348

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<210> 330

<211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 330
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Thr Trp Asn Ser Gly Ser Ile Asp Tyr Ala Asp 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 Phe Tyr Tyr Cys
 85 90 95
 Val Lys Glu Asp Glu Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115

<210> 331
 <211> 336
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 331
 gatattgtga tgacccagac tccactctcc tcacctgtca cccttggaca gccggcctcc 60
 atctcctgta ggtctagtca aagcctcgta cacagtgatg gaaacaccta tttgagttgg 120
 cttcagcaga ggccaggcca gcctccaaga ctccctaattt ataagatttc taaccgggttc 180
 tctgggggtcc cagacagaat cagtggcagt ggggcaggga cagatttcac actgaaaatc 240
 agcagggtgg aggctgagga tgtcggcgtt tattattgca tgcaagctac acaatttccg 300
 tacacttttg gccaggggac caagctggag atcaaa 336

<210> 332
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 332
 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
 20 25 30
 Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
 35 40 45
 Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 Asp Arg Ile Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
 85 90 95
 Thr Gln Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 333
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 333
 gaagtgcagc tgggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccggcaagct 120
 ccaggggaagg gcctggagtg ggtctcaggt attacttgga atagtggtag cataggctat 180
 gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
 ctgcaaataga acagtctgag agctgaggac acggccttgt attactgtgt aaaagaagat 300
 gaggccttttg actactgggg ccaggggaacc ctggtcaccg tctcctca 348

<210> 334
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 334
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Thr Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp 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
 Val Lys Glu Asp Glu Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115

<210> 335
 <211> 337
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 335
 gatattgtga tgaccagac tccactctcc tcacctgtca cccttgagaca gccggcctcc 60
 atctcctgca ggtctagtca aagcctcgta cacagtgatg gaaacaccta tttgagttgg 120
 cttcagcaga ggccaggcca gctccaaga ctctaattt ataagatttc taaccggttc 180

tctgggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgaaaatc 240
 agcaggggtgg aagctgagga tgtcgggggtt tattactgca tgcaagctac acaattttccg 300
 tacacttttg gccaggggac caagctggag atcaaac 337

<210> 336

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 336

Asp	Ile	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Ser	Pro	Val	Thr	Leu	Gly
1				5					10					15	
Gln	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	His	Ser
			20					25					30		
Asp	Gly	Asn	Thr	Tyr	Leu	Ser	Trp	Leu	Gln	Gln	Arg	Pro	Gly	Gln	Pro
		35					40					45			
Pro	Arg	Leu	Leu	Ile	Tyr	Lys	Ile	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro
	50					55					60				
Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ala	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile
65					70					75					80
Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys	Met	Gln	Ala
			85						90					95	
Thr	Gln	Phe	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys
			100					105						110	

<210> 337

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 337

gaggtgcaac tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttaga agttatacca tgacctgggt ccgccaggct 120
 ccagggaagg gactggattg ggtctcaggt attactgata gtggtgctgg cacatactac 180
 ggagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcaaataga acagcctgag agccgaggac acggccgtgt attactgtgt gaaagagggg 300
 gatagtggct acgatttgga ctactggggc cagggaacc tggtcaccgt ctccctca 357

<210> 338

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 338

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Arg	Ser	Tyr
			20					25					30		
Thr	Met	Thr	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Asp	Trp	Val
		35				40						45			
Ser	Gly	Ile	Thr	Asp	Ser	Gly	Ala	Gly	Thr	Tyr	Tyr	Gly	Asp	Ser	Val

[illegible]

```
<210> 339
<211> 24
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Synthetic

<400> 339
ggattcacct ttagaagtta tacc 24

```
<210> 340
<211> 8
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Synthetic

<400> 340
Gly Phe Thr Phe Arg Ser Tyr Thr
1 5

```
<210> 341
<211> 24
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Synthetic

<400> 341
attactgata gtggtgctgg caca 24

```
<210> 342
<211> 8
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Synthetic

```
<400> 342
Ile Thr Asp Ser Gly Ala Gly Thr
  1             5
```

$$\begin{array}{ll} \langle 210 \rangle & 343 \\ \langle 211 \rangle & 36 \end{array}$$

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 343

gtgaaagagg gggatagtgg ctacgatttg gactac

36

<210> 344

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 344

Val	Lys	Glu	Gly	Asp	Ser	Gly	Tyr	Asp	Leu	Asp	Tyr
1				5					10		

<210> 345

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 345

gacatccaga	tgacccagtc	tccatcctca	ctgtctgcat	ctgtaggaga	cagagtcacc	60
atcacttgtc	ggggagagtc	gggcattagt	acttatttag	cctgggttca	gcagaaacca	120
gggaaagccc	ctaagtcctt	gatctatgct	acatccagtt	tgcaaagtgg	ggtcccatca	180
aagttcagcg	gcagtagatc	tgggacagat	ttcactctca	ccatcagcag	cctgcagcct	240
gaagattttg	caacttatta	ctgccaacaa	tataagagtt	ccccgctcac	tttcggcgga	300
gggaccaagg	tggagatcaa	a				321

<210> 346

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 346

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5					10					15	
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Gly	Ile	Ser	Thr	Tyr
		20						25					30		
Leu	Ala	Trp	Leu	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Ser	Leu	Ile
		35					40					45			
Tyr	Ala	Thr	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Lys	Phe	Ser	Gly
	50					55					60				
Ser	Arg	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75				80	
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Tyr	Lys	Ser	Ser	Pro	Leu
				85					90					95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys					
			100					105							

<210> 347
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 347
cagggcatta gtacttat

18

<210> 348
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 348
Gln Gly Ile Ser Thr Tyr
1 5

<210> 349
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 349
gctacatcc

9

<210> 350
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 350
Ala Thr Ser
1

<210> 351
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 351
caacaatata agagttcccc gctcact

27

<210> 352
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 352
 Gln Gln Tyr Lys Ser Ser Pro Leu Thr
 1 5

<210> 353
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 353
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttaga agttatacca tgacctgggt ccgccaggct 120
 ccagggaagg gactggattg ggtctcaggt attactgata gtggtgctgg cacatactac 180
 ggagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcaaataga acagcctgag agccgaggac acggccgtgt attactgtgt gaaagagggg 300
 gatagtggct acgatttggg ctactggggc cagggaaccc tggtcaccgt ctcctca 357

<210> 354
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 354
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Tyr
 20 25 30
 Thr Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Asp Trp Val
 35 40 45
 Ser Gly Ile Thr Asp Ser Gly Ala Gly Thr Tyr Tyr Gly Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile 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
 Val Lys Glu Gly Asp Ser Gly Tyr Asp Leu Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 355
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 355

```

gacatccaga tgacccagtc tccatcctca ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgtc gggcgagtc gggcattagt acttatttag cctgggttca gcagaaacca 120
gggaaagccc ctaagtcctt gatctatgct acatccagtt tgcaaagtgg ggtcccatca 180
aagttcagcg gcagtagatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgccaacaa tataagagtt ccccgctcac tttcggcgga 300
gggaccaagg tggagatcaa a                                     321

```

<210> 356

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 356

```

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1           5           10           15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Thr Tyr
          20           25           30
Leu Ala Trp Leu Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
          35           40           45
Tyr Ala Thr Ser Ser Leu Gln Ser Gly Val Pro Ser Lys Phe Ser Gly
          50           55           60
Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65           70           75           80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Lys Ser Ser Pro Leu
          85           90           95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
          100          105

```

<210> 357

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 357

```

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttaga agttatacca tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcagct attactgata gtggtgctgg cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaataa acagcctgag agccgaggac acggccgtat attactgtgt gaaagagggg 300
gatagtggct acgatttgga ctactggggc cagggaaccc tggtcaccgt ctctca 357

```

<210> 358

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 358

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Tyr
 20 25 30
 Thr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ala Ile Thr Asp Ser Gly Ala Gly Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile 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
 Val Lys Glu Gly Asp Ser Gly Tyr Asp Leu Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 359
 <211> 322
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 359
 gacatccaga tgaccagtc tccatcctca ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgtc gggcgagtc gggcattagt acttatttag cctggtttca gcagaaacca 120
 gggaaagccc ctaagtccct gatctatgct acatccagtt tgcaaagtgg ggtcccatca 180
 aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
 gaagattttg caacttatta ctgccaaaca tataagagtt ccccgctcac ttctggcgga 300
 gggaccaagg tggagatcaa ac 322

<210> 360
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 360
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Thr Tyr
 20 25 30
 Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
 35 40 45
 Tyr Ala Thr Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Lys Ser Ser Pro Leu
 85 90 95
 Thr Phe Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 361
 <211> 348

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 361

```

gaagtgaac tgggtggagtc tgggggagac ttggtacagc ctggcaggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccggcaagct 120
ccagggaggg gcctagagtg ggtctcaggt attacttgga atagtggtag catggcctat 180
gcggactctg tggagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctacaaatga acagtctgag agctgaggac acggccttat attactgtgc aagagaaaaac 300
tgggcctttg actactgggg ccaggaacc ctggtcacgc tctctca 348

```

<210> 362

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 362

```

Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Gln Pro Gly Arg
 1             5             10             15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
      20             25             30
Ala Met His Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
      35             40             45
Ser Gly Ile Thr Trp Asn Ser Gly Thr Met Ala Tyr Ala Asp Ser Val
      50             55             60
Glu 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 Glu Asn Trp Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
      100             105             110
Thr Val Ser Ser
      115

```

<210> 363

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 363

ggattcacct ttgatgatta tgcc

24

<210> 364

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 364

Gly Phe Thr Phe Asp Asp Tyr Ala
 1 5

<210> 365
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 365
 attacttgga atagtgggtac catg 24

<210> 366
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 366
 Ile Thr Trp Asn Ser Gly Thr Met
 1 5

<210> 367
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 367
 gcaagagaaa actgggcctt tgactac 27

<210> 368
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 368
 Ala Arg Glu Asn Trp Ala Phe Asp Tyr
 1 5

<210> 369
 <211> 336
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 369

```

gatattgtga tgaccagac tccactctcc tcacctgtca cccttggaca gccggcctcc 60
atctcctgca ggtctagtca cagcctcgta cacagtgatg gaaacaccta cttgagttgg 120
cttcagcaga ggccaggcca gcctccaaga ctcctaattt ataagatttc taaccgggtc 180
tctgggggcc cagacagatt cagtggcagt gggccaggga cagatttcac actgaaaatc 240
agcaggggtg aagctgagga tgtcgggggt tatttctgca tgcaagctac acaatttccg 300
tacacttttg gccaggggac caagctggag atcaaa 336

```

<210> 370

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 370

```

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
1           5           10           15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser His Ser Leu Val His Ser
20          25          30
Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
35          40          45
Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
50          55          60
Asp Arg Phe Ser Gly Ser Gly Pro Gly Thr Asp Phe Thr Leu Lys Ile
65          70          75          80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Phe Cys Met Gln Ala
85          90          95
Thr Gln Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100         105         110

```

<210> 371

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 371

cacagcctcg tacacagtga tggaaacacc tac

33

<210> 372

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 372

```

His Ser Leu Val His Ser Asp Gly Asn Thr Tyr
1           5           10

```

<210> 373

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 373

aagatttct

9

<210> 374

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 374

Lys Ile Ser

1

<210> 375

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 375

atgcaagcta cacaatttcc gtacact

27

<210> 376

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 376

Met Gln Ala Thr Gln Phe Pro Tyr Thr

1

5

<210> 377

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 377

gaagtgcagc	tgggtggagtc	tggggggagac	ttggtacagc	ctggcaggtc	cctgagactc	60
tctgtgcag	cctctggatt	cacctttgat	gattatgcc	tgcactgggt	ccggcaagct	120
ccagggaggg	gcctagagtg	ggtctcaggt	attacttgga	atagtggtag	catggcctat	180
gcggactctg	tggagggccg	attcaccatc	tccagagaca	acgccaagaa	ctccctgtat	240
ctacaaatga	acagtctgag	agctgaggac	acggccttat	attactgtgc	aagagaaaac	300
tgggcctttg	actactgggg	ccaggaacc	ctggtcaccg	tctcctca		348

<210> 378

<211> 116

<212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 378
 Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Thr Trp Asn Ser Gly Thr Met Ala Tyr Ala Asp Ser Val
 50 55 60
 Glu 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 Glu Asn Trp Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115

<210> 379
 <211> 336
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 379
 gatattgtga tgacccagac tccactctcc tcacctgtca cccttgagaca gccggcctcc 60
 atctcctgca ggtctagtca cagcctcgta cacagtgatg gaaacaccta cttgagttgg 120
 cttcagcaga ggccaggcca gcctccaaga ctcctaattt ataagatttc taaccgggtc 180
 tctgggggtcc cagacagatt cagtggcagt gggccaggga cagatttcac actgaaaatc 240
 agcaggggtgg aagctgagga tgtcgggggt tattttctgca tgcaagctac acaatttccg 300
 tacacttttg gccaggggac caagctggag atcaaa 336

<210> 380
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 380
 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser His Ser Leu Val His Ser
 20 25 30
 Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
 35 40 45
 Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Pro Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Phe Cys Met Gln Ala

				85						90					95				
Thr	Gln	Phe	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys				
			100					105					110						

<210> 381
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 381
 gaagtgcagc tgggtggagtc tggggggaggc ttggtacagc ctggcaggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccggcaagct 120
 ccaggggaagg gcctggagtg ggtctcaggt attacttgga atagtggtag catgggctat 180
 gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
 ctgcaaatac acagtctgag agctgaggac acggccttgt attactgtgc aagagaaaaac 300
 tgggcctttg actactgggg ccaggggaacc ctggtcaccc tctctca 348

<210> 382
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 382
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Thr Trp Asn Ser Gly Thr Met Gly Tyr Ala Asp 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 Glu Asn Trp Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115

<210> 383
 <211> 337
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 383
 gatattgtga tgaccagac tccactctcc tcacctgtca cccttggaca gccggcctcc 60
 atctcctgca ggtctagtca cagcctcgta cacagtgatg gaaacaccta cttgagttgg 120
 cttcagcaga ggccaggcca gctccaaga ctcttaattt ataagatttc taaccggttc 180
 tctggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgaaaatc 240

agcaggggtgg aagctgagga tgtcgggggtt tattactgca tgcaagctac acaattttccg 300
 tacacttttg gccaggggac caagctggag atcaaac 337

<210> 384
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 384
 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser His Ser Leu Val His Ser
 20 25 30
 Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
 35 40 45
 Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
 85 90 95
 Thr Gln Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 385
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 385
 gaggtgcaac tgggtggagtc tgggggaaac gtggtacggc cgggggggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttgat gattatggca tgacctgggt ccgccaagtt 120
 ccggggaagg ggtctggagt ggtctctggt attaatgga atggtggtag tacagattat 180
 gcagactctg tgaagggccg attcaccata tctagagaca acgccaagaa ctccctgtat 240
 ctgcaaataa atagtctgag agccgaggac acggccttat attactgtgc gagagataag 300
 gggttctacg gtatggacgt ctggggccaa gggaccacgg tcaccgtctc ctca 354

<210> 386
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 386
 Glu Val Gln Leu Val Glu Ser Gly Gly Asn 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 Thr Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Asn Trp Asn Gly Gly Ser Thr Asp Tyr Ala Asp 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 Asp Lys Gly Phe Tyr Gly Met Asp Val Trp Gly Gln Gly Thr
 100 105 110
 Thr Val Thr Val Ser Ser
 115

<210> 387
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 387
 ggattcacct ttgatgatta tggc 24

<210> 388
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 388
 Gly Phe Thr Phe Asp Asp Tyr Gly
 1 5

<210> 389
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 389
 attaattgga atggtggtag taca 24

<210> 390
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 390
 Ile Asn Trp Asn Gly Gly Ser Thr
 1 5

<210> 391
 <211> 33
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 391

gcgagagata aggggttcta cggtatggac gtc

33

<210> 392

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 392

Ala Arg Asp Lys Gly Phe Tyr Gly Met Asp Val
1 5 10

<210> 393

<211> 339

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 393

gacatcgtga tgaccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60
atcaactgca agtccagcca gaatccttta tacaactcca acaaaaagaa gtacttagct 120
tggtaccagc agaaaccagg acagccccct aagctgggtca tttactgggc atctaccggg 180
gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcaccagcc tacaggctga agatgtggca gtttattact gtcaacaata ttatagtact 300
ccgtacactt ttggccaggg gaccaagctg gagatcaaa 339

<210> 394

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 394

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Asn Pro Leu Tyr Asn
20 25 30
Ser Asn Lys Lys Lys Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45
Pro Pro Lys Leu Val Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60
Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80
Ile Thr Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95
Tyr Tyr Ser Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
100 105 110
Lys

<210> 395
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 395
cagaatcctt tatacaactc caacaaaaag aagtac

36

<210> 396
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 396
Gln Asn Pro Leu Tyr Asn Ser Asn Lys Lys Lys Tyr
1 5 10

<210> 397
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 397
tgggcatct

9

<210> 398
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 398
Trp Ala Ser
1

<210> 399
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 399
caacaatatt atagtactcc gtacact

27

<210> 400
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 400
 Gln Gln Tyr Tyr Ser Thr Pro Tyr Thr
 1 5

<210> 401
 <211> 351
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 401
 gaggtgcagc tgggtggagtc tgggggaaac gtggtacggc cggggggggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttgat gattatggca tgacctgggt ccgccaagtt 120
 ccggggaagg ggcctggagt ggtctctggt attaatgga atggtggtag tacagattat 180
 gcagactctg tgaagggccg attcaccata tctagagaca acgccaagaa ctccctgtat 240
 ctgcaaataa atagtctgag agccgaggac acggccttat attactgtgc gagagataag 300
 gggttctacg gtatggacgt ctgggggcaa gggaccacgg tcaccgtctc c 351

<210> 402
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 402
 Glu Val Gln Leu Val Glu Ser Gly Gly Asn 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 Thr Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Asn Trp Asn Gly Gly Ser Thr Asp Tyr Ala Asp 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 Asp Lys Gly Phe Tyr Gly Met Asp Val Trp Gly Gln Gly Thr
 100 105 110
 Thr Val Thr Val Ser
 115

<210> 403
 <211> 339
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 403

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gacatcgtga tgaccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60
atcaactgca agtccagcca gaatccttta tacaactcca acaaaaagaa gtacttagct 120
tggtaccagc agaaaccagg acagccccct aagctgggtca tttactgggc atctaccgg 180
gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcaccagcc tacaggctga agatgtggca gtttattact gtcaacaata ttatagtact 300
ccgtacactt ttggccaggg gaccaagctg gagatcaaa 339

```

<210> 404

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 404

```

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1           5           10           15
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Asn Pro Leu Tyr Asn
      20           25           30
Ser Asn Lys Lys Lys Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
      35           40           45
Pro Pro Lys Leu Val Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
      50           55           60
Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65           70           75           80
Ile Thr Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
      85           90           95
Tyr Tyr Ser Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
      100          105          110
Lys

```

<210> 405

<211> 352

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 405

```

gaggtgcagc tgggtggagtc tgggggaggt gtggtacggc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttgat gattatggca tgagctgggt ccgccaagct 120
ccaggggaagg ggctggagtg ggtctctggt attaattgga atggtggtag tacagggttat 180
gcagactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaatga acagtctgag agccgaggac acggccttgt atcactgtgc gagagataag 300
gggttctacg gtatggacgt ctggggccaa gggaccacgg tcaccgtctc ct 352

```

<210> 406

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 406

```

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 Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35          40          45
Ser Gly Ile Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp 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 Asp Lys Gly Phe Tyr Gly Met Asp Val Trp Gly Gln Gly Thr
          100          105          110
Thr Val Thr Val Ser
          115

```

<210> 407

<211> 340

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 407

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gacatcgtaga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60
atcaactgca agtccagcca gaatccttta tacaactcca acaaaaagaa gtacttagct 120
tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctaccggg 180
gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcaggctga agatgtggca gtttattact gtcaacaata ttatagtact 300
ccgtacactt ttggccaggg gaccaagctg gagatcaaac 340

```

<210> 408

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 408

```

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1          5          10          15
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Asn Pro Leu Tyr Asn
          20          25          30
Ser Asn Lys Lys Lys Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
          35          40          45
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50          55          60
Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65          70          75          80
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
          85          90          95
Tyr Tyr Ser Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
          100          105          110
Lys

```

<210> 409
 <211> 384
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 409
 gaagtgcagc tgggtggagtc tggggggaggc ttggtacagc ctggcaggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccggcaagct 120
 ccagggaagg gcctggagtg ggtctcaggt attagttgga atagtggtag cataggctat 180
 gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
 ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgc aaaagataga 300
 ttccctccgt ataagtataa cagtgggtgt ttttctgatg cttttgaaat ctgggggccaa 360
 gggacaatgg tcaccgtctc ttca 384

<210> 410
 <211> 128
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 410
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp 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 Lys Asp Arg Phe Pro Pro Tyr Lys Tyr Asn Ser Gly Gly Phe Ser
 100 105 110
 Asp Ala Phe Glu Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
 115 120 125

<210> 411
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 411
 ggattcacct ttgatgatta tgcc

24

<210> 412
 <211> 8
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 412

Gly Phe Thr Phe Asp Asp Tyr Ala
1 5

<210> 413

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 413

attagttgga atagtggtag cata

24

<210> 414

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 414

Ile Ser Trp Asn Ser Gly Ser Ile
1 5

<210> 415

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 415

gcaaaagata gattccctcc gtataagtat aacagtgggtg gtttttctga tgcttttgaa 60
atc 63

<210> 416

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 416

Ala Lys Asp Arg Phe Pro Pro Tyr Lys Tyr Asn Ser Gly Gly Phe Ser
1 5 10 15
Asp Ala Phe Glu Ile
20

<210> 417
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 417
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtttttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtggt gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gttcaccgat caccttcggc 300
caagggacac gactggagat tgaa 324

<210> 418
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 418
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Phe Ser Ser Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95
Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Glu
100 105

<210> 419
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 419
cagagtttta gcagcagcta c 21

<210> 420
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 420

Gln Ser Phe Ser Ser Ser Tyr
1 5

<210> 421
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 421
ggtgcatcc

9

<210> 422
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 422
Gly Ala Ser
1

<210> 423
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 423
cagcagtatg gtagttcacc gatcacc

27

<210> 424
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 424
Gln Gln Tyr Gly Ser Ser Pro Ile Thr
1 5

<210> 425
<211> 384
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 425

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gaagtgcagc tgggtggagtc tggggggaggc ttggtacagc ctggcaggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccggcaagct 120
ccaggggaagg gcttgagtg ggtctcaggt attagttgga atagtggtag cataggctat 180
cgggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgc aaaagataga 300
ttccctccgt ataagtataa cagtgggtgt ttttctgatg cttttgaaat ctggggccaa 360
gggacaatgg tcaccgtctc ttca                                     384

```

<210> 426

<211> 128

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 426

```

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1             5             10             15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
          20             25             30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35             40             45
Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp 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 Lys Asp Arg Phe Pro Pro Tyr Lys Tyr Asn Ser Gly Gly Phe Ser
          100             105             110
Asp Ala Phe Glu Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
          115             120             125

```

<210> 427

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 427

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gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtc gagtttttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgt ttactgtcag cagtatggta gttcaccgat caccttcggc 300
caagggacac gactggagat taaa                                     324

```

<210> 428

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 428

```

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly

```

1		5		10		15									
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Phe	Ser	Ser	Ser
			20					25					30		
Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu
		35					40					45			
Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser
	50					55					60				
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu
65					70					75					80
Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Gly	Ser	Ser	Pro
			85						90					95	
Ile	Thr	Phe	Gly	Gln	Gly	Thr	Arg	Leu	Glu	Ile	Lys				
			100					105							

<210> 429

<211> 384

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 429

```

gaagtgcagc  tgggtggagtc  tggggggaggc  ttggtacagc  ctggcaggtc  cctgagactc  60
tcctgtgcag  cctctggatt  cacctttgat  gattatgcc  tgactgggt  ccggcaagct  120
ccaggaagg  gcctggagtg  ggtctcaggt  attagttgga  atagtggtag  cataggctat  180
gcggactctg  tgaagggccg  attcaccatc  tccagagaca  acgccaagaa  ctccctgtat  240
ctgcaaata  acagtctgag  agctgaggac  acggccttgt  attactgtgc  aaaagataga  300
ttccctccgt  ataagtataa  cagtgggtgt  ttttctgatg  cttttgaaat  ctggggccaa  360
gggacaatgg  tcaccgtctc  ttca

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<210> 430

<211> 128

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 430

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Arg
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Asp	Asp	Tyr
			20					25					30		
Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			
Ser	Gly	Ile	Ser	Trp	Asn	Ser	Gly	Ser	Ile	Gly	Tyr	Ala	Asp	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	Lys	Asp	Arg	Phe	Pro	Pro	Tyr	Lys	Tyr	Asn	Ser	Gly	Gly	Phe	Ser
		100						105					110		
Asp	Ala	Phe	Glu	Ile	Trp	Gly	Gln	Gly	Thr	Met	Val	Thr	Val	Ser	Ser
		115					120					125			

<210> 431

<211> 325

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 431

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gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtc gagtttttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacagggttca gtggcagtggt gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtta ttactgtcag cagtatggta gttcaccgat caccttcggc 300
caagggacac gactggagat taaac 325

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<210> 432

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 432

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Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1           5           10           15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Phe Ser Ser Ser
20           25           30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35           40           45
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50           55           60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65           70           75           80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85           90           95
Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100           105

```

<210> 433

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 433

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gaggtgcagc tgggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tctgtgacag cctctggatt caccttcagt agctacgaca tgcactgggt ccgccaagtt 120
acaggaaaag gtctggaatg ggtctcagtc atttggtactg ttggtgacac atactatcca 180
ggctccctga agggccgatt caccatctcc agagaaaatg ccaagaactc cttgtatctt 240
caaatgaaca ccctgagagc cggggacacg gctgtttatt actgtgcaag aactggagca 300
gcagcccact cgtactacta cggtatggac gtctggggcc aagggaccat gggtcaccgtc 360
tcctca 366

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<210> 434

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 434

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr
			20					25					30		
Asp	Met	His	Trp	Val	Arg	Gln	Val	Thr	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35				40						45			
Ser	Val	Ile	Gly	Thr	Val	Gly	Asp	Thr	Tyr	Tyr	Pro	Gly	Ser	Leu	Lys
	50					55					60				
Gly	Arg	Phe	Thr	Ile	Ser	Arg	Glu	Asn	Ala	Lys	Asn	Ser	Leu	Tyr	Leu
65					70					75					80
Gln	Met	Asn	Thr	Leu	Arg	Ala	Gly	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala
				85					90					95	
Arg	Thr	Gly	Ala	Ala	Ala	His	Ser	Tyr	Tyr	Tyr	Gly	Met	Asp	Val	Trp
			100					105					110		
Gly	Gln	Gly	Thr	Met	Val	Thr	Val	Ser	Ser						
		115					120								

<210> 435

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 435

ggattcacct tcagtagcta cgac

24

<210> 436

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 436

Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Asp
1				5			

<210> 437

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 437

attggtactg ttggtgacac a

21

<210> 438

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 438

Ile Gly Thr Val Gly Asp Thr

1

5

<210> 439

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 439

gcaagaactg gagcagcagc ccactcgtac tactacggta tggacgtc

48

<210> 440

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 440

Ala Arg Thr Gly Ala Ala Ala His Ser Tyr Tyr Tyr Gly Met Asp Val

1

5

10

15

<210> 441

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 441

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtc gagtggttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtggt gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtt ttactgtcag cagtatggta gctcaccac tttcggcgga 300
gggaccaagg tggagatcaa a 321

<210> 442

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 442

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly

1

5

10

15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser

	20		25		30										
Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu
	35		40		45										
Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser
	50		55		60										
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu
65			70		75										80
Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Gly	Ser	Ser	Pro
			85		90									95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys					
			100		105										

<210> 443
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 443
 cagagtgtta gcagcagcta c 21

<210> 444
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 444
 Gln Ser Val Ser Ser Ser Tyr
 1 5

<210> 445
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 445
 ggtgcatcc 9

<210> 446
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 446
 Gly Ala Ser
 1

<210> 447
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 447
 cagcagtatg gtagctcacc cact

24

<210> 448
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 448
 Gln Gln Tyr Gly Ser Ser Pro Thr
 1 5

<210> 449
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 449
 gaggtgcagc tgggtggagtc tggggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctctggatt caccttcagt agctacgaca tgcactgggt ccgccaagtt 120
 acaggaaaag gtctggaatg ggtctcagtc attggtactg ttggtgacac atactatcca 180
 ggctccctga agggccgatt caccatctcc agagaaaatg ccaagaactc cttgtatctt 240
 caaatgaaca ccctgagagc cggggacacg gctgtttatt actgtgcaag aactggagca 300
 gcagcccact cgtactacta cggtatggac gtctggggcc aaggggaccac ggtcaccgtc 360
 tcc 363

<210> 450
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 450
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Asp Met His Trp Val Arg Gln Val Thr Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Val Ile Gly Thr Val Gly Asp Thr Tyr Tyr Pro Gly Ser Leu Lys
 50 55 60
 Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80
 Gln Met Asn Thr Leu Arg Ala Gly Asp Thr Ala Val Tyr Tyr Cys Ala

				85						90					95				
Arg	Thr	Gly	Ala	Ala	Ala	His	Ser	Tyr	Tyr	Tyr	Gly	Met	Asp	Val	Trp				
			100					105					110						
Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser											
		115					120												

<210> 451
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 451
 gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcctgca gggccagtc gagtggttagc agcagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
 gacaggttca gtggcagtggt gtctgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtt ttactgtcag cagtatggta gctcaccac tttcggcgga 300
 gggaccaagg tggagatcaa a 321

<210> 452
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 452
 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45
 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 453
 <211> 364
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 453
 gaggtgcagc tgggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc 60
 tcctgtgcag cctctggatt caccttcagt agctacgaca tgcaactgggt ccgccaagct 120
 acaggaaaag gtctggagtg ggtctcagct atttggtactg ttggtgacac atactatcca 180
 ggctccgtga agggccgatt caccatctcc agagaaaatg ccaagaactc cttgtatctt 240

```

caaatgaaca gcctgagagc cggggacacg gctgtgtatt actgtgcaag aactggagca 300
gcagcccact cgtactacta cggatatggac gtctggggcc aagggaccac ggtcaccgtc 360
tcct 364

```

<210> 454
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 454

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1			5					10					15		
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr
		20						25				30			
Asp	Met	His	Trp	Val	Arg	Gln	Ala	Thr	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			
Ser	Ala	Ile	Gly	Thr	Val	Gly	Asp	Thr	Tyr	Tyr	Pro	Gly	Ser	Val	Lys
	50					55					60				
Gly	Arg	Phe	Thr	Ile	Ser	Arg	Glu	Asn	Ala	Lys	Asn	Ser	Leu	Tyr	Leu
65					70				75						80
Gln	Met	Asn	Ser	Leu	Arg	Ala	Gly	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala
			85					90						95	
Arg	Thr	Gly	Ala	Ala	Ala	His	Ser	Tyr	Tyr	Tyr	Gly	Met	Asp	Val	Trp
			100				105						110		
Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser							
		115					120								

<210> 455
 <211> 322
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 455

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gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagttg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gtcacccac tttcggcgga 300
gggaccaagg tggagatcaa ac 322

```

<210> 456
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 456

Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly
1			5					10						15	
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Ser
		20					25					30			
Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu

	35					40				45					
Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser
	50					55					60				
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu
65					70					75					80
Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Gly	Ser	Ser	Pro
				85					90					95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys					
			100					105							

<210> 457
 <211> 345
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 457
 gaggtgcagc tgggtggagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggctc 60
 tcttgtaagg cttctggatt caccttcacc gactactata tgcactgggt gcgacaggcc 120
 cctggacaag ggcttgagtg gctgggatgg atcaacccta agagtgggtg gacaaagtat 180
 gcacagaggt ttcagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240
 atggaactga acggactaag atctgacgac acggccggtt tttactgtgc gcgaactgat 300
 gcttttgata tctggggcca agggacaatg gtcaccgtct cttca 345

<210> 458
 <211> 115
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

Glu	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	Phe	Thr	Phe	Thr	Asp	Tyr
		20					25						30		
Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Leu
		35				40						45			
Gly	Trp	Ile	Asn	Pro	Lys	Ser	Gly	Ala	Thr	Lys	Tyr	Ala	Gln	Arg	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	Asn	Gly	Leu	Arg	Ser	Asp	Asp	Thr	Ala	Val	Phe	Tyr	Cys
			85					90					95		
Ala	Arg	Thr	Asp	Ala	Phe	Asp	Ile	Trp	Gly	Gln	Gly	Thr	Met	Val	Thr
			100					105					110		
Val	Ser	Ser													
		115													

<210> 459
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 459
ggattcacct tcaccgacta ctat 24

<210> 460
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 460
Gly Phe Thr Phe Thr Asp Tyr Tyr
1 5

<210> 461
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 461
atcaacccta agagtgggtgc gaca 24

<210> 462
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 462
Ile Asn Pro Lys Ser Gly Ala Thr
1 5

<210> 463
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 463
gcgcgaactg atgcttttga tatc 24

<210> 464
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 464

Ala Arg Thr Asp Ala Phe Asp Ile
 1 5

<210> 465
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 465
 gacatccagt tgacccagtc tccttcacc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgcc gggccagtca gagtgttagt aactgggttg cctggatatca gcagaaacca 120
 gggaaagccc ctaaactcct gatctattcg gcgtctactt tagaaagtgg ggtcccatca 180
 aggttcagcg gcagtgaatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240
 gatgatattg caacttatta ctgccaacac tataatagtt attggacgtt cggccaaggg 300
 accaaggtgg aaatcaaacg a 321

<210> 466
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 466
 Asp Ile Gln Leu 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 Gln Ser Val Ser Asn Trp
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ser Ala Ser Thr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Glu 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 His Tyr Asn Ser Tyr Trp Thr
 85 90 95
 Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 467
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 467
 cagagtgtta gtaactgg 18

<210> 468
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
<223> Synthetic

<400> 468
Gln Ser Val Ser Asn Trp
1 5

<210> 469
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 469
tcggcgtct

9

<210> 470
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 470
Ser Ala Ser
1

<210> 471
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 471
caacactata atagttattg gacg

24

<210> 472
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 472
Gln His Tyr Asn Ser Tyr Trp Thr
1 5

<210> 473
<211> 345
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 473

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caggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgtaagg cttctggatt caccttcacc gactactata tgcactgggt gcgacaggcc 120
cctggacaag ggcttgagtg gctgggatgg atcaacccta agagtgggtgc gacaaagtat 180
gcacagaggt ttcagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240
atggaactga acggactaag atctgacgac acggccgttt tttactgtgc gcgaactgat 300
gcttttgata tctggggcca agggacaatg gtcaccgtct cttca 345

```

<210> 474

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 474

```

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 Phe Thr Phe Thr Asp Tyr
      20             25             30
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Leu
      35             40             45
Gly Trp Ile Asn Pro Lys Ser Gly Ala Thr Lys Tyr Ala Gln Arg 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 Asn Gly Leu Arg Ser Asp Asp Thr Ala Val Phe Tyr Cys
      85             90             95
Ala Arg Thr Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr
100             105             110
Val Ser Ser
      115

```

<210> 475

<211> 318

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 475

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gacatccaga tgacccagtc tccttcacc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggccagtca gagggttagt aactgggttg cctgggtatca gcagaaacca 120
gggaaagccc cttaaactcct gatctattcg gcgtctactt tagaaagtgg ggtcccatca 180
aggttcagcg gcagtgaatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240
gatgatattt caacttatta ctgccaacac tataatagtt attggacggt cggccaaggg 300
accaaggtgg aaatcaaa 318

```

<210> 476

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 476

```

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 Gln Ser Val Ser Asn Trp
          20           25           30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35           40           45
Tyr Ser Ala Ser Thr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
          50           55           60
Ser Glu 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 His Tyr Asn Ser Tyr Trp Thr
          85           90           95
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
          100           105

```

<210> 477

<211> 345

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 477

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caggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggctc 60
tcttgcaagg cttctggatt caccttcacc gactactata tgcactgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggatgg atcaacccta agagtgggtgc gacaaactat 180
gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240
atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gcgaactgat 300
gcttttgata tctggggcca agggacaatg gtcaccgtct ctcca 345

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<210> 478

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 478

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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 Phe Thr Phe Thr Asp Tyr
          20           25           30
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
          35           40           45
Gly Trp Ile Asn Pro Lys Ser Gly Ala Thr Asn 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 Thr Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr
          100           105           110
Val Ser Ser
          115

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<210> 479
 <211> 319
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 479
 gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgcc gggccagtc gagtggttagt aactgggttg cctggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctattcg gcgtctagtt tagaaagtgg ggtcccatca 180
 aggttcagcg gcagtggtatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240
 gatgattttg caacttatta ctgccaacac tataatagtt attggacgtt cggccaaggg 300
 accaaggtgg aaatcaaac 319

<210> 480
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 480
 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 Gln Ser Val Ser Asn Trp
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ser Ala Ser Ser Leu Glu 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 His Tyr Asn Ser Tyr Trp Thr
 85 90 95
 Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 481
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 481
 gaggtgcagc tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
 tcctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120
 ccaggcaagg ggcctggagtg ggtggcagtt atatggtatg atggaagtaa taaatactat 180
 gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcaaataga acagcctgag agccgaggac acggctgtgt attactgtgc gagagatgga 300
 tatagtggct acgatgacta ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> 482
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 482

Glu	Val	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	Ser	Tyr
			20					25					30		
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			
Ala	Val	Ile	Trp	Tyr	Asp	Gly	Ser	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	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	Arg	Asp	Gly	Tyr	Ser	Gly	Tyr	Asp	Asp	Tyr	Trp	Gly	Gln	Gly	Thr
			100					105					110		
Leu	Val	Thr	Val	Ser	Ser										
			115												

<210> 483

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 483

ggattcacct tcagtagcta tggc

24

<210> 484

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 484

Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Gly
1				5			

<210> 485

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 485

atatggtatg atggaagtaa taaa

24

<210> 486

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 486

Ile Trp Tyr Asp Gly Ser Asn Lys
1 5

<210> 487

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 487

gcgagagatg gatatagtgg ctacgatgac tac 33

<210> 488

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 488

Ala Arg Asp Gly Tyr Ser Gly Tyr Asp Asp Tyr
1 5 10

<210> 489

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 489

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gggcattaga aatgatttag gctggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tacaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tggcacagat ttactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtctacaa gattacaatt accctcggac gttcggccaa 300
gggaccaagc tggaaatcaa a 321

<210> 490

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 490

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
 20 25 30
 Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Tyr Asn Tyr Pro Arg
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 491
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 491
 cagggcatta gaaatgat

18

<210> 492
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 492
 Gln Gly Ile Arg Asn Asp
 1 5

<210> 493
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 493
 gctgcatcc

9

<210> 494
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 494
 Ala Ala Ser
 1

<210> 495
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 495
 ctacaagatt acaattaccc tcggacg

27

<210> 496
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 496
 Leu Gln Asp Tyr Asn Tyr Pro Arg Thr
 1 5

<210> 497
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 497
 caggtgcagc tgggtggagtc tggggggaggc gtggtccagc ctggggaggtc cctgagactc 60
 tctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg ggtggcagtt atatggtatg atggaagtaa taaatactat 180
 gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa caccgtgtat 240
 ctgcaaataga acagcctgag agccgaggac acggctgtgt attactgtgc gagagatgga 300
 tatagtggct acgatgacta ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> 498
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 498
 Gln Val 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 Ser Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile 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	Arg	Asp	Gly	Tyr	Ser	Gly	Tyr	Asp	Asp	Tyr	Trp	Gly	Gln	Gly	Thr				
			100					105					110						
Leu	Val	Thr	Val	Ser	Ser														
			115																

<210> 499
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 499
 gccatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgcc gggcaagtca gggcattaga aatgatttag gctggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatgct gcatccagtt tacaaagtgg ggtcccatca 180
 aggttcagcg gcagtggatc tggcacagat ttcaactctca ccatcagcag cctgcagcct 240
 gaagattttg caacttatta ctgtctacaa gattacaatt accctcggac gttcggccaa 300
 gggaccaagg tggaaatcaa a 321

<210> 500
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 500
 Ala Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
 20 25 30
 Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Tyr Asn Tyr Pro Arg
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 501
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 501
 caggtgcagc tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
 tcctgtgcag cgtctggatt caccttcagt agctatggca tgcaactgggt ccgccaggct 120
 ccaggcaagg ggctagagtg ggtggcagtt atatggtatg atggaagtaa taaatactat 180
 gcagactccg tgaaggggccc attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaataga acagcctgag agccgaggac acggctgtgt attactgtgc gagagatgga 300
tatagtggct acgatgacta ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> 502

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 502

Gln	Val	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	Ser	Tyr
			20					25					30		
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			
Ala	Val	Ile	Trp	Tyr	Asp	Gly	Ser	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	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	Arg	Asp	Gly	Tyr	Ser	Gly	Tyr	Asp	Asp	Tyr	Trp	Gly	Gln	Gly	Thr
			100					105					110		
Leu	Val	Thr	Val	Ser	Ser										
			115												

<210> 503

<211> 322

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 503

gccatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gggcattaga aatgatttag gctggatatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tacaaaagggt ggtcccatca 180
aggttcagcg gcagtggatc tggcacagat ttactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtctacaa gattacaatt accctcggac gttcggccaa 300
gggaccaagg tggaaatcaa ac 322

<210> 504

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 504

Ala	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1			5					10					15		
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Gly	Ile	Arg	Asn	Asp
			20					25					30		
Leu	Gly	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Tyr Asn Tyr Pro Arg
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 505
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 505
 gaggtgcagc tgggtgcagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccgacaaggc 120
 ccagggaagg gcctggagtg ggtctcaggt attagttgga atggtggtag cgcaggctat 180
 gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
 ctgcaattga acagtctgag agctgaggac acggccttgt attactgtgc aaaagaagac 300
 tatgcttttg atatctgggg ccaagggaca atggtcaccg tctcctca 348

<210> 506
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 506
 Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Gly Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Ser Trp Asn Gly Gly Ser Ala Gly Tyr Ala Asp 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 Leu Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95
 Ala Lys Glu Asp Tyr Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
 100 105 110
 Thr Val Ser Ser
 115

<210> 507
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 507
ggattcacct ttgatgatta tgcc 24

<210> 508
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 508
Gly Phe Thr Phe Asp Asp Tyr Ala
1 5

<210> 509
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 509
attagttgga atggtggtag cgca 24

<210> 510
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 510
Ile Ser Trp Asn Gly Gly Ser Ala
1 5

<210> 511
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 511
gcaaaagaag actatgcttt tgatatac 27

<210> 512
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 512
Ala Lys Glu Asp Tyr Ala Phe Asp Ile

1

5

<210> 513

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 513

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gacatcgtga tgacccagac tccactctcc tcacctgtca cccttggaca gccggcctcc 60
atctcctgca ggtctagtca aagcctcgta cacagtgatg gaaacaccta cttgagttgg 120
cttcagcaga ggccaggcca gcctccaaga ctcctaattt ataagatttc taaccggttc 180
tctggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgaaaatc 240
agcaggggtg aagctgagga tgtcggggtt tattactgca tgcaagctac acaatttccg 300
tacacttttg gccaggggac caaggtggag atcaaaa 336

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<210> 514

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 514

```

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
1           5           10           15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20           25           30
Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
35           40           45
Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
50           55           60
Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65           70           75           80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
85           90           95
Thr Gln Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100          105          110

```

<210> 515

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 515

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caaagcctcg tacacagtga tggaaacacc tac

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33

<210> 516

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 516

Gln Ser Leu Val His Ser Asp Gly Asn Thr Tyr
1 5 10

<210> 517

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 517

aagatttct

9

<210> 518

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 518

Lys Ile Ser

1

<210> 519

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 519

atgcaagcta cacaatttcc gtacact

27

<210> 520

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 520

Met Gln Ala Thr Gln Phe Pro Tyr Thr

1

5

<210> 521

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 521

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gaagtgcagc tgggtggagtc tggggggaggc ttggtacagc ctggcaggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttgat gattatgcca tgactgggt cgcacaaggt 120
ccagggaagg gcctggagtg ggtctcaggt attagttgga atggtggtag cgcaggctat 180
gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaattga acagtctgag agctgaggac acggccttgt attactgtgc aaaagaagac 300
tatgcttttg atatctgggg ccaagggaca atggtcaccg tctcttca 348

```

<210> 522

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 522

```

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1             5             10             15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
      20             25             30
Ala Met His Trp Val Arg Gln Gly Pro Gly Lys Gly Leu Glu Trp Val
      35             40             45
Ser Gly Ile Ser Trp Asn Gly Gly Ser Ala Gly Tyr Ala Asp 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 Leu Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
      85             90             95
Ala Lys Glu Asp Tyr Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
      100            105            110
Thr Val Ser Ser
      115

```

<210> 523

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 523

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gatattgtga tgaccagac tccactctcc tcacctgtca cccttggaca gccggcctcc 60
atctcctgca ggtctagtca aagcctcgta cacagtgatg gaaacaccta cttgagttgg 120
cttcagcaga ggccaggcca gcctccaaga ctccctaattt ataagatttc taaccggttc 180
tctgggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgaaaatc 240
agcaggggtgg aagctgagga tgtcgggggtt tattactgca tgcaagctac acaatttccg 300
tacacttttg gccagggggac caagctggag atcaaa 336

```

<210> 524

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 524

```

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1              5              10              15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
              20              25              30
Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
              35              40              45
Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
              50              55              60
Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65              70              75              80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
              85              90              95
Thr Gln Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
              100              105              110

```

<210> 525

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 525

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gaagtgcagc tgggtggagtc tggggggaggc ttggtacagc ctggcaggtc cctgagactc 60
tcctgtgcag cctctggatt caccctttgat gattatgcca tgcactgggt ccggaagct 120
ccagggaagg gctctggagt ggtctcaggt attagttgga atggtggtag cgcaggctat 180
gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgc aaaagaagac 300
tatgcttttg atatctgggg ccaagggaca atggtcaccg tctcttca 348

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<210> 526

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 526

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1              5              10              15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
              20              25              30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
              35              40              45
Ser Gly Ile Ser Trp Asn Gly Gly Ser Ala Gly Tyr Ala Asp 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 Lys Glu Asp Tyr Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val
              100              105              110
Thr Val Ser Ser
              115

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<210> 527

<211> 337
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 527
 gatattgtga tgacccagac tccactctcc tcacctgtca cccttgagaca gccggcctcc 60
 atctcctgca ggtctagtca aagcctcgta cacagtgatg gaaacaccta cttgagttgg 120
 cttcagcaga ggccaggcca gcctccaaga ctccctaattt ataagatttc taaccgggttc 180
 tctgggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgaaaatc 240
 agcagggtgg aagctgagga tgtcgggggtt tattactgca tgcaagctac acaatttccg 300
 tacacttttg gccaggggac caagctggag atcaaac 337

<210> 528
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 528
 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
 20 25 30
 Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
 35 40 45
 Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
 85 90 95
 Thr Gln Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 529
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 529
 gaggtgcagc tgggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttgaa gattatgcca tgcaactgggt ccggcaagct 120
 ccagggaagg gcctggaatg ggtctcaggt attacttggga atagtataaa taaaggctat 180
 gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagta ctccctgtat 240
 ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgc aaaagaggac 300
 tgggcgtttg actactgggg ccagggaacc ctggtcaccg tctcctca 348

<210> 530
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 530

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1             5             10             15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Asp Tyr
                20             25             30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
                35             40             45
Ser Gly Ile Thr Trp Asn Ser Asp Asn Lys Gly Tyr Ala Asp Ser Val
 50             55             60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Tyr 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 Lys Glu Asp Trp Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
                100            105            110
Thr Val Ser Ser
                115

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<210> 531

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 531

ggattcacct ttgaagatta tgcc

24

<210> 532

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 532

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Gly Phe Thr Phe Glu Asp Tyr Ala
 1             5

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<210> 533

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 533

attacttgga atagtgataa taaa

24

<210> 534

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 534

Ile Thr Trp Asn Ser Asp Asn Lys

1

5

<210> 535

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 535

gcaaaagagg actgggcggtt tgactac

27

<210> 536

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 536

Ala Lys Glu Asp Trp Ala Phe Asp Tyr

1

5

<210> 537

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 537

gacatccaga tgacccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgtc gtgcgagtc gggatattaac agttggtag cctggatatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctacgct gcatccagtt tgcagagtgg ggtcccatca 180
 aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcgg cctccagcct 240
 gaagattttg caacttacta ttgtcaacag gctaacagtt tcccgtacac ttttggccag 300
 gggaccaagg tggaaatcaa a 321

<210> 538

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 538

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly

1

5

10

15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Asn Ser Trp

			20						25					30			
Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile		
			35				40					45					
Tyr	Ala	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly		
			50			55					60						
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Gly	Leu	Gln	Pro		
65					70					75					80		
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ala	Asn	Ser	Phe	Pro	Tyr		
				85					90					95			
Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys							
			100					105									

<210> 539
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 539
 cagggtatta acagttgg 18

<210> 540
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 540
 Gln Gly Ile Asn Ser Trp
 1 5

<210> 541
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 541
 gctgcatcc 9

<210> 542
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 542
 Ala Ala Ser
 1

<210> 543
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 543
 caacaggcta acagtttccc gtacact

27

<210> 544
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 544
 Gln Gln Ala Asn Ser Phe Pro Tyr Thr
 1 5

<210> 545
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 545
 gaagtgcagc tgggtggagtc tggggggaggc ttggtacagc ctggcaggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttgaa gattatgcca tgcactgggt ccggcaagct 120
 ccagggaagg gcctggaatg ggtctcaggt attacttgga atagtataa taaaggctat 180
 gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagta ctccctgtat 240
 ctgcaaataa acagtctgag agctgaggac acggccttgt attactgtgc aaaagaggac 300
 tgggcgcttg actactgggg ccagggaacc ctggtcaccg tctcctca 348

<210> 546
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 546
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Asp Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Thr Trp Asn Ser Asp Asn Lys Gly Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Tyr 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 Lys Glu Asp Trp Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115

<210> 547
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 547
 gacatccaga tgacccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgtc gtgcgagtc gggattaaac agttggtag cctggatatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctacgct gcatccagtt tgcagagtgg ggtcccatca 180
 aggttcagcg gcagtggatc tgggacagat ttactctca ccatcagcgg cctccagcct 240
 gaagattttg caacttacta ttgtcaacag gctaacagtt tcccgtacac ttttggccag 300
 gggaccaagc tggagatcaa a 321

<210> 548
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 548
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Asn Ser Trp
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Gly Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 549
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 549
 gaagtgcagc tgggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttgaa gattatgcca tgactgggt ccggcaagct 120
 ccagggaagg gcctggagtg ggtctcaggt attacttga atagtataa taaaggctat 180
 gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
 ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgc aaaagaggac 300

tgggcggttg actactgggg ccaggaacc ctggtcaccg tctcctca

348

<210> 550

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 550

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Arg
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Glu	Asp	Tyr
			20					25					30		
Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			
Ser	Gly	Ile	Thr	Trp	Asn	Ser	Asp	Asn	Lys	Gly	Tyr	Ala	Asp	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	Lys	Glu	Asp	Trp	Ala	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val
			100					105						110	
Thr	Val	Ser	Ser												
			115												

<210> 551

<211> 322

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 551

gacatccaga	tgacccagtc	tccatcttct	gtgtctgcat	ctgtaggaga	cagagtcacc	60
atcacttgtc	ggcgagtc	gggtattaac	agttggtag	cctggtagca	gcagaaacca	120
gggaaagccc	ctaagctcct	gatctatgct	gcatccagtt	tgcaaagtgg	gggtcccatca	180
aggttcagcg	gcagtggatc	tggaacagat	ttcactctca	ctatcagcag	cctgcagcct	240
gaagattttg	caacttacta	ttgtcaacag	gctaacagtt	tcccgtacac	ttttggccag	300
gggaccaagc	tggagatcaa	ac				322

<210> 552

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 552

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Val	Ser	Ala	Ser	Val	Gly
1				5					10					15	
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Gly	Ile	Asn	Ser	Trp
			20					25					30		
Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35				40						45			
Tyr	Ala	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly

50		55		60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro				
65		70		75
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Tyr				80
	85		90	95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys				
	100		105	

<210> 553
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 553
 gaggtgcagc tgggtgcagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccggcaagct 120
 ccagggaagg gcctggagtg ggtctcaggt attagttaga atagtggtag caaaggctat 180
 gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
 ctgcaaataga acagtctgag acgtgaggac acggccttgt attactgtgt aaaagaggac 300
 tgggcgcttg actactgggg ccagggaacc ctggtcaccg tctcctca 348

<210> 554
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 554
 Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Ser Trp Asn Ser Gly Ser Lys Gly Tyr Ala Asp 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 Arg Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95
 Val Lys Glu Asp Trp Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115

<210> 555
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 555

ggattcacct ttgatgatta tgcc

24

<210> 556

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 556

Gly Phe Thr Phe Asp Asp Tyr Ala

1

5

<210> 557

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 557

attagttgga atagtggtag caaa

24

<210> 558

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 558

Ile Ser Trp Asn Ser Gly Ser Lys

1

5

<210> 559

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 559

gtaaaagagg actgggcggtt tgactac

27

<210> 560

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 560

Val Lys Glu Asp Trp Ala Phe Asp Tyr

1

5

<210> 561
 <211> 315
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 561
 gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgcc aggcgagtca ggacattagc aactatttaa attggtatca acaaaaacca 120
 gggaaagccc ctaagttcct gatctacgat gcatccaatt tgggaacagg ggtcccatca 180
 aggttcagtg gaagtggatc tgggacagat ttactttca ccatcagcag cctgcagcct 240
 gaagatattg cgacatatta ctgtcaacag tatgataatc tccctttcgg cggagggacc 300
 aaggtggaaa tcaaa 315

<210> 562
 <211> 105
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 562
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Phe Leu Ile
 35 40 45
 Tyr Asp Ala Ser Asn Leu Gly Thr Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Phe
 85 90 95
 Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 563
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 563
 caggacatta gcaactat 18

<210> 564
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 564
Gln Asp Ile Ser Asn Tyr
1 5

<210> 565
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 565
gatgcatcc

9

<210> 566
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 566
Asp Ala Ser
1

<210> 567
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 567
caacagtatg ataatctccc t

21

<210> 568
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 568
Gln Gln Tyr Asp Asn Leu Pro
1 5

<210> 569
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 569
 gaagtgcagc tgggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttgat gattatgcc tgcactgggt ccggcaagct 120
 ccagggaagg gcctggagtg ggtctcaggt attagttgga atagtggtag caaaggctat 180
 gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
 ctgcaaatac acagtctgag acgtgaggac acggccttgt attactgtgt aaaagaggac 300
 tgggcgtttg actactgggg ccagggaacc ctggtcaccg tctcctca 348

<210> 570

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 570

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Arg
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Asp	Asp	Tyr
			20					25					30		
Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
			35				40					45			
Ser	Gly	Ile	Ser	Trp	Asn	Ser	Gly	Ser	Lys	Gly	Tyr	Ala	Asp	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	Arg	Glu	Asp	Thr	Ala	Leu	Tyr	Tyr	Cys
			85						90				95		
Val	Lys	Glu	Asp	Trp	Ala	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val
			100					105					110		
Thr	Val	Ser	Ser												
			115												

<210> 571

<211> 315

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 571

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgcc aggcgagtc ggacattagc aactatttaa attggtatca acaaaaacca 120
 gggaaagccc ctaagttcct gatctacgat gcatccaatt tgggaacagg ggtcccatca 180
 aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240
 gaagatattg cgacatatta ctgtcaacag tatgataatc tccctttcgg cggaggggacc 300
 aaggtggaga tcaaaa 315

<210> 572

<211> 105

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 572

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1           5           10           15
Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
          20           25           30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Phe Leu Ile
          35           40           45
Tyr Asp Ala Ser Asn Leu Gly Thr Gly Val Pro Ser Arg Phe Ser Gly
          50           55           60
Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65           70           75           80
Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Phe
          85           90           95
Gly Gly Gly Thr Lys Val Glu Ile Lys
          100          105

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<210> 573
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

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<400> 573
gaagtgcagc tgggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttgat gattatgcc tgcactgggt ccggcaagct 120
ccagggaagg gcctggagtg ggtctcaggt attagttgga atagtggtag caaaggctat 180
gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgt aaaagaggac 300
tgggcgtttg actactgggg ccagggaacc ctggtcaccc tctcctca 348

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<210> 574
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

```

<400> 574
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1           5           10           15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
          20           25           30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35           40           45
Ser Gly Ile Ser Trp Asn Ser Gly Ser Lys Gly Tyr Ala Asp 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
Val Lys Glu Asp Trp Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
          100          105          110
Thr Val Ser Ser
          115

```

<210> 575
 <211> 316

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 575

```

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc aggcgagtc ggacattagc aactatttaa attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctacgat gcatccaatt tggaaacagg ggtcccatca 180
aggttcagtg gaagtggatc tgggacagat ttacttttca ccatcagcag cctgcagcct 240
gaagatattg caacatatta ctgtcaacag tatgataatc tccctttcgg cggaggggacc 300
aaggtggaga tcaaac                                     316

```

<210> 576

<211> 105

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 576

```

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1             5             10             15
Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
      20             25             30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
      35             40             45
Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
      50             55             60
Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65             70             75             80
Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Phe
      85             90             95
Gly Gly Gly Thr Lys Val Glu Ile Lys
      100             105

```

<210> 577

<211> 375

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 577

```

caggtgcagc tgggtgcagtc aggtccagga ctggtgaagc cctcgcagac cctctcactc 60
acctgtgcca tctccgggga cagtgtctct agcaacagtg ctgcttgga ctggatcagg 120
cagtcccat cgagaggcct tgagtggctg ggaaggacat actacaggtc caagtgggat 180
aatgattatg cagtatctgt gaaaagtcga ataaccatca acccagacac atccaagaac 240
cagttctccc tgcagctgaa ctctgtgact cccgaggaca cggctgtgta ttactgtgca 300
agaggggtata gcagcagctg gtacgggggt gcttttgata tctggggcca agggacaatg 360
gtcaccgtct cttca                                     375

```

<210> 578

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 578

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Gln
1				5					10					15	
Thr	Leu	Ser	Leu	Thr	Cys	Ala	Ile	Ser	Gly	Asp	Ser	Val	Ser	Ser	Asn
			20					25					30		
Ser	Ala	Ala	Trp	Asn	Trp	Ile	Arg	Gln	Ser	Pro	Ser	Arg	Gly	Leu	Glu
		35					40					45			
Trp	Leu	Gly	Arg	Thr	Tyr	Tyr	Arg	Ser	Lys	Trp	Tyr	Asn	Asp	Tyr	Ala
	50					55					60				
Val	Ser	Val	Lys	Ser	Arg	Ile	Thr	Ile	Asn	Pro	Asp	Thr	Ser	Lys	Asn
65					70					75					80
Gln	Phe	Ser	Leu	Gln	Leu	Asn	Ser	Val	Thr	Pro	Glu	Asp	Thr	Ala	Val
				85					90					95	
Tyr	Tyr	Cys	Ala	Arg	Gly	Tyr	Ser	Ser	Ser	Trp	Tyr	Gly	Gly	Ala	Phe
			100					105					110		
Asp	Ile	Trp	Gly	Gln	Gly	Thr	Met	Val	Thr	Val	Ser	Ser			
		115					120					125			

<210> 579

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 579

ggggacagtg tctctagcaa cagtgtgtgct

30

<210> 580

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 580

Gly	Asp	Ser	Val	Ser	Ser	Asn	Ser	Ala	Ala
1				5					10

<210> 581

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 581

acatactaca ggtccaagtg gtataat

27

<210> 582

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 582

Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn

1

5

<210> 583

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 583

gcaagagggg atagcagcag ctggtacggg ggtgcttttg atatc

45

<210> 584

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 584

Ala Arg Gly Tyr Ser Ser Ser Trp Tyr Gly Gly Ala Phe Asp Ile

1

5

10

15

<210> 585

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 585

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgcc gggcaagtca gagcattagc agttatttaa gttggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
 aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg caacttacta ctgtcaacag agttacagta cccattcac tttcggccct 300
 gggaccaagg tggaaatcaa a 321

<210> 586

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 586

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1

5

10

15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr

				20						25						30			
Leu	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile				
			35				40					45							
Tyr	Ala	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly				
		50				55					60								
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro				
65					70					75					80				
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Tyr	Ser	Thr	Pro	Phe				
				85					90					95					
Thr	Phe	Gly	Pro	Gly	Thr	Lys	Val	Glu	Ile	Lys									
			100					105											

<210> 587
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 587
cagagcatta gcagttat 18

<210> 588
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 588
Gln Ser Ile Ser Ser Tyr
1 5

<210> 589
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 589
gctgcatcc 9

<210> 590
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 590
Ala Ala Ser
1

<210> 591
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 591
 caacagagtt acagtacccc attcact

27

<210> 592
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 592
 Gln Gln Ser Tyr Ser Thr Pro Phe Thr
 1 5

<210> 593
 <211> 375
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 593
 caggtacagc tgcagcagtc aggtccagga ctggtgaagc cctcgcagac cctctcactc 60
 acctgtgcc tctccgggga cagtgtctct agcaacagtg ctgcttgga ctggatcagg 120
 cagtcccat cgagaggcct tgagtggctg ggaaggacat actacaggtc caagtggat 180
 aatgattatg cagtatctgt gaaaagtcga ataaccatca acccagacac atccaagaac 240
 cagttctccc tgcagctgaa ctctgtgact cccgaggaca cggctgtgta ttactgtgca 300
 agaggggtata gcagcagctg gtacgggggt gcttttgata tctggggcca agggacaatg 360
 gtcaccgtct cttca 375

<210> 594
 <211> 125
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 594
 Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
 20 25 30
 Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
 35 40 45
 Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
 50 55 60
 Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
 65 70 75 80
 Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val

				85					90					95					
Tyr	Tyr	Cys	Ala	Arg	Gly	Tyr	Ser	Ser	Ser	Trp	Tyr	Gly	Gly	Ala	Phe				
			100					105					110						
Asp	Ile	Trp	Gly	Gln	Gly	Thr	Met	Val	Thr	Val	Ser	Ser							
		115					120					125							

<210> 595
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 595
 gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgcc gggcaagtca gagcattagc agttatttaa gttggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
 aggttcagtg gcagtggtac tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg caacttacta ctgtcaacag agttacagta cccattcac tttcggccct 300
 gggaccaaag tggatatcaa a 321

<210> 596
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 596
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
 20 25 30
 Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Phe
 85 90 95
 Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
 100 105

<210> 597
 <211> 375
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 597
 caggtacagc tgcagcagtc aggtccagga ctggtgaagc cctcgcagac cctctcactc 60
 acctgtgcc tctccgggga cagtgtctct agcaacagtg ctgcttgga atggatcagg 120
 cagtcccat cgagaggcct tgagtggctg ggaaggacat actacaggtc caagtggat 180
 aatgattatg cagtatctgt gaaaagtcga ataaccatca acccagacac atccaagaac 240

```

cagttctccc tgcagctgaa ctctgtgact cccgaggaca cggctgtgta ttactgtgca 300
agaggggtata gcagcagctg gtacgggggt gcttttgata tctggggcca agggacaatg 360
gtcaccgtct cttca 375

```

<210> 598
 <211> 125
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

```

<400> 598
Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1      5      10      15
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
20     25     30
Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
35     40     45
Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50     55     60
Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65     70     75     80
Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85     90     95
Tyr Tyr Cys Ala Arg Gly Tyr Ser Ser Ser Trp Tyr Gly Gly Ala Phe
100    105    110
Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115    120    125

```

<210> 599
 <211> 322
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

```

<400> 599
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattagc agttatttaa attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggtac tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccattcac tttcggccct 300
gggaccaaag tggatatcaa ac 322

```

<210> 600
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

```

<400> 600
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1      5      10      15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20     25     30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

```

	35					40					45					
Tyr	Ala	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	
	50					55					60					
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	
65					70					75					80	
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Tyr	Ser	Thr	Pro	Phe	
				85					90					95		
Thr	Phe	Gly	Pro	Gly	Thr	Lys	Val	Asp	Ile	Lys						
			100					105								

```
<210> 601
<211> 357
<212> DNA
<213> Artificial Sequence
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<220>
<223> Synthetic

<400>	601					
cagggtgcagc	tgcaggagtc	tgggggaggc	tcggtacagc	ctgggggggtc	cctgcgactc	60
tcctgtgcaa	cctctggatt	cacctttacc	aactttgcc	taagctgggt	ccgccaggct	120
ccaggcagtg	ggctggagtg	ggtctcatct	attactggta	gtggtgatta	cgcatactac	180
gcagactccg	tgaagggccg	gttcaccatc	tccagagaca	gttccaagaa	cacgctctat	240
ctacaaatga	acagcctgag	agccgacgac	acggccgtat	atttctgtac	gagagaagac	300
tatattaact	cgctcctttga	ctactggggc	caggaacca	cggtcacctg	ctctctca	357

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<210> 602
<211> 119
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Synthetic

[illegible]

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<210> 603
<211> 24
<212> DNA
<213> Artificial Sequence
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<220>
<223> Synthetic

<400> 603
ggattcacct ttaccaactt tgcc 24

<210> 604
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 604
Gly Phe Thr Phe Thr Asn Phe Ala
1 5

<210> 605
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 605
attactggta gtggtgatta cgca 24

<210> 606
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 606
Ile Thr Gly Ser Gly Asp Tyr Ala
1 5

<210> 607
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 607
acgagagaag actatattaa ctcgtccttt gactac 36

<210> 608
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 608

Thr Arg Glu Asp Tyr Ile Asn Ser Ser Phe Asp Tyr
 1 5 10

<210> 609
 <211> 333
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 609
 gacatccaga tgacccagac tccactctcc tcacctgtca cccttggaca gccggcctcc 60
 atctcctgta ggtctagtca gagcctcgta cacagtgatg gaaataccta cttgagttgg 120
 cttcagcgga ggccaggcca gcctccaaga ctcctaattt ataagatttc taaccggttc 180
 tctgggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgaaaatc 240
 agcaggggtgg aagctgagga tgtcgggggtt tattactgca tgcaagctac acaacttccg 300
 acgttcgggcc aagggaacaa ggtggaaatc aaa 333

<210> 610
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 610
 Asp Ile Gln Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
 20 25 30
 Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Arg Arg Pro Gly Gln Pro
 35 40 45
 Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
 85 90 95
 Thr Gln Leu Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105 110

<210> 611
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 611
 cagagcctcg tacacagtga tggaaatacc tac 33

<210> 612
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 612

Gln	Ser	Leu	Val	His	Ser	Asp	Gly	Asn	Thr	Tyr
1				5					10	

<210> 613

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 613

aagatttct

9

<210> 614

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 614

Lys	Ile	Ser
1		

<210> 615

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 615

atgcaagcta cacaacttcc gacg

24

<210> 616

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 616

Met	Gln	Ala	Thr	Gln	Leu	Pro	Thr
1				5			

<210> 617

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 617

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gaggtgcagc tgttgagtc tgggggaggc tcggtacagc ctgggggggc cctgcgactc 60
tcctgtgcaa cctctggatt cacctttacc aactttgcc aagctgggt ccgccaggct 120
ccaggcagtg ggctggagtg ggtctcatct attactggta gtggtgatta cgcatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca gttccaagaa cagctcttat 240
ctacaaatga acagcctgag agccgacgac acggccgtat atttctgtac gagagaagac 300
tatattaact cgtcctttga ctactggggc caggggaacc tggtcaccgt ctctca 357

```

<210> 618

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 618

```

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Ser Val Gln Pro Gly Gly
1          5          10          15
Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Thr Asn Phe
20          25          30
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Ser Gly Leu Glu Trp Val
35          40          45
Ser Ser Ile Thr Gly Ser Gly Asp Tyr Ala Tyr Tyr Ala Asp Ser Val
50          55          60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Ser Ser Lys Asn Thr Leu Tyr
65          70          75          80
Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Phe Cys
85          90          95
Thr Arg Glu Asp Tyr Ile Asn Ser Ser Phe Asp Tyr Trp Gly Gln Gly
100          105          110
Thr Leu Val Thr Val Ser Ser
115

```

<210> 619

<211> 333

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 619

```

gatattgtga tgaccagac tccactctcc tcacctgtca cccttggaca gccggcctcc 60
atctcctgta ggtctagtca gagcctcgta cacagtgatg gaaataccta cttgagttgg 120
cttcagcggg gccaggcca gcctccaaga ctcttaattt ataagatttc taaccgggtc 180
tctgggggtc cagacagatt cagtggcagt ggggcaggga cagatttcac actgaaaatc 240
agcaggggtg aagctgagga tgtcgggggt tattactgca tgcaagctac acaacttccg 300
acgttcgggc aagggaacca ggtggaaatc aaa 333

```

<210> 620

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 620

```

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1           5           10           15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
      20           25           30
Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Arg Arg Pro Gly Gln Pro
      35           40           45
Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
      50           55           60
Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65           70           75           80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
      85           90           95
Thr Gln Leu Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
      100          105          110

```

<210> 621

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 621

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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttacc aactttgcca tgagctgggt ccgccaggct 120
ccaggggaagg ggcctggagtg ggtctcagct attactggta gtggtgatta cgcatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaataga acagcctgag agccgaggac acggccgtat attactgtac gagagaagac 300
tatattaact cgtcctttga ctactggggc caggggaacc tggtcaccgt ctccctca 357

```

<210> 622

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 622

```

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1           5           10           15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Asn Phe
      20           25           30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
      35           40           45
Ser Ala Ile Thr Gly Ser Gly Asp Tyr Ala Tyr Tyr Ala Asp Ser Val
      50           55           60
Lys Gly Arg Phe Thr Ile 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
Thr Arg Glu Asp Tyr Ile Asn Ser Ser Phe Asp Tyr Trp Gly Gln Gly
      100          105          110
Thr Leu Val Thr Val Ser Ser
      115

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<210> 623
 <211> 334
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 623
 gatattgtga tgacccagac tccactctcc tcacctgtca cccttggaca gccggcctcc 60
 atctcctgca ggtctagtca gaggctcgta cacagtgatg gaaataccta cttgagttgg 120
 cttcagcaga ggccaggcca gcctccaaga ctccctaattt ataagatttc taaccgggttc 180
 tctgggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgaaaatc 240
 agcagggtgg aagctgagga tgtcgggggtt tattactgca tgcaagctac acaacttccg 300
 acgttcggcc aagggaacca ggtggaaatc aaac 334

<210> 624
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 624
 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
 20 25 30
 Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
 35 40 45
 Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
 85 90 95
 Thr Gln Leu Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105 110

<210> 625
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 625
 cagggtgcagc tgggtggagtc tggggggaggc gtgggtccagc ctgggatgtc cctgagactc 60
 tcctgtgcag cgtccggatt taccttcagg agatatggca tgcactgggt ccgccagggt 120
 ccaggcaagg ggtctggagtg ggtggcagtt atatggtatg atggaagtaa taaatattat 180
 gtagattccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcaaataga acagcctgag agccgaggac acggctgtgt attactgtgc gagcgaaatt 300
 acagttgggg actggttcga cccctggggc cagggaaccc tggtcaccgt ctccctca 357

<210> 626
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 626

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Met
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Arg Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Val Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile 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 Ser Glu Ile Thr Val Gly Asp Trp Phe Asp Pro Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 627

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 627

ggatttacct tcaggagata tggc

24

<210> 628

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 628

Gly Phe Thr Phe Arg Arg Tyr Gly
 1 5

<210> 629

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 629

atatggtatg atggaagtaa taaa

24

<210> 630

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 630

Ile Trp Tyr Asp Gly Ser Asn Lys
1 5

<210> 631

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 631

gcgagcgaaa ttacagttgg ggactggttc gacccc

36

<210> 632

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 632

Ala Ser Glu Ile Thr Val Gly Asp Trp Phe Asp Pro
1 5 10

<210> 633

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 633

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgtc gggcaagtca gggcattaga aatgatttag gctggtatca gcagaaacca 120
gggaaagccc ctaaactcct gatctatgct gcatccagtt tacacagtgg ggtcccatca 180
aggttcagcg gcagtggatc tggcacagat ttactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtctacag gatttcaatt accctctcac tttcggcgga 300
gggaccaagg tggagatcaa a 321

<210> 634

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 634

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

Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Gly	Ile	Arg	Asn	Asp
			20					25					30		
Leu	Gly	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			
Tyr	Ala	Ala	Ser	Ser	Leu	His	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75					80
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Leu	Gln	Asp	Phe	Asn	Tyr	Pro	Leu
				85					90					95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys					
			100					105							

<210> 635
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 635
 cagggcatta gaaatgat

18

<210> 636
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 636
 Gln Gly Ile Arg Asn Asp
 1 5

<210> 637
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 637
 gctgcatcc

9

<210> 638
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 638
 Ala Ala Ser
 1

<210> 639
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 639
 ctacaggatt tcaattaccc tctcact

27

<210> 640
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 640
 Leu Gln Asp Phe Asn Tyr Pro Leu Thr
 1 5

<210> 641
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 641
 cagggtgcagc tgggtggagtc tgggggaggc gtggtccagc ctgggatgtc cctgagactc 60
 tctgtgacag cgtccggatt taccttcagg agatatggca tgcactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg ggtggcagtt atatggtatg atggaagtaa taaatattat 180
 gtagattccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcaaataga acagcctgag agccgaggac acggctgtgt attactgtgc gagcgaaatt 300
 acagttgggg actggttcga cccctggggc caggggaacc tggtcaccgt ctcctca 357

<210> 642
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 642
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Met
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Arg Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Val Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile 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 Ser Glu Ile Thr Val Gly Asp Trp Phe Asp Pro Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 643
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 643
 gccatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgtc gggcaagtca gggcattaga aatgatttag gctggtatca gcagaaacca 120
 gggaaagccc ctaaactcct gatctatgct gcatccagtt tacacagtgg ggtcccatca 180
 aggttcagcg gcagtggatc tggcacagat ttcactctca ccatcagcag cctgcagcct 240
 gaagattttg caacttatta ctgtctacag gattttcaatt accctctcac tttcggcgga 300
 gggaccaagg tggagatcaa a 321

<210> 644
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 644
 Ala Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
 20 25 30
 Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ala Ala Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Phe Asn Tyr Pro Leu
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 645
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 645
 caggtgcagc tgggtggagtc tgggggaggc gtgggtccagc ctgggaggtc cctgagactc 60
 tcctgtgcag cgtctggatt taccttcagg agatatggca tgactgggt ccgccaggct 120
 ccaggcaagg ggcctggagt ggtggcagtt atatggtatg atggaagtaa taaatactat 180
 gcagactccg tgaagggccg attcaccatc tccagagaca actccaagaa cacgctgtat 240

ctgcaaataga acagcctgag agccgaggac acggctgtgt attactgtgc gagcgaaatt 300
 acagttggggg actggttcga cccctggggc cagggaaccc tggtcaccgt ctccctca 357

<210> 646

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 646

Gln	Val	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	Arg	Arg	Tyr
			20					25					30		
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			
Ala	Val	Ile	Trp	Tyr	Asp	Gly	Ser	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	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	Ser	Glu	Ile	Thr	Val	Gly	Asp	Trp	Phe	Asp	Pro	Trp	Gly	Gln	Gly
			100					105					110		
Thr	Leu	Val	Thr	Val	Ser	Ser									
			115												

<210> 647

<211> 322

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 647

gccatccaga	tgacccagtc	tccatcctcc	ctgtctgcat	ctgtaggaga	cagagtcacc	60
atcacttgcc	gggcaagtca	gggcattaga	aatgatttag	gctgggtatca	gcagaaacca	120
gggaaagccc	ctaagctcct	gatctatgct	gcatccagtt	tacaaagtgg	ggtcccatca	180
aggttcagcg	gcagtggatc	tggcacagat	ttcactctca	ccatcagcag	cctgcagcct	240
gaagattttg	caacttatta	ctgtctacag	gatttcaatt	accctctcac	tttcggcgga	300
gggaccaagg	tggagatcaa	ac				322

<210> 648

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 648

Ala	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1			5					10					15		
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Gly	Ile	Arg	Asn	Asp
			20					25					30		
Leu	Gly	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Phe Asn Tyr Pro Leu
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 649
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 649
 caggtgcagc tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
 tcctgtgtag cctctggatt caccttcagt agatatggca tgcactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg gctgatagtt atatcatatg atggaattaa taaatactat 180
 gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacggtgtat 240
 ctgcaaatga acagcctgag agctgaggac acgggagtggt attactgtgc gaaaggggac 300
 ttttgagtg gttactttga ctactggggc caggggaacc tggtcactgt ctccctca 357

<210> 650
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 650
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Arg Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu
 35 40 45
 Ile Val Ile Ser Tyr Asp Gly Ile Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Gly Val Tyr Tyr Cys
 85 90 95
 Ala Lys Gly Asp Phe Trp Ser Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 651
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 651
ggattcacct tcagtagata tggc 24

<210> 652
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 652
Gly Phe Thr Phe Ser Arg Tyr Gly
1 5

<210> 653
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 653
atatcatatg atggaattaa taaa 24

<210> 654
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 654
Ile Ser Tyr Asp Gly Ile Asn Lys
1 5

<210> 655
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 655
gcgaaagggg acttttggag tggttacttt gactac 36

<210> 656
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 656
Ala Lys Gly Asp Phe Trp Ser Gly Tyr Phe Asp Tyr

1 5 10

<210> 657
 <211> 336
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 657
 gacatcgtga tgacccagac tccactctcc tcacctgtca cccttggaca gccggcctcc 60
 atctcctgca ggtctagtca aagcctcgtc cacagtgatg gaaacaccta cttgagttgg 120
 cttcaccaga ggccaggcca gcctccaaga ctcctaattt ataagatttc taaccggttc 180
 tctggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgcaaadc 240
 agcaggggtg aagctgagga tgtcgggatt tattactgca tgcaaggtag acaatttccg 300
 actttcggcg gagggacca ggtggagatc aaacga 336

<210> 658
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 658
 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
 20 25 30
 Asp Gly Asn Thr Tyr Leu Ser Trp Leu His Gln Arg Pro Gly Gln Pro
 35 40 45
 Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Gln Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Val Gly Ile Tyr Tyr Cys Met Gln Gly
 85 90 95
 Thr Gln Phe Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
 100 105 110

<210> 659
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 659
 caaagcctcg tccacagtga tggaaacacc tac 33

<210> 660
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 660

Gln Ser Leu Val His Ser Asp Gly Asn Thr Tyr
1 5 10

<210> 661

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 661

aagatttct

9

<210> 662

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 662

Lys Ile Ser

1

<210> 663

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 663

atgcaaggta cacaatttcc gact

24

<210> 664

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 664

Met Gln Gly Thr Gln Phe Pro Thr

1

5

<210> 665

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 665

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tcctgtgtag cctctggatt caccttcagt agatatggca tgcactgggt ccgccaggct 120
ccaggcaagg ggcctggagtg gctgatagtt atatcatatg atggaattaa taaatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgggtgtat 240
ctgcaaataga acagcctgag agctgaggac acgggagtggt attactgtgc gaaaggggac 300
ttttggagtg gttactttga ctactggggc caggggaaccc tggtcaccgt ctctca 357
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<210> 666

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 666

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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1           5           10           15
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Arg Tyr
 20           25           30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu
 35           40           45
Ile Val Ile Ser Tyr Asp Gly Ile Asn Lys Tyr Tyr Ala Asp Ser Val
 50           55           60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
 65           70           75           80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Gly Val Tyr Tyr Cys
 85           90           95
Ala Lys Gly Asp Phe Trp Ser Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
 100          105          110
Thr Leu Val Thr Val Ser Ser
 115
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<210> 667

<211> 333

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 667

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atctcctgca ggtctagtca aagcctcgtc cacagtgatg gaaacaccta cttgagttgg 120
cttcaccaga ggccaggcca gcctccaaga ctctaattt ataagatttc taaccggttc 180
tctggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgcaaatac 240
agcaggggtgg aagctgagga tgtcgggatt tattactgca tgcaaggtac acaatttccg 300
actttcggcg gagggaccaaa ggtggagatc aaa 333
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<210> 668

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 668

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Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1           5           10           15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
          20           25           30
Asp Gly Asn Thr Tyr Leu Ser Trp Leu His Gln Arg Pro Gly Gln Pro
          35           40           45
Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
          50           55           60
Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Gln Ile
65           70           75           80
Ser Arg Val Glu Ala Glu Asp Val Gly Ile Tyr Tyr Cys Met Gln Gly
          85           90           95
Thr Gln Phe Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
          100          105          110

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<210> 669

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 669

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caggtgcagc tgggtggagtc tggggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt agatatggca tgcactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaattaa taaatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gaaaggggac 300
ttttggagtg gttactttga ctactggggc caggggaacc tggtcaccgt ctccctca 357

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<210> 670

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 670

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Gln Val 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 Arg Tyr
          20           25           30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35           40           45
Ala Val Ile Ser Tyr Asp Gly Ile Asn Lys Tyr Tyr Ala Asp Ser Val
          50           55           60
Lys Gly Arg Phe Thr Ile 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 Lys Gly Asp Phe Trp Ser Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
          100          105          110
Thr Leu Val Thr Val Ser Ser
          115

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<210> 671

<211> 334
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 671
 gatattgtga tgacccagac tccactctcc tcacctgtca cccttggaca gccggcctcc 60
 atctcctgca ggtctagtca aagcctcgtc cacagtgatg gaaacaccta cttgagttgg 120
 cttcagcaga ggccaggcca gcctccaaga ctccctaattt ataagatttc taaccgggttc 180
 tctgggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgaaaatc 240
 agcagggtgg aagctgagga tgtcgggggtt tattactgca tgcaaggtag acaatttccg 300
 actttcggcg gagggaccaa ggtggagatc aaac 334

<210> 672
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 672
 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
 20 25 30
 Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
 35 40 45
 Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly
 85 90 95
 Thr Gln Phe Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105 110

<210> 673
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 673
 caggtgcagc tgggtgcagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
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 ccaggcaagg ggctggagtg ggtggtagtt atatcatatg atggaattaa taaatactat 180
 gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacggtgtat 240
 ctgcaaatga acagcctgag agctgaggac acggctgtgt atcactgtgc gaaaggggac 300
 ttttgagagt gttactttga ctactggggc caggaaccc tggtcaccgt ctccctca 357

<210> 674
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 674

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Arg Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Val Val Ile Ser Tyr Asp Gly Ile Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys
 85 90 95
 Ala Lys Gly Asp Phe Trp Ser Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 675

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 675

ggattcacct tcagtagata tggc

24

<210> 676

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 676

Gly Phe Thr Phe Ser Arg Tyr Gly
 1 5

<210> 677

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 677

atatcatatg atggaattaa taaa

24

<210> 678

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 678

Ile Ser Tyr Asp Gly Ile Asn Lys

1

5

<210> 679

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 679

gcgaaagggg acttttggag tggttacttt gactac

36

<210> 680

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 680

Ala Lys Gly Asp Phe Trp Ser Gly Tyr Phe Asp Tyr

1

5

10

<210> 681

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 681

gacatcgtga tgaccagac tccactctcc tcacctgtca cccttggaca gccggcctcc 60
 atctcctgca ggtctagtca aagcctcgta cacagtgatg gaaacaccta cttgagttgg 120
 cttcaccaga ggccaggcca gcctccaaga ctcttaattt ataagatttc taaccggttc 180
 tctggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgcaaadc 240
 agcagggtgg aagctgagga tgtcgggatt tattactgca tgcaagcaac acaatttccg 300
 actttcggcg gagggacca ggtggaaatc aaacga 336

<210> 682

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 682

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly

1

5

10

15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser

			20						25					30			
Asp	Gly	Asn	Thr	Tyr	Leu	Ser	Trp	Leu	His	Gln	Arg	Pro	Gly	Gln	Pro		
		35					40					45					
Pro	Arg	Leu	Leu	Ile	Tyr	Lys	Ile	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro		
		50				55					60						
Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ala	Gly	Thr	Asp	Phe	Thr	Leu	Gln	Ile		
65					70					75					80		
Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Ile	Tyr	Tyr	Cys	Met	Gln	Ala		
				85					90					95			
Thr	Gln	Phe	Pro	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg		
			100					105						110			

<210> 683
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 683
caaagcctcg tacacagtga tggaaacacc tac 33

<210> 684
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 684
Gln Ser Leu Val His Ser Asp Gly Asn Thr Tyr
1 5 10

<210> 685
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 685
aagatttct 9

<210> 686
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 686
Lys Ile Ser
1

<210> 687
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 687
 atgcaagcaa cacaatttcc gact

24

<210> 688
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 688
 Met Gln Ala Thr Gln Phe Pro Thr
 1 5

<210> 689
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 689
 caggtgcagc tgggtggagtc tggggggaggc gtggtccagc ctgggaggtc cctgagactc 60
 tcctgtgtag cctctggatt caccttcagt agatatggca tgcactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg ggtggtagtt atatcatatg atggaattaa taaatactat 180
 gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacggtgtat 240
 ctgcaaataga acagcctgag agctgaggac acggctgtgt atcactgtgc gaaaggggac 300
 ttttgagagt gttactttga ctactggggc caggggaacc tggtcaccgt ctctca 357

<210> 690
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 690
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Arg Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Val Val Ile Ser Tyr Asp Gly Ile Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys
 85 90 95

Ala Lys Gly Asp Phe Trp Ser Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 691
 <211> 333
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 691
 gatattgtga tgaccagac tccactctcc tcacctgtca cccttggaca gccggcctcc 60
 atctcctgca ggtctagtca aagcctcgta cacagtgatg gaaacaccta cttgagttgg 120
 cttcaccaga ggccaggcca gcctccaaga ctcctaattt ataagatttc taaccgggtc 180
 tctgggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgcaaata 240
 agcagggtgg aagctgagga tgtcgggatt tattactgca tgcaagcaac acaatttccg 300
 actttcggcg gagggacca ggtggagatc aaa 333

<210> 692
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 692
 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
 20 25 30
 Asp Gly Asn Thr Tyr Leu Ser Trp Leu His Gln Arg Pro Gly Gln Pro
 35 40 45
 Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Gln Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Val Gly Ile Tyr Tyr Cys Met Gln Ala
 85 90 95
 Thr Gln Phe Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105 110

<210> 693
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 693
 caggtgcagc tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
 tcctgtgcag cctctggatt caccttcagt agatatggca tgcaactggg cgcaccaggct 120
 ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaattaa taaatactat 180
 gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gaaaggggac 300

ttttggagtg gttactttga ctactggggc caggggaaccc tggtcaccgt ctcctca 357

<210> 694

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 694

Gln	Val	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	Arg	Tyr
			20					25					30		
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			
Ala	Val	Ile	Ser	Tyr	Asp	Gly	Ile	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	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	Lys	Gly	Asp	Phe	Trp	Ser	Gly	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly
			100					105					110		
Thr	Leu	Val	Thr	Val	Ser	Ser									

<210> 695

<211> 334

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 695

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cttcagcaga	ggccaggcca	gctccaaga	ctcctaattt	ataagatttc	taaccggttc	180
tctggggtcc	cagacagatt	cagtggcagt	ggggcaggga	cagatttcac	actgaaaatc	240
agcagggtgg	aagctgagga	tgtcgggggt	tattactgca	tgcaagcaac	acaatttcgc	300
actttcggcg	gagggacca	ggtggagatc	aaac			334

<210> 696

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 696

Asp	Ile	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Ser	Pro	Val	Thr	Leu	Gly
1				5					10					15	
Gln	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	His	Ser
			20					25					30		
Asp	Gly	Asn	Thr	Tyr	Leu	Ser	Trp	Leu	Gln	Gln	Arg	Pro	Gly	Gln	Pro
		35					40					45			
Pro	Arg	Leu	Leu	Ile	Tyr	Lys	Ile	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro

50		55		60
Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile				
65		70		75
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala				
	85		90	
Thr Gln Phe Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys				
	100		105	110

<210> 697
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 697
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 tcctgtgtag cctctggatt caccttcagt agatatggca tacactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg ggtgatagtt atatcatatg atggaattaa taaatactat 180
 gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacggtatat 240
 ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gaaaggggac 300
 ttttgagtg gttactttga ctattggggc caggggaacc tggtcaccgt ctctca 357

<210> 698
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 698
 Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Arg Tyr
 20 25 30
 Gly Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ile Val Ile Ser Tyr Asp Gly Ile Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val 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 Lys Gly Asp Phe Trp Ser Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 699
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 699

ggattcacct tcagtagata tggc

24

<210> 700

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 700

Gly Phe Thr Phe Ser Arg Tyr Gly

1

5

<210> 701

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 701

atatcatatg atggaattaa taaa

24

<210> 702

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 702

Ile Ser Tyr Asp Gly Ile Asn Lys

1

5

<210> 703

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 703

gcgaaagggg acttttggag tggttacttt gactat

36

<210> 704

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 704

Ala Lys Gly Asp Phe Trp Ser Gly Tyr Phe Asp Tyr

1

5

10

<210> 705
 <211> 336
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 705
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 atctcctgta ggtctaatca aagcctcgta cacagtgatg gaaacaccta cttgagttgg 120
 cttcaccaga ggccaggcca gcctccaaga ctcttaattt ataagatttc taaccgggttc 180
 tctgggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgcaaadc 240
 agcagggtgg aagctgagga tgtcgggtatt tattactgca tgcaagctac acaatttcgc 300
 actttcggcg gagggacca ggtggaaac aaacga 336

<210> 706
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 706
 Glu Ile Val Leu Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Arg Ser Asn Gln Ser Leu Val His Ser
 20 25 30
 Asp Gly Asn Thr Tyr Leu Ser Trp Leu His Gln Arg Pro Gly Gln Pro
 35 40 45
 Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Gln Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Val Gly Ile Tyr Tyr Cys Met Gln Ala
 85 90 95
 Thr Gln Phe Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
 100 105 110

<210> 707
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 707
 caaagcctcg tacacagtga tggaaacacc tac 33

<210> 708
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 708
Gln Ser Leu Val His Ser Asp Gly Asn Thr Tyr
1 5 10

<210> 709
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 709
aagatttct 9

<210> 710
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 710
Lys Ile Ser
1

<210> 711
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 711
atgcaagcta cacaatttcc gact 24

<210> 712
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 712
Met Gln Ala Thr Gln Phe Pro Thr
1 5

<210> 713
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 713
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 tcctgtgtag cctctggatt caccttcagt agatatggca tacactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg ggtgatagtt atatcatatg atggaattaa taaatactat 180
 gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacggtatat 240
 ctgcaaatac acagcctgag agccgaggac acggctgtgt attactgtgc gaaaggggac 300
 ttttgagtg gttactttga ctattggggc caggaaccc tggtcaccgt ctccctca 357

<210> 714
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 714
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Arg Tyr
 20 25 30
 Gly Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ile Val Ile Ser Tyr Asp Gly Ile Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val 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 Lys Gly Asp Phe Trp Ser Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 715
 <211> 333
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 715
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 atctcctgta ggtctaatca aagcctcgta cacagtgatg gaaacaccta cttgagttgg 120
 cttcaccaga ggccaggcca gctccaaga ctctaatatt ataagatttc taaccggttc 180
 tctgggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgcaaatac 240
 agcaggggtgg aagctgagga tgtcggtatt tattactgca tgcaagctac acaatttccg 300
 actttcggcg gagggacca ggtggagatc aaa 333

<210> 716
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 716

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Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1           5           10           15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Asn Gln Ser Leu Val His Ser
          20           25           30
Asp Gly Asn Thr Tyr Leu Ser Trp Leu His Gln Arg Pro Gly Gln Pro
          35           40           45
Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
          50           55           60
Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Gln Ile
65           70           75           80
Ser Arg Val Glu Ala Glu Asp Val Gly Ile Tyr Tyr Cys Met Gln Ala
          85           90           95
Thr Gln Phe Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
          100          105          110

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<210> 717
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

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<400> 717
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ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaattaa taaatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaataga acagcctgag agctgaggac acggctgtgt attactgtgc gaaaggggac 300
ttttggagtg gttactttga ctattggggc caggggaacc tggtcaccgt ctccctca 357

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<210> 718
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

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<400> 718
Gln Val 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 Arg Tyr
          20           25           30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35           40           45
Ala Val Ile Ser Tyr Asp Gly Ile Asn Lys Tyr Tyr Ala Asp Ser Val
          50           55           60
Lys Gly Arg Phe Thr Ile 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 Lys Gly Asp Phe Trp Ser Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
          100          105          110
Thr Leu Val Thr Val Ser Ser
          115

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<210> 719
 <211> 334

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 719

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gatattgtga tgacccagac tccactctcc tcacctgtca cccttggaca gccggcctcc 60
atctcctgca ggtctagtca aagcctcgta cacagtgatg gaaacaccta cttgagttgg 120
cttcagcaga ggccaggcca gcctccaaga ctcctaattt ataagatttc taaccgggtc 180
tctgggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgaaaatc 240
agcaggggtgg aagctgagga tgtcgggggtt tattactgca tgcaagctac acaatttccg 300
actttcggcg gagggacca ggtggagatc aaac 334

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<210> 720

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 720

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Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
1           5           10           15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20           25           30
Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
35           40           45
Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
50           55           60
Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65           70           75           80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
85           90           95
Thr Gln Phe Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100          105          110

```

<210> 721

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 721

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caggtgcagc tgggtggagtc tgggggaggc gtggtccagc ctgggatgct cctgagactc 60
tctgttacag cgtccggatt tacgttcagg agatatggca tgcactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtggcagtt atttggtatg atggaagtaa taaatattat 180
gcagactccg tgaagggacg attcaccata accagagaca attccaagaa cacgttgtat 240
ctgcaaataga acagcctgag agccgaggac acggctatat atttttgtgc gagcgaaata 300
acaattgggg actggttcga cccccggggc cagggaaccc tggtcaccgt ctccctca 357

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<210> 722

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 722

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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Met
 1              5              10              15
Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Arg Arg Tyr
              20              25              30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
              35              40              45
Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
              50              55              60
Lys Gly Arg Phe Thr Ile Thr 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 Ile Tyr Phe Cys
              85              90              95
Ala Ser Glu Ile Thr Ile Gly Asp Trp Phe Asp Pro Arg Gly Gln Gly
              100              105              110
Thr Leu Val Thr Val Ser Ser
              115

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<210> 723

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 723

ggatttacgt tcaggagata tggc

24

<210> 724

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 724

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Gly Phe Thr Phe Arg Arg Tyr Gly
 1              5

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<210> 725

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 725

atttggtatg atggaagtaa taaa

24

<210> 726

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 726

Ile Trp Tyr Asp Gly Ser Asn Lys

1

5

<210> 727

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 727

gcgagcgaaa taacaattgg ggactgggtc gacccc

36

<210> 728

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 728

Ala Ser Glu Ile Thr Ile Gly Asp Trp Phe Asp Pro

1

5

10

<210> 729

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 729

gccatccaga tgaccagtc tccatcctcc ctgtctgcat ctgttgaga cagagtcacc 60
 atcacttgtc gggcaagtca gggcattaga aatgatttag gctggtttca acagaaacca 120
 gggaaagtcc ctaaactcct gatctatgct gcatccactt tacacagtgg ggtcccatca 180
 aggttcagcg gcagtggatt tggcacagat ttcactctca ccatcagcag cctgcagcct 240
 gaagattttg caacttatta ctgtctacag gatttcaatt accctctcac ttctggcgga 300
 gggaccaagg tggagatcaa acga 324

<210> 730

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 730

Ala Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1

5

10

15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp

20

25

30

Leu Gly Trp Phe Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ala Ala Ser Thr Leu His Ser Gly Val 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
 Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Phe Asn Tyr Pro Leu
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 731
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 731
 cagggcatta gaaatgat

18

<210> 732
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 732
 Gln Gly Ile Arg Asn Asp
 1 5

<210> 733
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 733
 gctgcatcc

9

<210> 734
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 734
 Ala Ala Ser
 1

<210> 735

<211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 735
 ctacaggatt tcaattaccc tctcact

27

<210> 736
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 736
 Leu Gln Asp Phe Asn Tyr Pro Leu Thr
 1 5

<210> 737
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 737
 cagggtgcagc tgggtggagtc tgggggaggc gtgggtccagc ctgggatgtc cctgagactc 60
 tctgtacag cgtccggatt tacgttcagg agatatggca tgcactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg ggtggcagtt atttggtatg atggaagtaa taaatattat 180
 gcagactccg tgaagggacg attcaccata accagagaca attccaagaa cacgttgtat 240
 ctgcaaataga acagcctgag agccgaggac acggctatat atttttgtgc gagcgaaata 300
 acaattggggg actggttcga cccccggggc cagggaaccc tggtcaccgt ctctca 357

<210> 738
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 738
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Met
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Arg Arg Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Thr 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 Ile Tyr Phe Cys
 85 90 95
 Ala Ser Glu Ile Thr Ile Gly Asp Trp Phe Asp Pro Arg Gly Gln Gly

100
Thr Leu Val Thr Val Ser Ser
115

105

110

<210> 739
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 739
gccatccaga tgacccagtc tccatcctcc ctgtctgcat ctgttggaga cagagtcacc 60
atcacttgtc gggcaagtca gggcattaga aatgatttag gctggtttca acagaaacca 120
gggaaagtcc ctaaactcct gatctatgct gcatccactt tacacagtgg ggtcccatca 180
aggttcagcg gcagtggatt tggcacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtctacag gatttcaatt accctctcac tttcggcgga 300
gggaccaagg tggagatcaa a 321

<210> 740
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 740
Ala Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
20 25 30
Leu Gly Trp Phe Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
35 40 45
Tyr Ala Ala Ser Thr Leu His Ser Gly Val 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
Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Phe Asn Tyr Pro Leu
85 90 95
Thr Phe Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 741
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 741
caggtgcagc tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tctgtgcag cgtctggatt tacgttcagg agatatggca tgcactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtggcagtt atttggtatg atggaagtaa taaatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca actccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagcgaaata 300
acaattgggg actggttcga cccccggggc cagggaaccc tggtcaccgt ctccctca 357

<210> 742
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 742
 Gln Val 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 Arg Arg Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile 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 Ser Glu Ile Thr Ile Gly Asp Trp Phe Asp Pro Arg Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 743
 <211> 322
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 743
 gccatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgcc gggcaagtca gggcattaga aatgatttag gctggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatgct gcatccagtt tacaaagtgg ggtcccatca 180
 aggttcagcg gcagtggatc tggcacagat ttcactctca ccatcagcag cctgcagcct 240
 gaagattttg caacttatta ctgtctacag gatttcaatt accctctcac tttcggcgga 300
 gggaccaagg tggagatcaa ac 322

<210> 744
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 744
 Ala Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
 20 25 30
 Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Phe Asn Tyr Pro Leu
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 745
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 745
 cagggtgcagc tgggtgcagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
 tcctgtgtag cctctggatt caccttcagt agatatggca tgcactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg ggtggtagtt atatcatatg atggaattaa taaatactat 180
 gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacggtgtat 240
 ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gaaaggggac 300
 ttttgagagt gttactttga ctactggggc caggaaccc tggtcaccgt ctctca 357

<210> 746
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 746
 Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Arg Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Val Val Ile Ser Tyr Asp Gly Ile Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val 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 Lys Gly Asp Phe Trp Ser Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 747
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 747
 ggattcacct tcagtagata tggc

<210> 748
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 748
Gly Phe Thr Phe Ser Arg Tyr Gly
1 5

<210> 749
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 749
atatcatatg atggaattaa taaa

24

<210> 750
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 750
Ile Ser Tyr Asp Gly Ile Asn Lys
1 5

<210> 751
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 751
gcgaaagggg acttttggag tggttacttt gactac

36

<210> 752
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 752
Ala Lys Gly Asp Phe Trp Ser Gly Tyr Phe Asp Tyr
1 5 10

<210> 753
 <211> 336
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 753
 gaaattgtgc tgactcagac tccactctcc tcacctgtca cccttgagaca gccggcctcc 60
 atctcctgca ggtctagtca aagcctcgta cacagtgatg gaaacaccta cttgagttgg 120
 cttcaccaga ggccaggcca gcctccaaga ctcttaattt ataagatttc taaccgggttc 180
 tctgggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgcaaatac 240
 agcagggtgg aagctgagga tgtcgggatt tattactgca tgcaagctac acaatttccg 300
 actttcggcg gagggaccaaa ggtggagatc aaacga 336

<210> 754
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 754
 Glu Ile Val Leu Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
 20 25 30
 Asp Gly Asn Thr Tyr Leu Ser Trp Leu His Gln Arg Pro Gly Gln Pro
 35 40 45
 Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Gln Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Val Gly Ile Tyr Tyr Cys Met Gln Ala
 85 90 95
 Thr Gln Phe Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
 100 105 110

<210> 755
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 755
 caaagcctcg tacacagtga tggaaacacc tac 33

<210> 756
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 756
Gln Ser Leu Val His Ser Asp Gly Asn Thr Tyr
1 5 10

<210> 757
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 757
aagatttct

9

<210> 758
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 758
Lys Ile Ser
1

<210> 759
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 759
atgcaagcta cacaatttcc gact

24

<210> 760
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 760
Met Gln Ala Thr Gln Phe Pro Thr
1 5

<210> 761
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 761
 caggtgcagc tgggtggagtc tggggggaggc gtggtccagc ctgggaggtc cctgagactc 60
 tcctgtgtag cctctggatt caccttcagt agatatggca tgcactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg ggtggtagtt atatcatatg atggaattaa taaatactat 180
 gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacggtgtat 240
 ctgcaaatac acagcctgag agctgaggac acggctgtgt attactgtgc gaaaggggac 300
 ttttggagtg gttactttga ctactggggc caggggaacc tggtcaccgt ctcctca 357

<210> 762
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 762
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Arg Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Val Val Ile Ser Tyr Asp Gly Ile Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val 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 Lys Gly Asp Phe Trp Ser Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 763
 <211> 333
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 763
 gatattgtga tgaccagac tccactctcc tcacctgtca cccttgagca gccggcctcc 60
 atctcctgca ggtctagtca aagcctcgta cacagtgatg gaaacaccta cttgagttgg 120
 cttcaccaga ggccaggcca gcctccaaga ctcttaattt ataagatttc taaccggttc 180
 tctgggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgcaaata 240
 agcagggtgg aagctgagga tgtcgggatt tattactgca tgcaagctac acaatttccg 300
 actttcggcg gagggacca ggtggagatc aaa 333

<210> 764
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 764
 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly

1				5					10					15			
Gln	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	His	Ser		
			20					25					30				
Asp	Gly	Asn	Thr	Tyr	Leu	Ser	Trp	Leu	His	Gln	Arg	Pro	Gly	Gln	Pro		
		35					40					45					
Pro	Arg	Leu	Leu	Ile	Tyr	Lys	Ile	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro		
		50				55					60						
Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ala	Gly	Thr	Asp	Phe	Thr	Leu	Gln	Ile		
65					70					75					80		
Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Ile	Tyr	Tyr	Cys	Met	Gln	Ala		
				85					90					95			
Thr	Gln	Phe	Pro	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys			
			100					105						110			

<210> 765

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 765

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caggtgcagc tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt agatatggca tgcactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaattaa taaatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatac acagcctgag agctgaggac acggctgtgt attactgtgc gaaaggggac 300
ttttggagtg gttactttga ctactggggc caggaacc tggtcaccgt ctccctca 357

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<210> 766

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 766

Gln	Val	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	Arg	Tyr		
			20					25					30				
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val		
		35					40					45					
Ala	Val	Ile	Ser	Tyr	Asp	Gly	Ile	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val		
		50				55					60						
Lys	Gly	Arg	Phe	Thr	Ile	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	Lys	Gly	Asp	Phe	Trp	Ser	Gly	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly		
			100					105						110			
Thr	Leu	Val	Thr	Val	Ser	Ser											
			115														

<210> 767

<211> 334

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 767

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gatattgtga tgacccagac tccactctcc tcacctgtca cccttggaca gccggcctcc 60
atctcctgca ggtctagtca aagcctcgta cacagtgatg gaaacaccta cttgagttgg 120
cttcagcaga ggccaggcca gcctccaaga ctccctaattt ataagatttc taaccggttc 180
tctgggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgaaaatc 240
agcaggggtgg aagctgagga tgtcgggggtt tattactgca tgcaagctac acaatttccg 300
actttcggcg gagggaccaaa ggtggagatc aaac 334

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<210> 768

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 768

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Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
1           5           10           15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20          25          30
Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
35          40          45
Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
50          55          60
Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65          70          75          80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
85          90          95
Thr Gln Phe Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100         105         110

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<210> 769

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 769

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gaggtgcagc tgggtgcagtc tggggggaggc gtggtccagc ctggggaggtc cctgagactc 60
tctgtgttag cctctggatt caccttcagt agatatggca tgcactgggt ccgccaggct 120
ccaggcaagg ggctggagtg gctgatagtt atatcatatg atggaattaa taaatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacggtgtat 240
ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gaaaggggac 300
ttttggagtg gatactttga ctactggggc caggaaccc tggtcaccgt ctccctca 357

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<210> 770

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 770

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Arg Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu
 35 40 45
 Ile Val Ile Ser Tyr Asp Gly Ile Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val 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 Lys Gly Asp Phe Trp Ser Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 771

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 771

ggattcacct tcagtagata tggc

24

<210> 772

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 772

Gly Phe Thr Phe Ser Arg Tyr Gly
 1 5

<210> 773

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 773

atatcatatg atggaattaa taaa

24

<210> 774

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 774

Ile Ser Tyr Asp Gly Ile Asn Lys
1 5

<210> 775

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 775

gcgaaagggg acttttggag tggatacttt gactac

36

<210> 776

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 776

Ala Lys Gly Asp Phe Trp Ser Gly Tyr Phe Asp Tyr
1 5 10

<210> 777

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 777

gacatcgtga tgaccagac tccactctcc tcacctgtca cccttggaca gccggcctcc 60
atctcctgca ggtctagtca aagcctcgta cacagtgatg gaaacaccta cttgagttgg 120
cttcaccaga ggccaggcca gcctccaaga ctcctaattt ataagatttc taaccggttc 180
tctgggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgcaaatac 240
agcaggggtgg aagctgagga tgtcgggatt tattactgca tgcaaggtac acaatttccg 300
actttcggcg gagggaccaaa ggtggagatc aaacga 336

<210> 778

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 778

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
1 5 10 15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30
Asp Gly Asn Thr Tyr Leu Ser Trp Leu His Gln Arg Pro Gly Gln Pro

35 40 45
Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Gln Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Ile Tyr Tyr Cys Met Gln Gly
85 90 95
Thr Gln Phe Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

<210> 779
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 779
caaagcctcg tacacagtga tggaaacacc tac 33

<210> 780
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 780
Gln Ser Leu Val His Ser Asp Gly Asn Thr Tyr
1 5 10

<210> 781
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 781
aagatttct 9

<210> 782
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 782
Lys Ile Ser
1

<210> 783
<211> 24

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 783
 atgcaaggta cacaatttcc gact

24

<210> 784
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 784
 Met Gln Gly Thr Gln Phe Pro Thr
 1 5

<210> 785
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 785
 cagggtgcagc tgggtggagtc tggggggaggc gtgggtccagc ctggggaggtc cctgagactc 60
 tcctgtgtag cctctggatt caccttcagt agatatggca tgcactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg gctgatagtt atatcatatg atggaattaa taaatactat 180
 gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacggtgtat 240
 ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gaaaggggac 300
 ttttgagtg gatactttga ctactggggc cagggaaccc tggtcaccgt ctccctca 357

<210> 786
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 786
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Arg Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu
 35 40 45
 Ile Val Ile Ser Tyr Asp Gly Ile Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val 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 Lys Gly Asp Phe Trp Ser Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 787
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 787
gatattgtga tgaccagac tccactctcc tcacctgtca cccttggaca gccggcctcc 60
atctcctgca ggtctagtca aagcctcgta cacagtgatg gaaacaccta cttgagttgg 120
cttcaccaga ggccaggcca gcctccaaga ctccctaattt ataagatttc taaccggttc 180
tctgggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgcaaadc 240
agcaggggtgg aagctgagga tgtcgggatt tattactgca tgcaaggtac acaatttccg 300
actttcggcg gagggacca ggtggagatc aaa 333

<210> 788
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 788
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
1 5 10 15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30
Asp Gly Asn Thr Tyr Leu Ser Trp Leu His Gln Arg Pro Gly Gln Pro
35 40 45
Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Gln Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Ile Tyr Tyr Cys Met Gln Gly
85 90 95
Thr Gln Phe Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 789
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 789
caggtgcagc tgggtggagtc tggggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cctctggatt cacccttcagt agatatggca tgcactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaattaa taaatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cagcgtgtat 240
ctgcaaataga acagcctgag agctgaggac acggctgtgt attactgtgc gaaaggggac 300
ttttggagtg gatactttga ctactggggc cagggaaccc tggtcaccgt ctccctca 357

<210> 790
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 790
 Gln Val 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 Arg Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Val Ile Ser Tyr Asp Gly Ile Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile 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 Lys Gly Asp Phe Trp Ser Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 791
 <211> 334
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 791
 gatattgtga tgaccagac tccactctcc tcacctgtca cccttggaca gccggcctcc 60
 atctcctgca ggtctagtca aagcctcgta cacagtgatg gaaacaccta cttgagttgg 120
 cttcagcaga ggccaggcca gcctccaaga ctccctaattt ataagatttc taaccgggttc 180
 tctgggggtcc cagacagatt cagtggcagt ggggcaggga cagatttcac actgaaaatc 240
 agcagggtgg aagctgagga tgtcgggggtt tattactgca tgcaaggtag acaatttccg 300
 actttcggcg gagggacca ggtggagatc aaac 334

<210> 792
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 792
 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
 20 25 30
 Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
 35 40 45
 Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile

65					70					75					80
Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys	Met	Gln	Gly
				85					90					95	
Thr	Gln	Phe	Pro	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	
			100					105						110	

<210> 793
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 793
 caggtgcagc tgcaggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
 tcctgtgtag cctctggatt caccttcagt agatatggca tgcactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg ggtggtagtt atatcatatg atggaattaa taaatactat 180
 gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacggtgtat 240
 ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gaaaggggac 300
 ttttgagagt gttactttga ctactggggc caggaaccc tggtcaccgt ctctca 357

<210> 794
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 794
 Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Arg Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Val Val Ile Ser Tyr Asp Gly Ile Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val 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 Lys Gly Asp Phe Trp Ser Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 795
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 795
 ggattcacct tcagtagata tggc

<210> 796
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 796
Gly Phe Thr Phe Ser Arg Tyr Gly
1 5

<210> 797
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 797
atatcatatg atggaattaa taaa

24

<210> 798
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 798
Ile Ser Tyr Asp Gly Ile Asn Lys
1 5

<210> 799
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 799
gcgaaagggg acttttggag tggttacttt gactac

36

<210> 800
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 800
Ala Lys Gly Asp Phe Trp Ser Gly Tyr Phe Asp Tyr
1 5 10

<210> 801
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 801
 gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgcc gggcaagtca gggcattaga aatgatttag gctggtatca gcagaaacca 120
 gggaaagccc ctaagcgcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
 aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240
 gaagattttg caacttatta ctgtctacag cataatagtt accctccgac gttcggccaa 300
 gggaccaagg tggagatcaa a 321

<210> 802
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 802
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
 20 25 30
 Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
 35 40 45
 Tyr Ala Ala Ser Ser Leu Gln 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
 Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Pro
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 803
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 803
 cagggcatta gaaatgat 18

<210> 804
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 804

Gln Gly Ile Arg Asn Asp
 1 5

<210> 805
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 805
 gctgcatcc

9

<210> 806
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 806
 Ala Ala Ser
 1

<210> 807
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 807
 ctacagcata atagttaccc tccgacg

27

<210> 808
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 808
 Leu Gln His Asn Ser Tyr Pro Pro Thr
 1 5

<210> 809
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 809

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caggtgcagc tgggtggagtc tggggggaggc gtggtccagc ctggggaggtc cctgagactc 60
tcctgtgtag cctctggatt caccttcagt agatatggca tgcactgggt ccgccaggct 120
ccaggcaagg ggcctggagtg ggtggtagtt atatcatatg atggaattaa taaatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgggtgtat 240
ctgcaaataga acagcctgag agctgaggac acggcctgtgt attactgtgc gaaaggggac 300
ttttggagtg gttactttga ctactggggc caggggaacc tggtcaccgt ctccctca 357

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<210> 810

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 810

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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1             5             10             15
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Arg Tyr
      20             25             30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
      35             40             45
Val Val Ile Ser Tyr Asp Gly Ile Asn Lys Tyr Tyr Ala Asp Ser Val
      50             55             60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val 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 Lys Gly Asp Phe Trp Ser Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
      100            105            110
Thr Leu Val Thr Val Ser Ser
      115

```

<210> 811

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 811

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gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gggcattaga aatgatttag gctggtatca gcagaaacca 120
gggaaagccc ctaagcgccct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtctacag cataatagtt accctccgac gttcggccaa 300
gggaccaagg tggaaatcaa a                                     321

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<210> 812

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 812

```

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

```

```

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
      20      25      30
Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
      35      40      45
Tyr Ala Ala Ser Ser Leu Gln 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
Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Pro
      85      90      95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
      100      105

```

<210> 813
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

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<400> 813
caggtgcagc tgggtggagtc tggggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt agatatggca tgcactgggt ccgccagggt 120
ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaattaa taaatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaataga acagcctgag agctgaggac acggctgtgt attactgtgc gaaaggggac 300
ttttggagtg gttactttga ctactggggc caggaaccc tggtcaccgt ctcctca 357

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<210> 814
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

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<400> 814
Gln Val 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 Arg Tyr
      20      25      30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
      35      40      45
Ala Val Ile Ser Tyr Asp Gly Ile Asn Lys Tyr Tyr Ala Asp Ser Val
      50      55      60
Lys Gly Arg Phe Thr Ile 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 Lys Gly Asp Phe Trp Ser Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
      100      105      110
Thr Leu Val Thr Val Ser Ser
      115

```

<210> 815
 <211> 322
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 815

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gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gggcattaga aatgatttag gctggtatca gcagaaacca 120
gggaaagccc ctaagcgcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtctacag cataatagtt accctccgac gttcggccaa 300
gggaccaagg tggaaatcaa ac                                     322

```

<210> 816

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 816

```

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1           5           10           15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
          20           25           30
Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
          35           40           45
Tyr Ala Ala Ser Ser Leu Gln 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
Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Pro
          85           90           95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
          100          105

```

<210> 817

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 817

```

gaggtgcagc tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgtag cctctggatt caccttcagt agatatggca tgcactgggt ccgccaggct 120
ccaggcaagg ggctggagtg gctgatagtt atatcatatg atggaattaa taaatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacggtgtat 240
ctgcaaatac acagcctgag agttgaggac acgggagtggt attactgtgc gaaaggggac 300
ttttggagtg gttactttga ctactggggc caggggaacc tggtcaccgt ctccctca 357

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<210> 818

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 818

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Arg Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu
 35 40 45
 Ile Val Ile Ser Tyr Asp Gly Ile Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Gly Val Tyr Tyr Cys
 85 90 95
 Ala Lys Gly Asp Phe Trp Ser Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 819

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 819

ggattcacct tcagtagata tggc

24

<210> 820

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 820

Gly Phe Thr Phe Ser Arg Tyr Gly
 1 5

<210> 821

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 821

atatcatatg atggaattaa taaa

24

<210> 822

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 822

Ile Ser Tyr Asp Gly Ile Asn Lys
 1 5

<210> 823

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 823

gcgaaagggg acttttggag tggttacttt gactac

36

<210> 824

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 824

Ala Lys Gly Asp Phe Trp Ser Gly Tyr Phe Asp Tyr
 1 5 10

<210> 825

<211> 327

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 825

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
 gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcaccgtg gacgttcggc 300
 caagggacca aggtggaaat caaacga 327

<210> 826

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 826

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser
	50					55					60				
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu
65					70					75					80
Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Gly	Ser	Ser	Pro
				85					90					95	
Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg			
			100					105							

<210> 827
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 827
 cagagtgtta gcagcagcta c 21

<210> 828
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 828
 Gln Ser Val Ser Ser Ser Tyr
 1 5

<210> 829
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 829
 ggtgcatcc 9

<210> 830
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 830
 Gly Ala Ser
 1

<210> 831
 <211> 27
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 831

cagcagtatg gtagctcacc gtggacg

27

<210> 832

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 832

Gln Gln Tyr Gly Ser Ser Pro Trp Thr

1

5

<210> 833

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 833

cagggtgcagc tgggtggagtc tggggggaggc gtggtccagc ctgggaggtc cctgagactc 60
 tcctgtgtag cctctggatt caccttcagt agatatggca tgcactgggt ccgccaggct 120
 ccaggcaagg ggcctggagt gctgatagtt atatcatatg atggaattaa taaatactat 180
 gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacggtgtat 240
 ctgcaaatga acagcctgag agttgaggac acgggagtggt attactgtgc gaaaggggac 300
 ttttgagtg gttactttga ctactggggc caggaaccc tggtcaccgt ctccctca 357

<210> 834

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 834

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Arg Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu
 35 40 45
 Ile Val Ile Ser Tyr Asp Gly Ile Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Gly Val Tyr Tyr Cys
 85 90 95
 Ala Lys Gly Asp Phe Trp Ser Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser

115

<210> 835
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 835
 gaaattgtgt tgaogcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
 gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcaccgtg gacgttcggc 300
 caagggacca aggtggaaat caaa 324

<210> 836
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 836
 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45
 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95
 Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 837
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 837
 caggtgcagc tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
 tcctgtgcag cctctggatt caccttcagt agatatggca tgcactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaattaa taaatactat 180
 gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gaaaggggac 300
 tttttggagtg gttactttga ctactggggc caggggaacc tggtcaccgt ctctctca 357

<210> 838

<211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 838
 Gln Val 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 Arg Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Val Ile Ser Tyr Asp Gly Ile Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile 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 Lys Gly Asp Phe Trp Ser Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 839
 <211> 325
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 839
 gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcctgca gggccagtca gagggttagc agcagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
 gacaggttca gtggcagtg gtctgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgt ttactgtcag cagtatggta gctcaccgtg gacgttcggc 300
 caagggacca aggtggaaat caaac 325

<210> 840
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 840
 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45
 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Gly	Ser	Ser	Pro
				85					90					95	
Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys				
			100					105							

<210> 841
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <221> VARIANT
 <222> (1)...(1)
 <223> Xaa = Gly

<220>
 <221> VARIANT
 <222> (2)...(2)
 <223> Xaa = Phe

<220>
 <221> VARIANT
 <222> (3)...(3)
 <223> Xaa = Thr

<220>
 <221> VARIANT
 <222> (4)...(4)
 <223> Xaa = Phe

<220>
 <221> VARIANT
 <222> (5)...(5)
 <223> Xaa = Ser or Arg

<220>
 <221> VARIANT
 <222> (6)...(6)
 <223> Xaa = Ser or Arg

<220>
 <221> VARIANT
 <222> (7)...(7)
 <223> Xaa = Tyr

<220>
 <221> VARIANT
 <222> (8)...(8)
 <223> Xaa = Gly, Ala, or Thr

<400> 841
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5

<210> 842
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <221> VARIANT
 <222> (1)...(1)
 <223> Xaa = Ile

<220>
 <221> VARIANT
 <222> (2)...(2)
 <223> Xaa = Ser, Gly, or Thr

<220>
 <221> VARIANT
 <222> (3)...(3)
 <223> Xaa = Tyr, Gly, or Asp

<220>
 <221> VARIANT
 <222> (4)...(4)
 <223> Xaa = Asp, Gly, or Ser

<220>
 <221> VARIANT
 <222> (5)...(5)
 <223> Xaa = Gly or Arg

<220>
 <221> VARIANT
 <222> (6)...(6)
 <223> Xaa = Ile, Gly, or Ala

<220>
 <221> VARIANT
 <222> (7)...(7)
 <223> Xaa = Asn, Ser, Arg, or Gly

<220>
 <221> VARIANT
 <222> (8)...(8)
 <223> Xaa = Lys, Ala, or Thr

<400> 842
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5

<210> 843
 <211> 12

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> VARIANT
<222> (1)...(1)
<223> Xaa = Ala or Val

<220>
<221> VARIANT
<222> (2)...(2)
<223> Xaa = Lys

<220>
<221> VARIANT
<222> (3)...(3)
<223> Xaa = Gly or Glu

<220>
<221> VARIANT
<222> (4)...(4)
<223> Xaa = Asp or Gly

<220>
<221> VARIANT
<222> (5)...(5)
<223> Xaa = Phe or Asp

<220>
<221> VARIANT
<222> (6)...(6)
<223> Xaa = Trp or Ser

<220>
<221> VARIANT
<222> (7)...(7)
<223> Xaa = Ser or Gly

<220>
<221> VARIANT
<222> (8)...(8)
<223> Xaa = Gly or Tyr

<220>
<221> VARIANT
<222> (9)...(9)
<223> Xaa = Tyr or Asp

<220>
<221> VARIANT
<222> (10)...(10)
<223> Xaa = Phe or Leu

<220>
 <221> VARIANT
 <222> (11)...(11)
 <223> Xaa = Asp or Ala

<220>
 <221> VARIANT
 <222> (12)...(12)
 <223> Xaa = Tyr

<400> 843
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10

<210> 844
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <221> VARIANT
 <222> (1)...(1)
 <223> Xaa = Gln

<220>
 <221> VARIANT
 <222> (2)...(2)
 <223> Xaa = Ser or Gly

<220>
 <221> VARIANT
 <222> (3)...(3)
 <223> Xaa = Leu or Ile

<220>
 <221> VARIANT
 <222> (4)...(4)
 <223> Xaa = Val or Ser

<220>
 <221> VARIANT
 <222> (5)...(5)
 <223> Xaa = His, Asn, or Thr

<220>
 <221> VARIANT
 <222> (6)...(6)
 <223> Xaa = Ser, Asn, or Tyr

<220>
 <221> VARIANT

<222> (7)...(7)
 <223> Xaa = Asp or absent

<220>
 <221> VARIANT
 <222> (8)...(8)
 <223> Xaa = Gly or absent

<220>
 <221> VARIANT
 <222> (9)...(9)
 <223> Xaa = Asn or absent

<220>
 <221> VARIANT
 <222> (10)...(10)
 <223> Xaa = Thr or absent

<220>
 <221> VARIANT
 <222> (11)...(11)
 <223> Xaa = Tyr or absent

<400> 844
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10

<210> 845
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <221> VARIANT
 <222> (1)...(1)
 <223> Xaa = Lys or Ala

<220>
 <221> VARIANT
 <222> (2)...(2)
 <223> Xaa = Ile, Ala, or Thr

<220>
 <221> VARIANT
 <222> (3)...(3)
 <223> Xaa = Ser

<400> 845
 Xaa Xaa Xaa
 1

<210> 846

<211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <221> VARIANT
 <222> (1)...(1)
 <223> Xaa = Met or Gln

<220>
 <221> VARIANT
 <222> (2)...(2)
 <223> Xaa = Gln

<220>
 <221> VARIANT
 <222> (3)...(3)
 <223> Xaa = Ala or Tyr

<220>
 <221> VARIANT
 <222> (4)...(4)
 <223> Xaa = Thr or Lys

<220>
 <221> VARIANT
 <222> (5)...(5)
 <223> Xaa = Gln, Ser, or Ile

<220>
 <221> VARIANT
 <222> (6)...(6)
 <223> Xaa = Phe or Ser

<220>
 <221> VARIANT
 <222> (7)...(7)
 <223> Xaa = Pro

<220>
 <221> VARIANT
 <222> (8)...(8)
 <223> Xaa = Thr or Leu

<220>
 <221> VARIANT
 <222> (9)...(9)
 <223> Xaa = Thr or absent

<400> 846
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5

<210> 847
 <211> 330
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 847
 Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
 1 5 10 15
 Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20 25 30
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 65 70 75 80
 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95
 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 100 105 110
 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 115 120 125
 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 130 135 140
 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 145 150 155 160
 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 165 170 175
 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 180 185 190
 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 195 200 205
 Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 210 215 220
 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
 225 230 235 240
 Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 245 250 255
 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 260 265 270
 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 275 280 285
 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 290 295 300
 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 305 310 315 320
 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 325 330

<210> 848
 <211> 327
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 848

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Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 1          5          10          15
Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
      20          25          30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
      35          40          45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
      50          55          60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65          70          75          80
Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
      85          90          95
Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro
      100          105          110
Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
      115          120          125
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
      130          135          140
Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145          150          155          160
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
      165          170          175
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
      180          185          190
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
      195          200          205
Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
      210          215          220
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225          230          235          240
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
      245          250          255
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
      260          265          270
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
      275          280          285
Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
      290          295          300
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305          310          315          320
Leu Ser Leu Ser Leu Gly Lys
      325

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<210> 849

<211> 327

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 849

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Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 1          5          10          15
Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
      20          25          30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
      35          40          45

```

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
 65 70 75 80
 Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95
 Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
 100 105 110
 Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 115 120 125
 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 130 135 140
 Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
 145 150 155 160
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
 165 170 175
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 180 185 190
 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
 195 200 205
 Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 210 215 220
 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
 225 230 235 240
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 245 250 255
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 260 265 270
 Thr Thr Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 275 280 285
 Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
 290 295 300
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 305 310 315 320
 Leu Ser Leu Ser Leu Gly Lys
 325

<210> 850

<211> 1194

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 850

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 aagggtgatg gcacatccca cgtcactgga aaaggagtta cagttgaaac agtcttttct 180
 gtggatgagt tttctgcatc tgtcctcact ggaaaactga ccacggtctt ccttccaatt 240
 gtctacacaa ttgtgtttgt ggtgggtttg ccaagtaacg gcatggccct gtgggtcttt 300
 cttttccgaa ctaagaagaa gcaccctgct gtgatttaca tggccaatct ggccttggct 360
 gacctcctct ctgtcatctg gttccccttg aagattgcct atcacataca tgccaacaac 420
 tggatttatg ggggaagctct ttgtaatgtg cttattggct ttttctatgg caacatgtac 480
 tgttccattc tcttcatgac ctgcctcagt gtgcagaggt attgggtcat cgtgaacccc 540
 atggggcact ccaggaagaa ggcaaacatt gccattggca tctccctggc aatatggctg 600
 ctgattctgc tggtcacat ccctttgtat gtcgtgaagc agaccatctt cattcctgcc 660
 ctgaacatca cgacctgtca tgatgttttg cctgagcagc tcttggtggg agacatgttc 720
 aattacttcc tctctctggc cattgggggtc tttctgttcc cagccttcc cagagcctct 780
 gcctatgtgc tgatgatcag aatgctgcga tcttctgcca tggatgaaaa ctcagagaag 840

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aaaaggaaga gggccatcaa actcattgtc actgtcctgg ccatgtacct gatctgcttc 900
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<210> 851

<211> 397

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 851

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Ser Lys Gly Arg Ser Leu Ile Gly Lys Val Asp Gly Thr Ser His Val
      35           40           45
Thr Gly Lys Gly Val Thr Val Glu Thr Val Phe Ser Val Asp Glu Phe
      50           55           60
Ser Ala Ser Val Leu Thr Gly Lys Leu Thr Thr Val Phe Leu Pro Ile
65           70           75           80
Val Tyr Thr Ile Val Phe Val Val Gly Leu Pro Ser Asn Gly Met Ala
      85           90           95
Leu Trp Val Phe Leu Phe Arg Thr Lys Lys Lys His Pro Ala Val Ile
      100          105          110
Tyr Met Ala Asn Leu Ala Leu Ala Asp Leu Leu Ser Val Ile Trp Phe
      115          120          125
Pro Leu Lys Ile Ala Tyr His Ile His Ala Asn Asn Trp Ile Tyr Gly
      130          135          140
Glu Ala Leu Cys Asn Val Leu Ile Gly Phe Phe Tyr Gly Asn Met Tyr
145          150          155          160
Cys Ser Ile Leu Phe Met Thr Cys Leu Ser Val Gln Arg Tyr Trp Val
      165          170          175
Ile Val Asn Pro Met Gly His Ser Arg Lys Lys Ala Asn Ile Ala Ile
      180          185          190
Gly Ile Ser Leu Ala Ile Trp Leu Leu Ile Leu Leu Val Thr Ile Pro
      195          200          205
Leu Tyr Val Val Lys Gln Thr Ile Phe Ile Pro Ala Leu Asn Ile Thr
      210          215          220
Thr Cys His Asp Val Leu Pro Glu Gln Leu Leu Val Gly Asp Met Phe
225          230          235          240
Asn Tyr Phe Leu Ser Leu Ala Ile Gly Val Phe Leu Phe Pro Ala Phe
      245          250          255
Leu Thr Ala Ser Ala Tyr Val Leu Met Ile Arg Met Leu Arg Ser Ser
      260          265          270
Ala Met Asp Glu Asn Ser Glu Lys Lys Arg Lys Arg Ala Ile Lys Leu
      275          280          285
Ile Val Thr Val Leu Ala Met Tyr Leu Ile Cys Phe Thr Pro Ser Asn
      290          295          300
Leu Leu Leu Val Val His Tyr Phe Leu Ile Lys Ser Gln Gly Gln Ser
305          310          315          320
His Val Tyr Ala Leu Tyr Ile Val Ala Leu Cys Leu Ser Thr Leu Asn
      325          330          335
Ser Cys Ile Asp Pro Phe Val Tyr Tyr Phe Val Ser His Asp Phe Arg
      340          345          350
Asp His Ala Lys Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val Lys

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355 360 365
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 370 375 380
 Ser Tyr Ser Ser Ser Ser Thr Thr Val Lys Thr Ser Tyr
 385 390 395

<210> 852
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 <212> PRT
 <213> Human

<400> 852
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 1 5 10 15
 Gly Thr

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 <212> PRT
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<400> 853
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 <213> Artificial Sequence

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 35 40 45
 Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu
 50 55 60
 Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu
 65 70 75 80
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<213> Mouse
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Leu Ala Pro Gly Arg Asn Asn Ser Lys Gly Arg Ser Leu Ile Gly Arg
 1          5          10          15
Leu Glu Thr Gln
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<210>	857
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Gly Thr Asn Arg Ser Ser Lys Gly Arg Ser Leu Ile Gly Arg Val Asp
1 5 10 15
Gly Thr

<210>	858
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<212>	PRT
<213>	Rat

<400> 858
Gly Pro Asn Ser Lys Gly Arg Ser Leu Ile Gly Arg Leu Asp Thr Pro
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$\langle 210 \rangle$	859
$\langle 211 \rangle$	18

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<213> Rabbit

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Gly Thr Asn Lys Thr Ser Lys Gly Arg Ser Leu Ile Gly Arg Asn Thr
1 5 10 15
Gly Ser

<210> 860
<211> 18
<212> PRT
<213> Dog

<400> 860
Gly Thr Asn Arg Thr Ser Lys Gly Arg Ser Leu Ile Gly Lys Thr Asp
1 5 10 15
Ser Ser

<210> 861
<211> 18
<212> PRT
<213> Pig

<400> 861
Gly Thr Ser Arg Pro Ser Lys Gly Arg Ser Leu Ile Gly Lys Ala Asp
1 5 10 15
Asn Thr

<210> 862
<211> 18
<212> PRT
<213> Human

<400> 862
Ala Thr Asn Ala Thr Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro
1 5 10 15
Asn Asp

<210> 863
<211> 18
<212> PRT
<213> Human

<400> 863
Asp Thr Asn Asn Leu Ala Lys Pro Thr Leu Pro Ile Lys Thr Phe Arg
1 5 10 15
Gly Ala

<210> 864
<211> 19
<212> PRT

<213> Human

<400> 864

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

<210> 865

<211> 2772

<212> DNA

<213> Mouse

<400> 865

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2772

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<211> 399

<212> PRT

<213> Mouse

<400> 866

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 20          25          30
Asn Asn Ser Lys Gly Arg Ser Leu Ile Gly Arg Leu Glu Thr Gln Pro
 35          40          45
Pro Ile Thr Gly Lys Gly Val Pro Val Glu Pro Gly Phe Ser Ile Asp
 50          55          60
Glu Phe Ser Ala Ser Ile Leu Thr Gly Lys Leu Thr Thr Val Phe Leu
 65          70          75          80
Pro Val Val Tyr Ile Ile Val Phe Val Ile Gly Leu Pro Ser Asn Gly
 85          90          95
Met Ala Leu Trp Ile Phe Leu Phe Arg Thr Lys Lys Lys His Pro Ala
 100          105          110
Val Ile Tyr Met Ala Asn Leu Ala Leu Ala Asp Leu Leu Ser Val Ile
 115          120          125
Trp Phe Pro Leu Ala Ile Ala Tyr His Leu His Gly Asn Asn Trp Val
 130          135          140
Tyr Gly Glu Ala Leu Cys Lys Val Leu Ile Gly Phe Phe Tyr Gly Asn
 145          150          155          160
Met Tyr Cys Ser Ile Leu Phe Met Thr Cys Leu Ser Val Gln Arg Tyr
 165          170          175
Trp Val Ile Val Asn Pro Met Gly His Pro Arg Lys Lys Ala Asn Ile
 180          185          190
Ala Val Gly Val Ser Leu Ala Ile Trp Leu Leu Ile Phe Leu Val Thr
 195          200          205
Ile Pro Leu Tyr Val Met Lys Gln Thr Ile Tyr Ile Pro Ala Leu Asn
 210          215          220
Ile Thr Thr Cys His Asp Val Leu Pro Glu Glu Val Leu Val Gly Asp
 225          230          235          240
Met Phe Asn Tyr Phe Leu Ser Leu Ala Ile Gly Val Phe Leu Phe Pro
 245          250          255
Ala Ile Leu Thr Ala Ser Ala Tyr Val Leu Met Ile Lys Thr Leu Arg
 260          265          270
Ser Ser Ala Met Asp Glu His Ser Glu Lys Lys Arg Gln Arg Ala Ile
 275          280          285
Arg Leu Ile Ile Thr Val Leu Ala Met Tyr Phe Ile Cys Phe Ala Pro
 290          295          300
Ser Asn Leu Leu Leu Val Val His Tyr Phe Leu Ile Lys Thr Gln Arg
 305          310          315          320
Gln Ser His Val Tyr Ala Leu Tyr Leu Val Ala Leu Cys Leu Ser Thr
 325          330          335
Leu Asn Ser Cys Ile Asp Pro Phe Val Tyr Tyr Phe Val Ser Lys Asp
 340          345          350
Phe Arg Asp His Ala Arg Asn Ala Leu Leu Cys Arg Ser Val Arg Thr
 355          360          365
Val Asn Arg Met Gln Ile Ser Leu Ser Ser Asn Lys Phe Ser Arg Lys
 370          375          380
Ser Gly Ser Tyr Ser Ser Ser Thr Ser Val Lys Thr Ser Tyr
 385          390          395

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<210> 867

<211> 3011

<212> DNA

<213> Rat

<400> 867

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<210> 868

<211> 397

<212> PRT

<213> Rat

<400> 868

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 20          25          30
Ser Lys Gly Arg Ser Leu Ile Gly Arg Leu Asp Thr Pro Pro Pro Ile
 35          40          45
Thr Gly Lys Gly Ala Pro Val Glu Pro Gly Phe Ser Val Asp Glu Phe
 50          55          60
Ser Ala Ser Val Leu Thr Gly Lys Leu Thr Thr Val Phe Leu Pro Val
 65          70          75          80
Ile Tyr Ile Ile Val Phe Val Ile Gly Leu Pro Ser Asn Gly Met Ala
 85          90          95
Leu Trp Val Phe Phe Arg Thr Lys Lys Lys His Pro Ala Val Ile
100          105          110
Tyr Met Ala Asn Leu Ala Leu Ala Asp Leu Leu Ser Val Ile Trp Phe
115          120          125
Pro Leu Lys Ile Ser Tyr His Leu His Gly Asn Asp Trp Thr Tyr Gly
130          135          140
Asp Ala Leu Cys Lys Val Leu Ile Gly Phe Phe Tyr Gly Asn Met Tyr
145          150          155          160
Cys Ser Ile Leu Phe Met Thr Cys Leu Ser Val Gln Arg Tyr Trp Val
165          170          175
Ile Val Asn Pro Met Gly His Ser Arg Lys Arg Ala Asn Ile Ala Val
180          185          190
Gly Val Ser Leu Ala Ile Trp Leu Leu Ile Phe Leu Val Thr Ile Pro
195          200          205
Leu Tyr Val Met Arg Gln Thr Ile Tyr Ile Pro Ala Leu Asn Ile Thr
210          215          220
Thr Cys His Asp Val Leu Pro Glu Glu Val Leu Val Gly Asp Met Phe
225          230          235          240
Ser Tyr Phe Leu Ser Leu Ala Ile Gly Val Phe Leu Phe Pro Ala Leu
245          250          255
Leu Thr Ala Ser Ala Tyr Val Leu Met Ile Lys Thr Leu Arg Ser Ser
260          265          270
Ala Met Asp Glu His Ser Glu Lys Lys Arg Arg Arg Ala Ile Arg Leu
275          280          285
Ile Ile Thr Val Leu Ser Met Tyr Phe Ile Cys Phe Ala Pro Ser Asn
290          295          300
Val Leu Leu Val Val His Tyr Phe Leu Ile Lys Ser Gln Arg Gln Ser
305          310          315          320
His Val Tyr Ala Leu Tyr Leu Val Ala Leu Cys Leu Ser Thr Leu Asn
325          330          335
Ser Cys Ile Asp Pro Phe Val Tyr Tyr Phe Val Ser Lys Asp Phe Arg
340          345          350
Asp Gln Ala Arg Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val Lys
355          360          365
Arg Met Gln Ile Ser Leu Thr Ser Asn Lys Phe Ser Arg Lys Ser Ser
370          375          380
Ser Tyr Ser Ser Ser Ser Thr Ser Val Lys Thr Ser Tyr
385          390          395

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<210> 869

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 869

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<210> 870

<211> 23

<212> PRT

<213> Artificial Sequence

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<223> Synthetic

<400> 870

Gly Arg Asn Asn Ser Lys Gly Arg Ser Leu Ile Gly Arg Leu Glu Thr
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<210> 871

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 871

Gly Thr Asn Arg Ser Ser Lys Gly Arg Ser Leu Ile Gly Lys Val Asp
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<210> 872

<211> 24

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<210> 873

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

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<400> 873

Gly Thr Asn Arg Ser Ser Lys Gly Ala Ser Leu Ile Gly Lys Val Asp
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Gly Thr Gly Gly Gly Gly Ser Lys
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<210> 874

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 874

Gly Thr Asn Arg Ser Ser Lys Gly Arg Ala Leu Ile Gly Lys Val Asp
1 5 10 15
Gly Thr Gly Gly Gly Gly Ser Lys
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<210> 875

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 875

Gly Thr Asn Arg Ser Ser Lys Gly Arg Ser Ala Ile Gly Lys Val Asp
1 5 10 15
Gly Thr Gly Gly Gly Gly Ser Lys
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<210> 876

<211> 24

<212> PRT

<213> Artificial Sequence

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<223> Synthetic

<400> 876

Gly Thr Asn Arg Ser Ser Lys Gly Arg Ser Leu Ala Gly Lys Val Asp
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Gly Thr Gly Gly Gly Gly Ser Lys
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<210> 877

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 877

Gly Thr Asn Arg Ser Ser Lys Gly Arg Ser Leu Ile Ala Lys Val Asp
1 5 10 15
Gly Thr Gly Gly Gly Gly Ser Lys
20

<210> 878
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<212> PRT
<213> Artificial Sequence

<220>
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<400> 878
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1 5 10 15
Gly Thr Gly Gly Gly Gly Ser Lys
20

<210> 879
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<400> 879
Gly Thr Asn Arg Ser Ser Lys Gly Arg Ser Leu Ile Gly Lys Ala Asp
1 5 10 15
Gly Thr Gly Gly Gly Gly Ser Lys
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<210> 880
<211> 24
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<220>
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<400> 880
Gly Thr Asn Arg Ser Ser Lys Gly Arg Ser Leu Ile Gly Lys Val Ala
1 5 10 15
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