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(12) **United States Patent**
Sleeman et al.(10) **Patent No.:** US 8,062,640 B2
(45) **Date of Patent:** Nov. 22, 2011(54) **HIGH AFFINITY HUMAN ANTIBODIES TO PCSK9**(75) Inventors: **Mark W. Sleeman**, Mahopac, NY (US); **Joel H. Martin**, Putnam Valley, NY (US); **Tammy T Huang**, Goldens Bridge, NY (US); **Douglas MacDonald**, New York, NY (US)(73) Assignee: **Regeneron Pharmaceuticals, Inc.**, Tarrytown, NY (US)

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(51) **Int. Cl.**

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C07K 16/00 (2006.01)
C12P 21/08 (2006.01)

(52) **U.S. Cl.** 424/158.1; 530/387.1; 530/387.9(58) **Field of Classification Search** None
See application file for complete search history.

(56)

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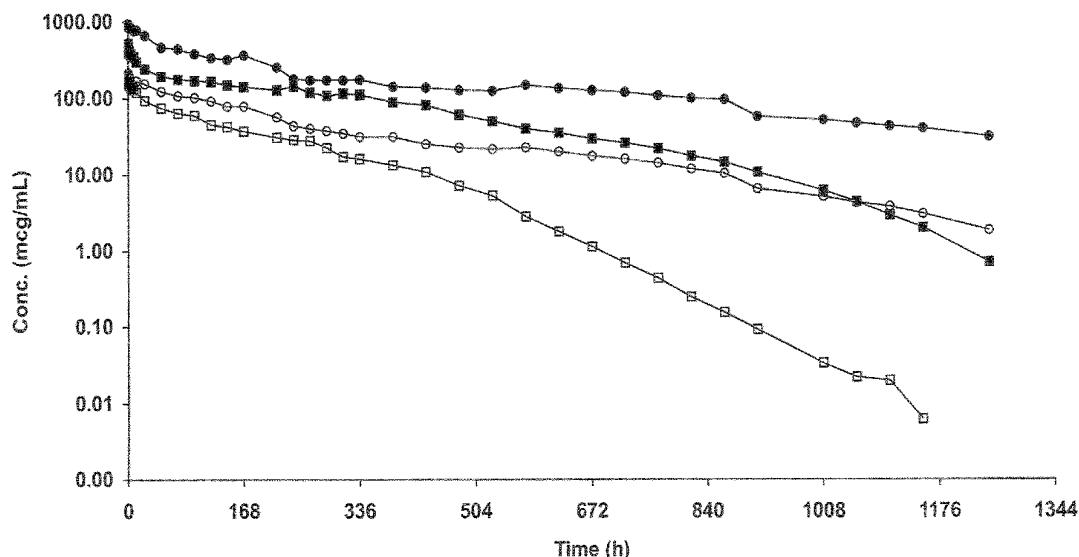
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Primary Examiner — Cherie M Woodward*(74) Attorney, Agent, or Firm* — Valeta Gregg; Frank R. Cottingham(57) **ABSTRACT**

An human antibody or antigen-binding fragment of a human antibody that specifically binds and inhibits human proprotein convertase subtilisin/kexin type 9 (hPCSK9) characterized by the ability to reduce serum LDL cholesterol by 40-80% over a 24, 60 or 90 day period relative to predose levels, with little or no reduction in serum HDL cholesterol and/or with little or no measurable effect on liver function, as determined by ALT and AST measurements.

3 Claims, 14 Drawing Sheets

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H1H316P VH (SEQ ID NO:90) EVQLVESGGGLVQPGGSLRLSCAASGFTFNNYAMNWVRQA PGKG
H1M300N VH (SEQ ID NO:218) EMQLVESGGGLVQPGGSLRLSCAASGFTFS SHWMKWVRQA PGKG

H1H316P VH (SEQ ID NO:90) LDWVSTISGSGGTTNYADSVKGRFII SRDSSKHTLYLQMNSLRA
H1M300N VH (SEQ ID NO:218) LEWVANINQDGSEKYYVDSVKGRFTI SRDNAKNSLFLQMNSLRA

CDR1

H1H316P VH (SEQ ID NO:90) EDTAVYYCAKDSNWGNFDL-----
H1M300N VH (SEQ ID NO:218) EDTAVYYCARDIVLMVYDMDYYYGMWDVWGWGQGTTVTVSS

CDR2

H1H316P VK (SEQ ID NO:92) DIVMTQSPDSDLAVSLGERATINCKSSS
H1M300N VK (SEQ ID NO:226) DIVMTQSPPLSLPVTPGEPA SISCRSSSQSLLHSGNNNY-LDWYLQ

CDR1

H1H316P VK (SEQ ID NO:92) KPGQPPNLIYWASSTRESSGV PDRFSSGSGT DFTLT
H1M300N VK (SEQ ID NO:226) KPGQSPQLLIVLGSNRASGV PDRFSSGSGT DFTLKI SREV EAED

CDR2

H1H316P VK (SEQ ID NO:92) VAVYYCQQYTTPYTFGQGTTKLEIK
H1M300N VK (SEQ ID NO:226) VGVYYCMATLQTPLTFGGGTKV EIK

CDR3

Fig. 1

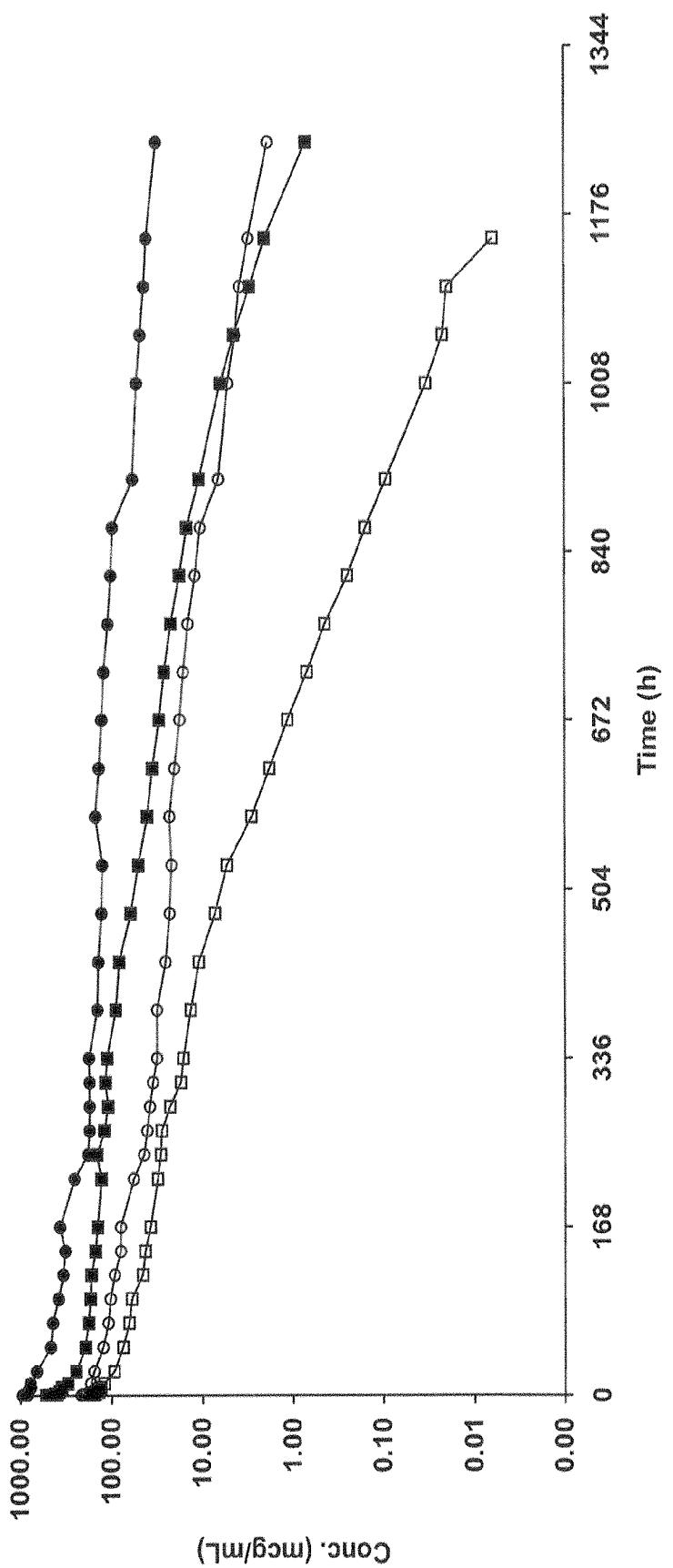


Fig. 2

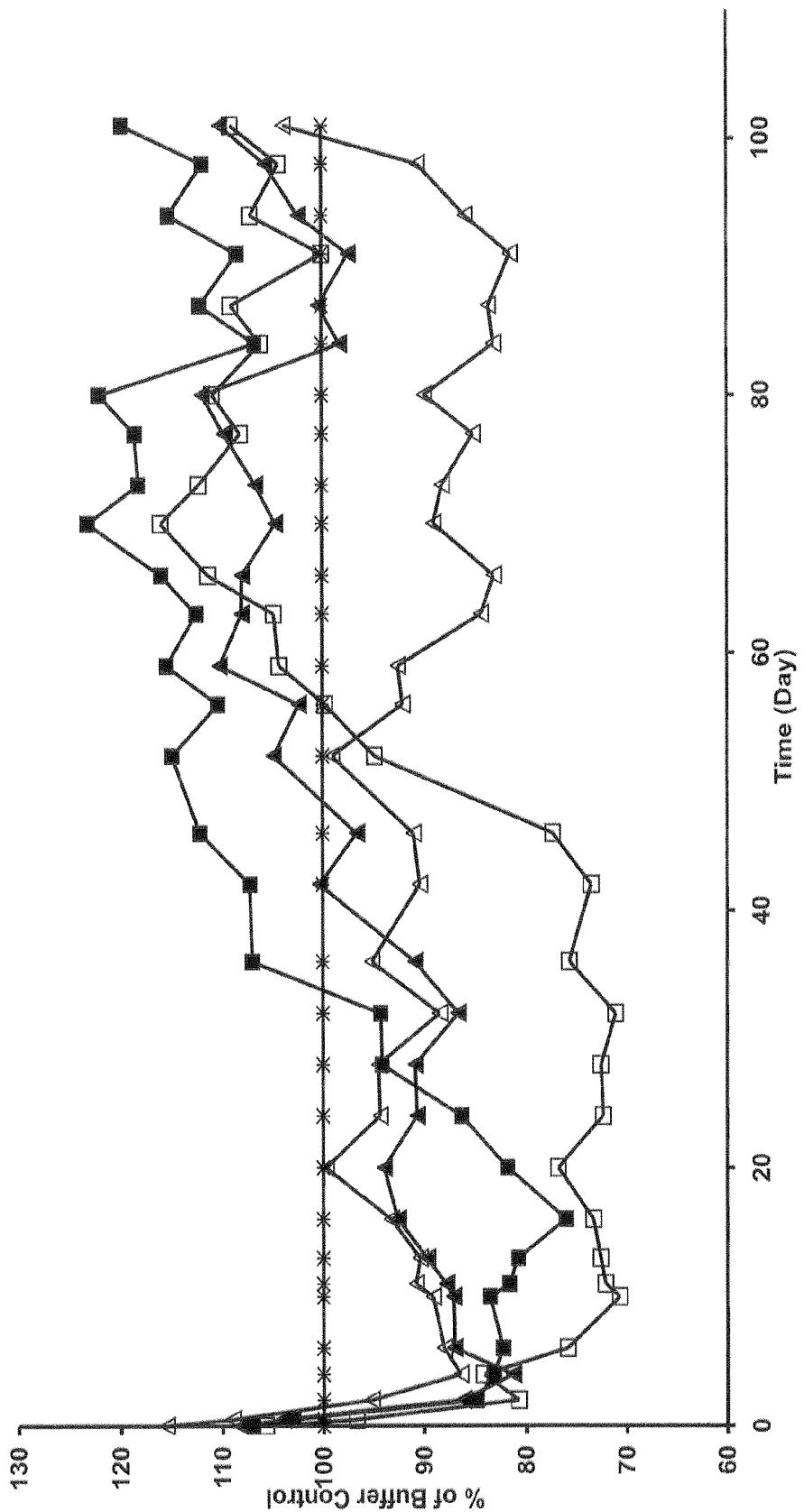


Fig. 3

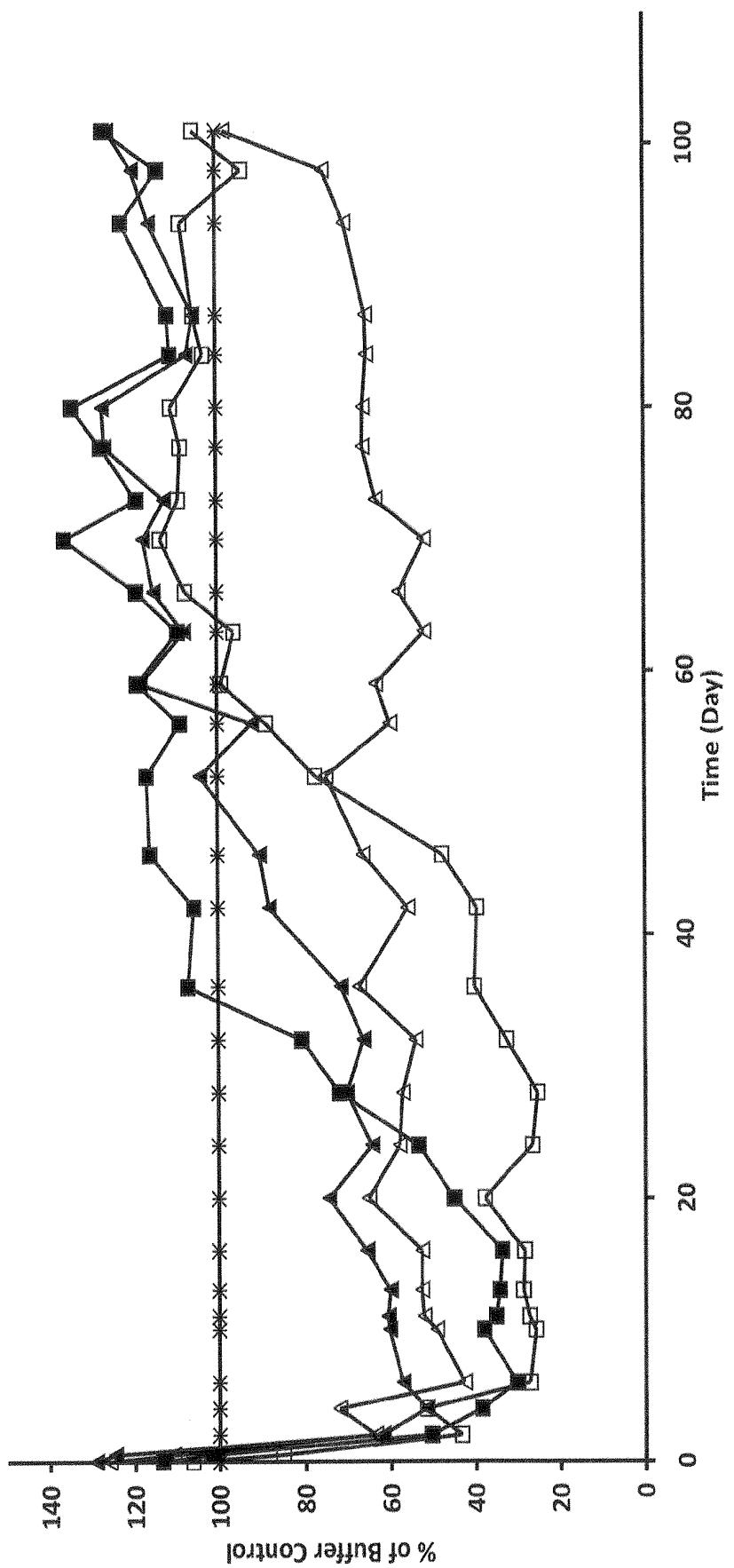


Fig. 4

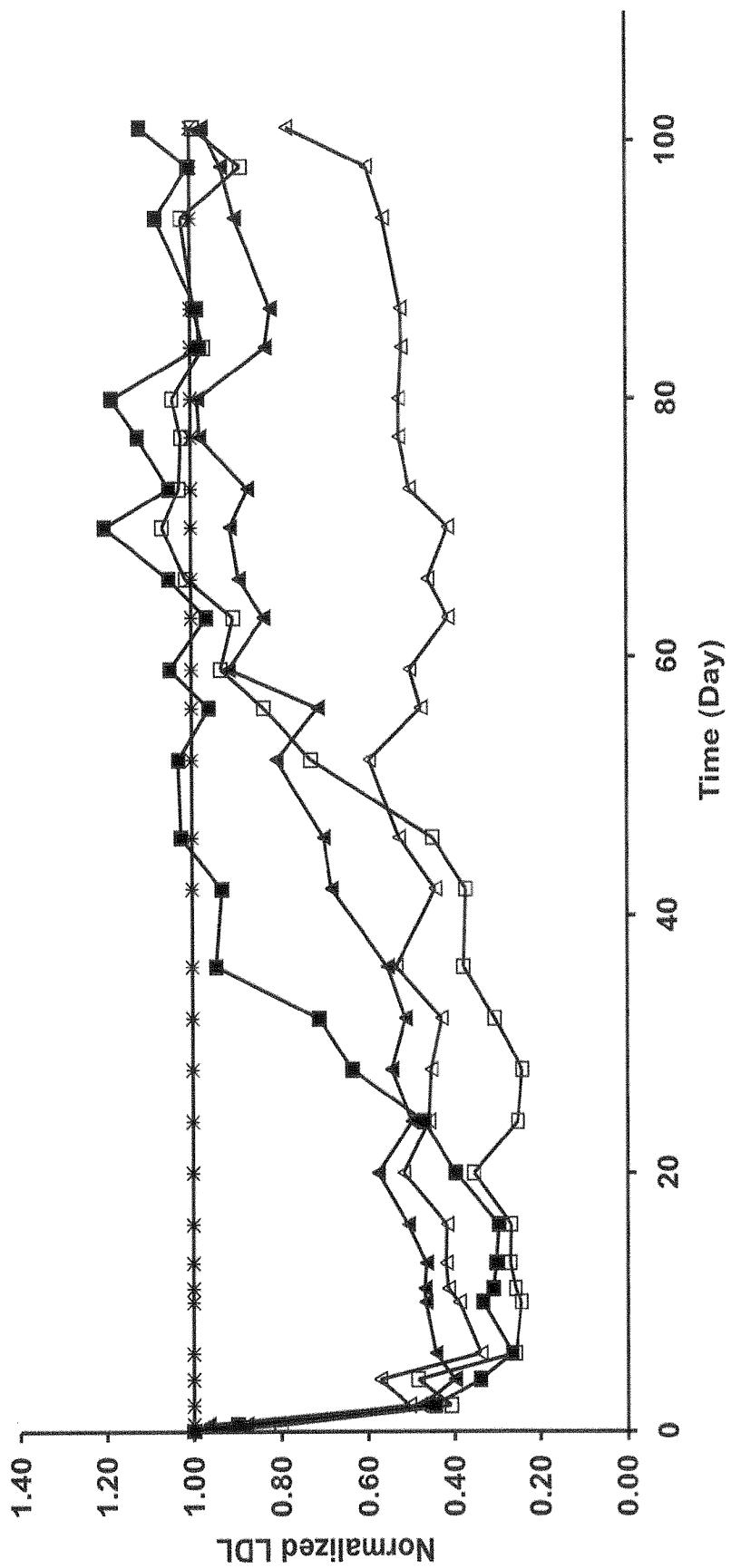


Fig. 5

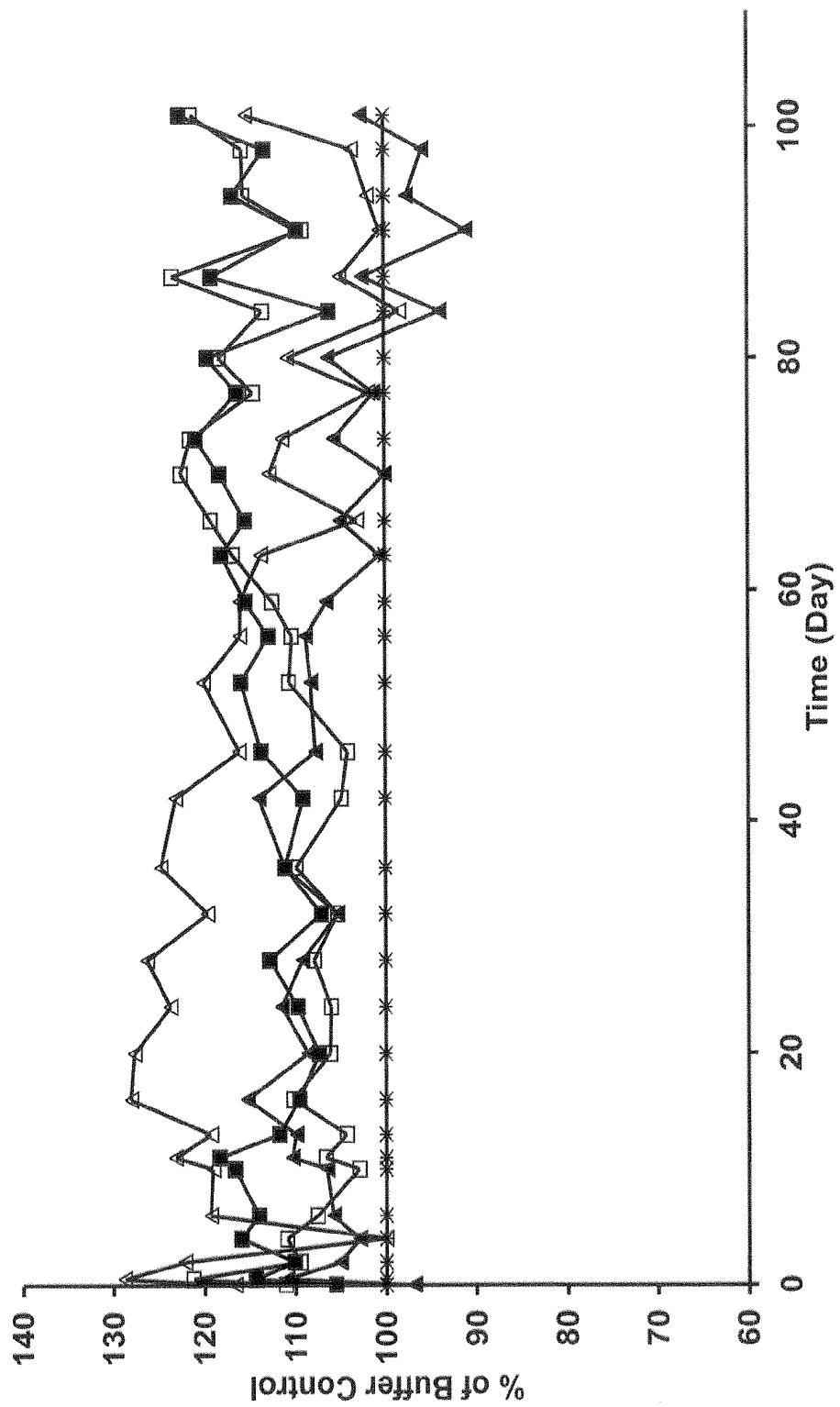


Fig. 6

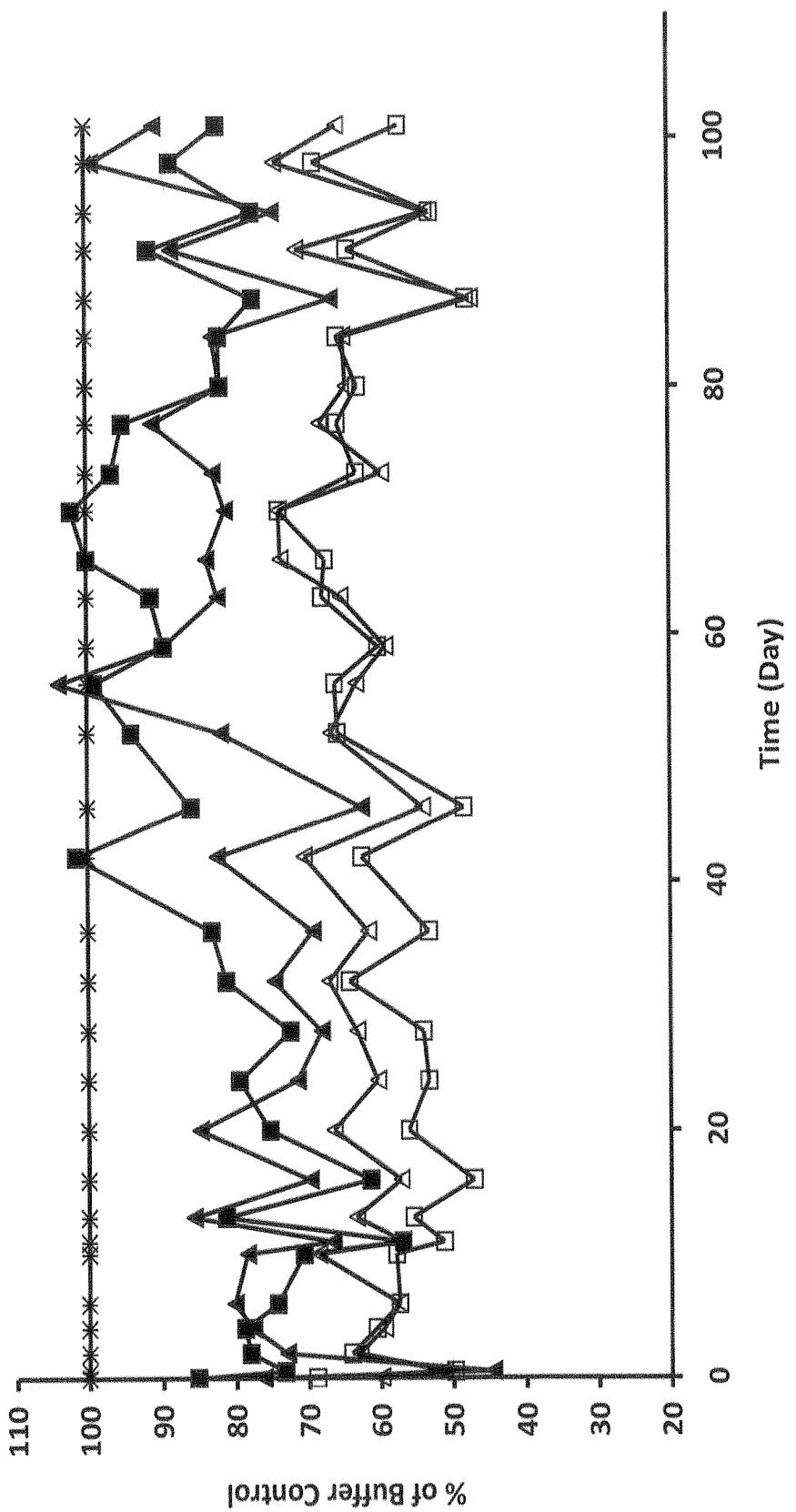


Fig. 7

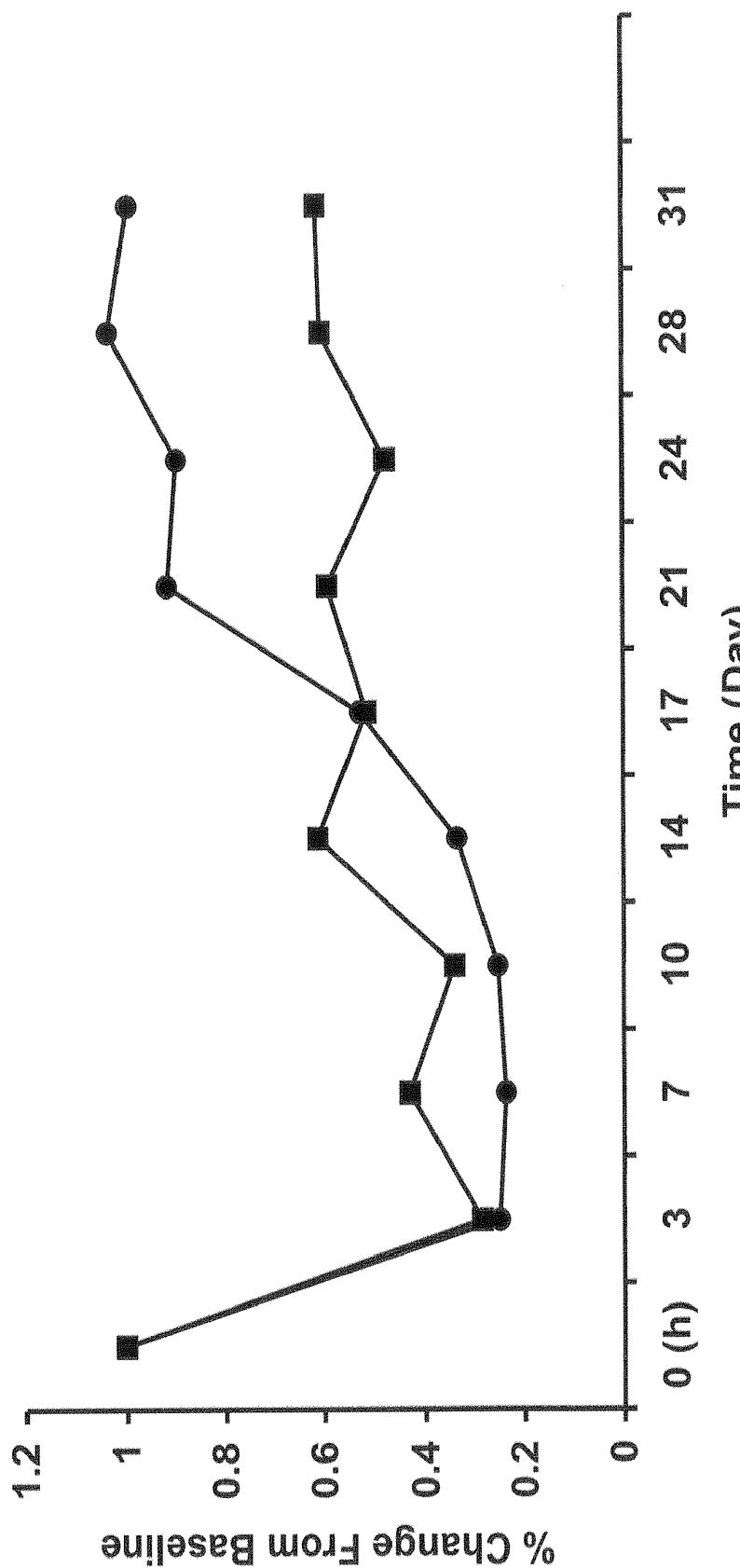


Fig. 8

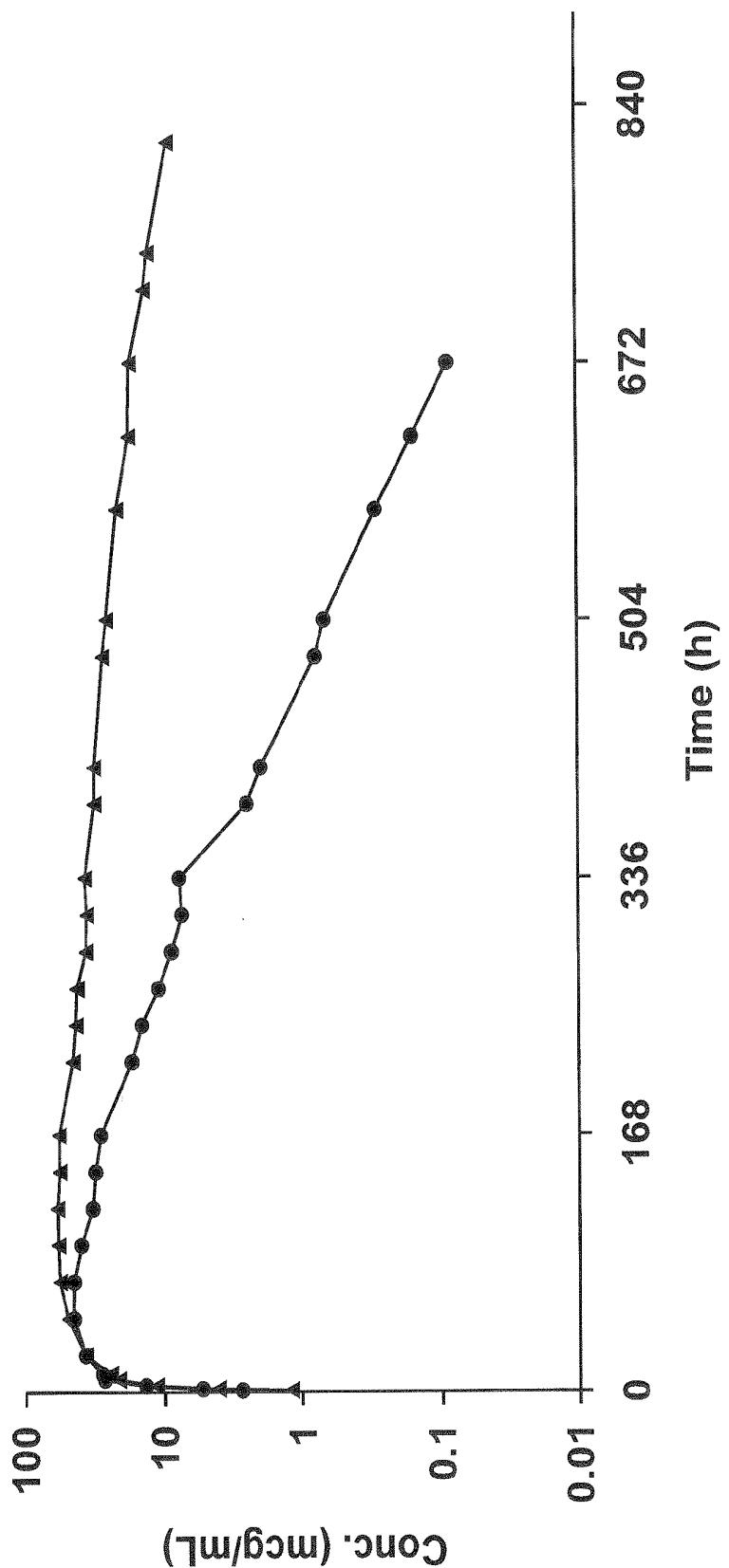


Fig. 9

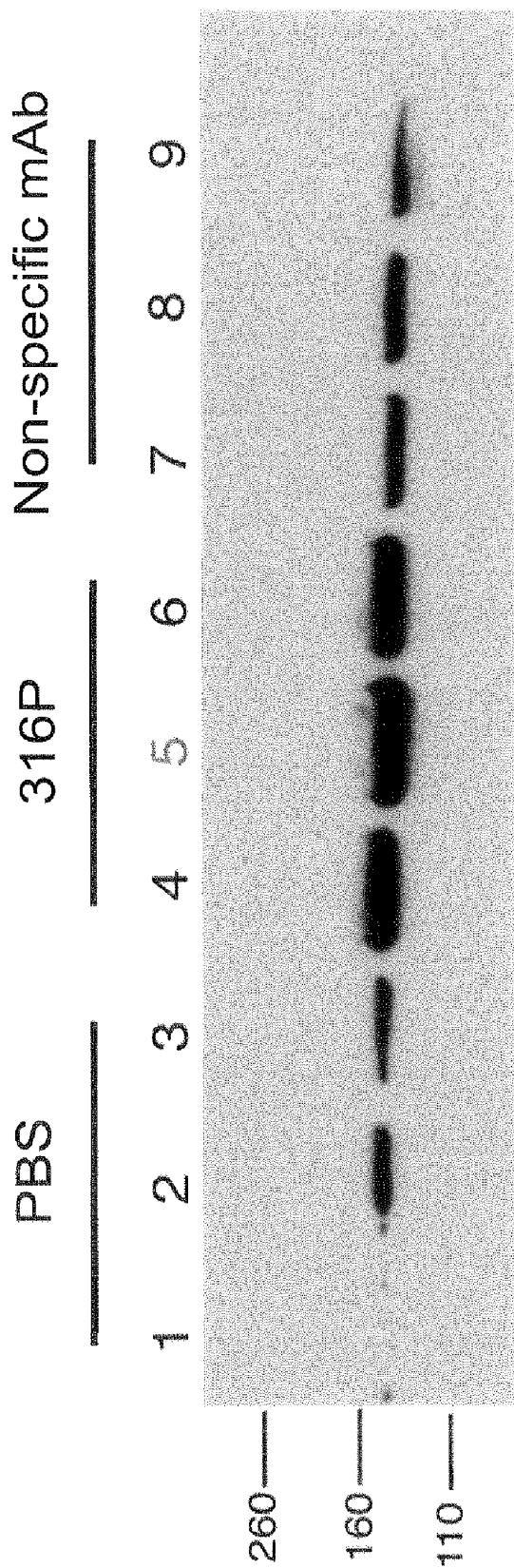


Fig. 10

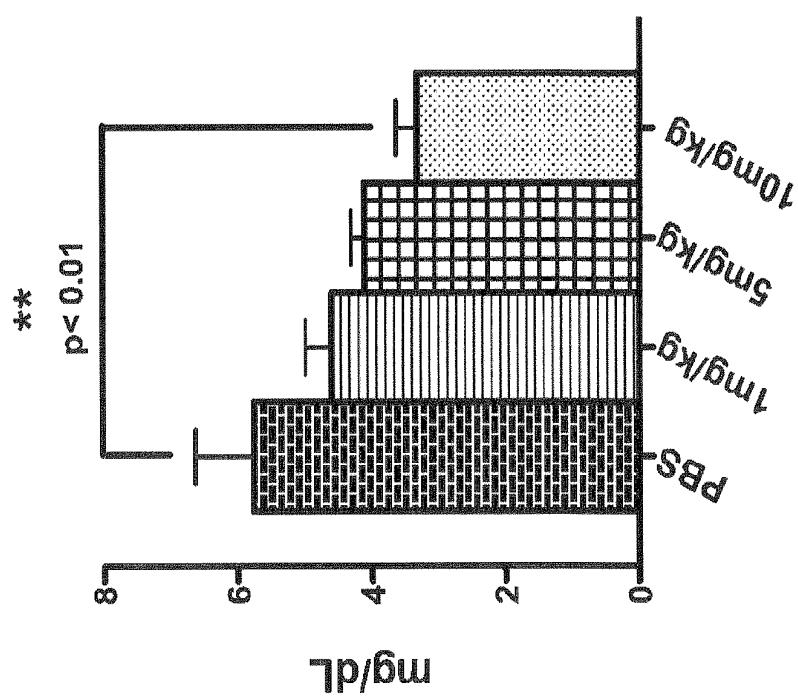


Fig. 11

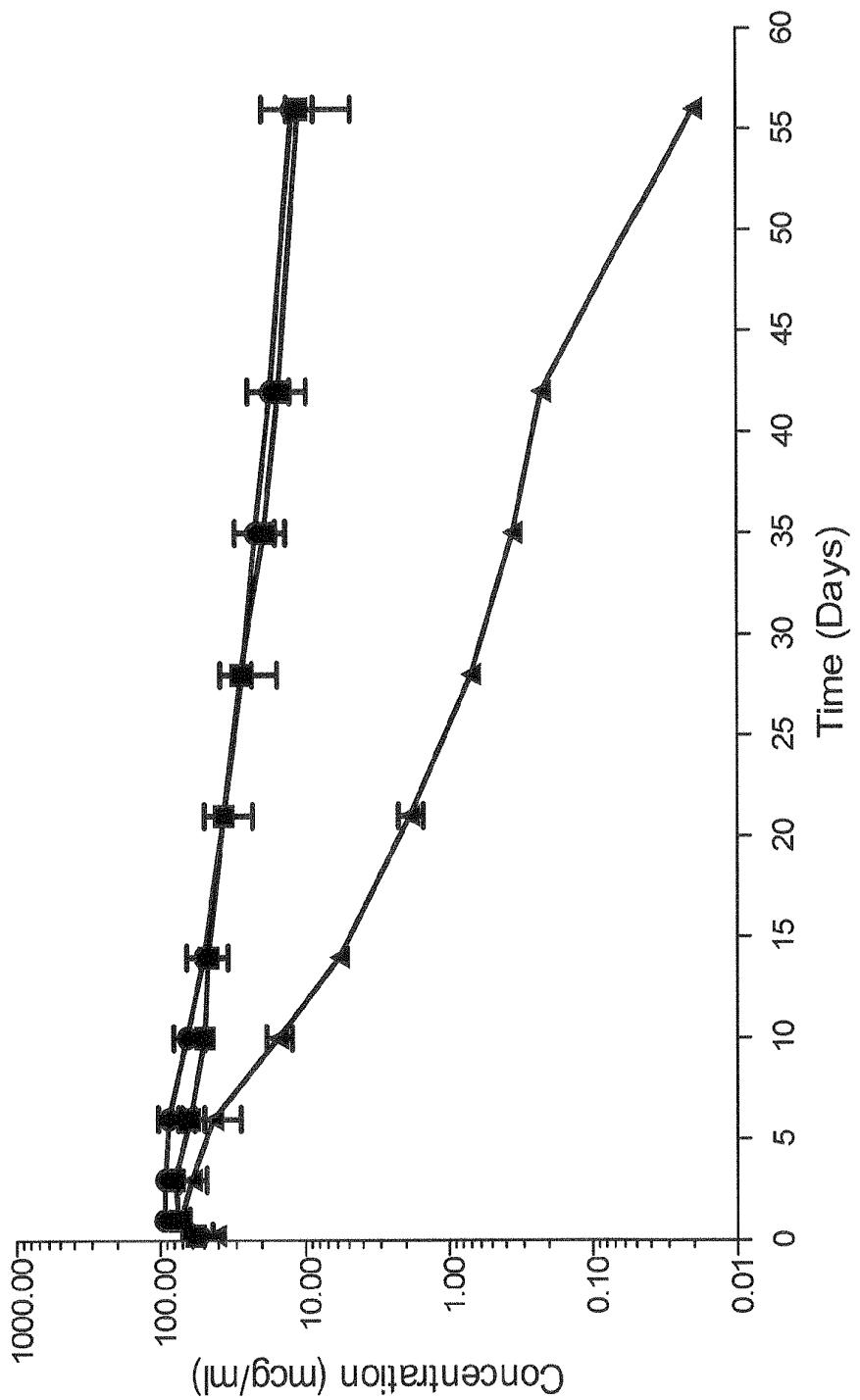


Fig. 12

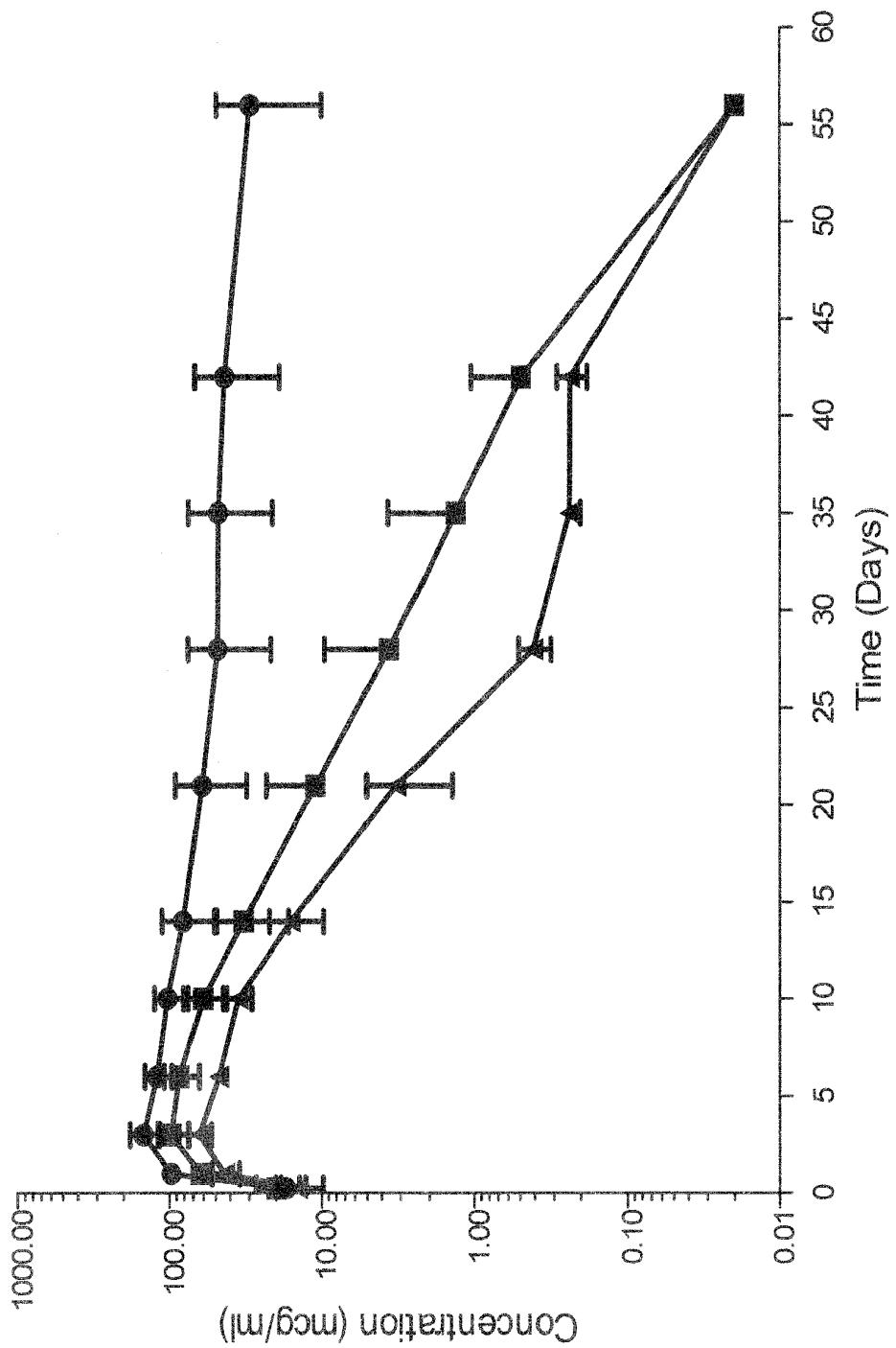


Fig. 13

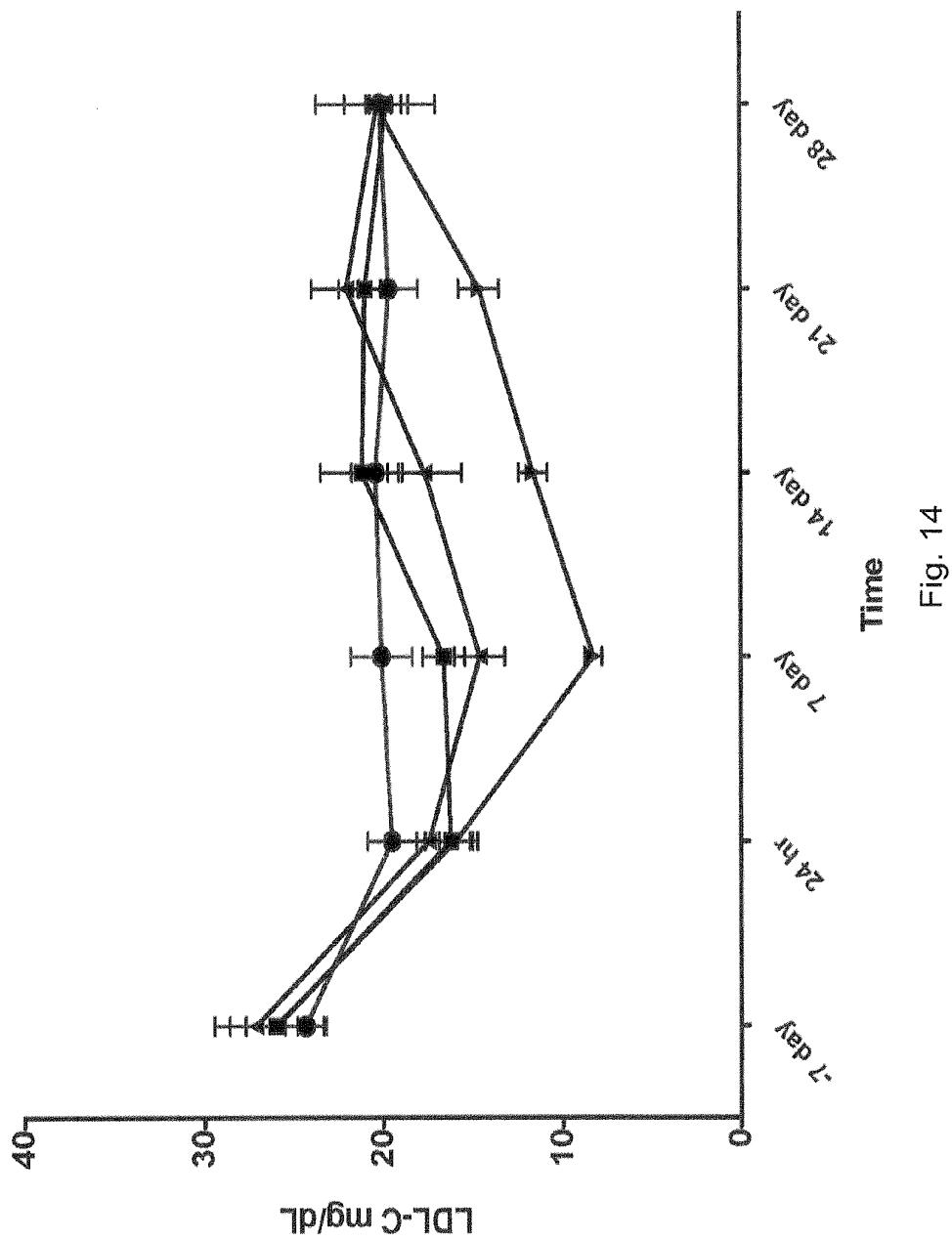


Fig. 14

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**HIGH AFFINITY HUMAN ANTIBODIES TO
PCSK9**

CROSS-REFERENCE TO RELATED
APPLICATIONS

This application claims the benefit under 35 USC §119(e) of U.S. Provisional 61/261,776 filed 17 Nov. 2009, 61/249,135 filed 6 Oct. 2009, 61/218,136 filed 18 Jun. 2009, 61/168,753 filed 13 Apr. 2009, 61/210,566 filed 18 Mar. 2009 and 61/1229,482 filed 15 Dec. 2008, which applications are herein specifically incorporated by reference in their entirety.

FIELD OF THE INVENTION

The present invention is related to human antibodies and antigen-binding fragments of human antibodies that specifically bind human proprotein convertase subtilisin/kexin type 9 (PCSK9), and therapeutic methods of using those antibodies.

SEQUENCE LISTING

An ASCII compliant text file of the sequence listing is filed concurrently with the present specification (37 CFR §1.52(e) and 37 CFR §1.821). The contents of the text file are herein incorporated by reference. The text file containing the sequence listing is named "PCSK9_SeqList", was created on 11 Dec. 2009, and contains approximately 418 kilobytes.

STATEMENT OF RELATED ART

Protein convertase subtilisin/kexin type 9 (PCSK9) is a proprotein convertase belonging to the proteinase K subfamily of the secretory subtilase family. The encoded protein is synthesized as a soluble zymogen that undergoes autocatalytic intramolecular processing in the endoplasmic reticulum. Evidence suggest that PCSK9 increases plasma LDL cholesterol by promoting degradation of the LDL receptor, which mediates LDL endocytosis in the liver, the major route of LDL clearance from circulation. The structure of PCSK9 protein shows that it has a signal sequence, followed by a prodomain, a catalytic domain that contains a conserved triad of residues (D186, H226 and S386), and a C-terminal domain. It is synthesized as a soluble 74-kDa precursor that undergoes autocatalytic cleavage in the ER, generating a 14-kDa prodomain and 60-kDa catalytic fragment. The autocatalytic activity has been shown to be required for secretion. After cleavage the prodomain remains tightly associated with the catalytic domain.

Antibodies to PCSK9 are described in, for example, WO 2008/057457, WO 2008/057458, WO 2008/057459, WO 2008/063382, WO 2008/125623, and US 2008/0008697.

BRIEF SUMMARY OF THE INVENTION

In a first aspect, the invention provides fully human monoclonal antibodies (mAbs) and antigen-binding fragments thereof that specifically bind and neutralize human PCSK9 (hPCSK9) activity.

In one embodiment, the invention comprises an antibody or antigen-binding fragment of an antibody that specifically binds hPCSK9 and is characterized by at least one of:

(i) capable of reducing serum total cholesterol at least about 25-35% and sustaining the reduction over at least a 24 day period relative to a predose level, preferably the reduction in serum total cholesterol is at least about 30-40%;

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- (ii) capable of reducing serum LDL cholesterol at least about 65-80% and sustaining the reduction over at least a 24 day period relative to a predose level;
- (iii) capable of reducing serum triglyceride at least about 25-40% relative to predose level;
- (iv) does not reduce serum HDL cholesterol or reduces serum HDL cholesterol no more than 5% relative to predose level.

In one embodiment, the invention comprises an antibody or antigen-binding fragment of an antibody that specifically binds hPCSK9 and is characterized by at least one of:

- (i) capable of reducing serum LDL cholesterol at least about 40-70% and sustaining the reduction over at least a 60 or 90 day period relative to a predose level;
- (ii) capable of reducing serum triglyceride at least about 25-40% relative to predose level;

(iii) does not reduce serum HDL cholesterol or reduces serum HDL cholesterol no more than 5% relative to predose level.

In one embodiment, the antibody or antigen-binding fragment is characterized as binding an epitope comprising amino acid residue 238 of hPCSK9 (SEQ ID NO:755). In a more specific embodiment, the antibody or antigen-binding fragment binds an epitope comprising one or more of amino acid residue 238, 153, 159 and 343 of hPCSK9 (SEQ ID NO:755). In a more specific embodiment, the antibody or fragment thereof is characterized as binding an epitope which does not comprise an amino acid residue at position 192, 194, 197 and/or 237 of SEQ ID NO:755.

In one embodiment, the antibody or antigen-binding fragment is characterized as binding an epitope comprising amino acid residue 366 of hPCSK9 (SEQ ID NO:755). In a more specific embodiment, the antibody or antigen-binding fragment binds an epitope comprising one or more of amino acid residue at position 147, 366 and 380 of SEQ ID NO:755. In a more specific embodiment, the antibody or antigen-binding fragment of an antibody is characterized as binding an epitope which does not comprise an amino acid residue at position 215 or 238 of SEQ ID NO:755.

In one embodiment, the antibody or antigen-binding fragment is characterized as exhibiting an enhanced binding affinity (K_D) for hPCSK9 at pH 5.5 relative to the K_D at pH 7.4, as measured by plasmon surface resonance. In a specific embodiment, the antibody or fragment thereof exhibits at least a 20-fold, at least a 40-fold or at least a 50-fold enhanced affinity for PCSK9 at an acidic pH relative to a neutral pH, as measured by surface plasmon resonance.

In one embodiment, the antibody or antigen-binding fragment is characterized as not exhibiting an enhanced binding affinity for PCSK9 at an acidic pH relative to a neutral pH, as measured by surface plasmon resonance. In a specific embodiment, the antibody or fragment thereof exhibits a decreased binding affinity at an acidic pH.

In another embodiment, the antibody or antigen-binding fragment binds human, human GOF mutation D374Y, cynomolgus monkey, rhesus monkey, mouse, rat and hamster PCSK9.

In one embodiment, the antibody or antigen-binding fragment binds human and monkey PCSK9, but does not bind mouse, rat or hamster PCSK9.

The mAbs can be full-length (e.g., an IgG1 or IgG4 antibody) or may comprise only an antigen-binding portion (e.g., 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).

In one embodiment, the invention comprises an antibody or antigen-binding fragment of an antibody comprising a heavy

chain variable region (HCVR) 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 and 742, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity. In one embodiment, the HCVR comprises an amino acid sequence selected from the group consisting of SEQ ID NO:50, 66, 70, 74, 90, 94, 122, 138, 142, 218, 234, 238, 242, 258, 262, 314, 330 and 334. In a more specific embodiment, the HCVR comprises SEQ ID NO:90 or 218.

In one embodiment, the antibody or fragment thereof further comprises a light chain variable region (LCVR) 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 and 744, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity. In one embodiment, the LCVR comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 58, 68, 72, 82, 92, 96, 130, 140, 144, 226, 236, 240, 250, 260, 264, 322, 332 and 336. In a more specific embodiment, the LCVR comprises SEQ ID NO:92 or 226.

In specific embodiments, the antibody or fragment thereof comprises 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, 508/516, 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, 718/720, 722/730, 738/740 and 742/744. In one embodiment, the HCVR and LCVR sequence pair comprises one of SEQ ID NO: 50/58, 66/68, 70/72, 74/82, 90/92, 94/96, 122/130, 138/140, 142/144, 218/226, 234/236, 238/240, 242/250, 258/260, 262/264, 314/322, 330/332 and 334/336. In a more specific embodiment, the HCVR/LCVR pair comprises SEQ ID NO:90/92 or 218/226.

In a second aspect, the invention features an antibody or antigen-binding fragment of an antibody comprising a heavy chain CDR3 (HCDR3) domain 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 and 728, 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 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 and 736, or substantially similar sequences thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity. In one embodiment, the HCDR3/LCDR3 sequence pair is selected from the group consisting of SEQ ID NO:56/64, 80/88, 128/136, 224/232, 248/256 and 320/328. In a more specific embodiment, the HCDR3/LCDR3 sequence pair comprises SEQ ID NO:80/88 or 224/232.

In a further embodiment, the invention comprising an antibody or fragment thereof further comprising a heavy chain CDR1 (HCDR1) domain 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 and 724, 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 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 and 726, 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 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 and 732, 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 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 and 734, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity. In one embodiment, the heavy and light chain CDR sequences comprise a sequence selected from the group consisting of SEQ ID NO:52, 54, 56, 60, 62, 64; 76, 78, 80, 84, 86, 88; 124, 126, 128, 132, 134, 136; 220, 222, 224, 228, 230, 232; 244, 246, 248, 252, 254, 256; and 316, 318, 320, 324, 326, 328. In more specific embodiments, the CDR sequences comprise SEQ ID NO: 76, 78, 80, 84, 86, 88; or 220, 222, 224, 228, 230, 232.

In a related embodiment, the invention comprises an antibody or antigen-binding fragment of an antibody which specifically binds hPCSK9, wherein the antibody or fragment comprises heavy and light chain CDR domains contained within heavy and light chain sequence pairs 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, 718/720, 722/730, 738/740 and 742/744. In one embodiment, the CDR sequences are contained within HCVR and LCVR selected from the amino acid sequence pairs of SEQ ID NO: 50/58, 66/68, 70/72, 74/82, 90/92, 94/96, 122/130, 138/140, 142/144, 218/226, 234/236, 238/240, 242/250, 258/260, 262/264, 314/322, 330/332 and 334/336. In more specific embodiment

ments, the CDR sequences are comprised within HCVR/LCVR sequences selected from SEQ ID NO: 90/92 or 218/226.

In one embodiment, the invention provides fully human monoclonal antibody or antigen-binding fragment thereof that specifically bind hPCSK9 and neutralize PCSK9 activity, wherein the antibody or fragment thereof exhibits one or more of the following characteristics: (i) capable of reducing serum total cholesterol at least about 25-35% and sustaining the reduction over at least a 24 day period relative to a predose level, preferably the reduction in serum total cholesterol is at least about 30-40%; (ii) capable of reducing serum LDL cholesterol at least about 65-80% and sustaining the reduction over at least a 24 day period relative to a predose level; (iii) capable of reducing serum triglyceride at least about 25-40% relative to predose level; (iv) does not reduce serum HDL cholesterol or reduces serum HDL cholesterol no more than 5% relative to predose level; (v) binds an epitope comprising amino acid residue 238 of hPCSK9 (SEQ ID NO:755); (vi) exhibits an enhanced binding affinity (K_D) for hPCSK9 at pH 5.5 relative to the K_D at pH 7.4, as measured by plasmon surface resonance, wherein the enhanced affinity is at least about a 20- to 50-fold increase in affinity; (vii) binds human, human GOF mutation D374Y, cynomolgus monkey, rhesus monkey, mouse, rat and hamster PCSK9; (viii) comprises heavy and light chain CDR3 sequences comprising SEQ ID NO:80 and 88; and (ix) comprises CDR sequences from SEQ ID NO:90 and 92.

In one embodiment, the invention provides fully human monoclonal antibody or antigen-binding fragment thereof that specifically bind human PCSK9 (hPCSK9) and neutralize PCSK9 activity, wherein the antibody or fragment thereof exhibits one or more of the following characteristics: (i) capable of reducing serum LDL cholesterol at least about 40-70% and sustaining the reduction over at least a 60 or 90 day period relative to a predose level; (ii) capable of reducing serum triglyceride at least about 25-40% relative to predose level; (iii) does not reduce serum HDL cholesterol or reduces serum HDL cholesterol no more than 5% relative to predose level; (iv) binds an epitope comprising amino acid residue 366 of hPCSK9 (SEQ ID NO:755); (v) does not exhibit an enhanced binding affinity for PCSK9 at an acidic pH relative to a neutral pH, as measured by surface plasmon resonance; (vi) binds human and monkey PCSK9, but does not bind mouse, rat or hamster PCSK9; (vii) comprises heavy and light chain CDR3 sequences comprising SEQ ID NO:224 and 232; and (viii) comprises CDR sequences from SEQ ID NO:218 and 226.

In a third aspect, the invention provides nucleic acid molecules encoding anti-PCSK9 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.

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 and 741, or a substantially identical

sequence having at least 90%, at least 95%, at least 98%, or at least 99% homology thereof. In one embodiment, the HCVR is encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO: 49, 65, 69, 73, 89, 93, 121, 137, 141, 217, 233, 237, 241, 257, 261, 313, 329 and 333. In more specific embodiments, the HCVR is encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO: 89 and 217.

In one embodiment, the antibody or fragment thereof further comprises 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 and 743, or a substantially identical sequence having at least 90%, at least 95%, at least 98%, or at least 99% homology thereof. In one embodiment, the LCVR is encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO: 57, 67, 71, 81, 91, 95, 129, 139, 143, 225, 235, 239, 249, 259, 263, 321, 331 and 335. In more specific embodiments, the LCVR is encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO: 91 and 225.

In one embodiment, the invention features 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 and 727, 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 and 735, or a substantially identical sequence having at least 90%, at least 95%, at least 98%, or at least 99% homology thereof. In one embodiment, the HCDR3 and LCDR3 comprise a sequence pair encoded by the nucleic acid sequence of SEQ ID NO: 55/63, 79/87, 127/135, 223/231, 247/255 and 319/327, respectively. In more specific embodiments, the HCDR3 and LCDR3 comprise a sequence pair encoded by the nucleic acid sequence of SEQ ID NO: 79/87 and 223/231.

In a further embodiment, the antibody or fragment thereof 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 and 723, 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 and 725, 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 and 731, 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 and 733, or a substantially identical sequence having at least 90%, at least 95%, at least 98%, or at least 99% homology thereof. In one embodiment, the heavy and light chain CDR sequences are encoded by the nucleic acid sequences of SEQ ID NO: 51, 53, 55, 59, 61, 63; 75, 77, 79, 83, 85, 87; 123, 125, 127, 131, 133, 135; 219, 221, 223, 227, 229, 231; 243, 245, 247, 251, 253, 255; and 315, 317, 319, 323, 325, 327. In more specific embodiments, the heavy and light chain CDR sequences are encoded by the nucleic acid sequences of SEQ ID NO: 75, 77, 79, 83, 85, 87; and 219, 221, 223, 227, 229, 231.

In a fourth aspect, the invention features an isolated antibody or antigen-binding fragment thereof that specifically binds hPCSK9, comprising a HCDR3 and a LCDR3, wherein HCDR3 comprises an amino acid sequence of the formula $X^1-X^2-X^3-X^4-X^5-X^6-X^7-X^8-X^9-X^{10}-X^{11}-X^{12}-X^{13}-X^{14}-X^{15}-X^{16}-X^{17}-X^{18}-X^{19}-X^{20}$ (SEQ ID NO:747), wherein X^1 is Ala, X^2 is Arg or Lys, X^3 is Asp, X^4 is Ser or Ile, X^5 is Asn or Val, X^6 is Leu or Trp, X^7 is Gly or Met, X^8 is Asn or Val, X^9 is Phe or Tyr, X^{10} is Asp, X^{11} is Leu or Met, X^{12} is Asp or absent, X^{13} is Tyr or absent, X^{14} is Tyr or absent, X^{15} is Tyr or absent, X^{16} is Tyr or absent, X^{17} is Gly or absent, X^{18} is Met or absent, X^{19} is Asp or absent, and X^{20} is Val or absent; and 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:750), wherein X^1 is Gln or Met, X^2 is Gln, X^3 is Tyr or Thr, X^4 is Tyr or Leu, X^5 is Thr or Gln, X^6 is Thr, X^7 is Pro, X^8 is Tyr or Leu, and X^9 is Thr.

In a further embodiment, the antibody or fragment thereof further comprise 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:745), wherein X^1 is Gly, X^2 is Phe, X^3 is Thr, X^4 is Phe, X^5 is Ser or Asn, X^6 is Ser or Asn, X^7 is Tyr or His, and X^8 is Ala or Trp; a HCDR2 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:746), wherein X^1 is Ile, X^2 is Ser or Asn, X^3 is Gly or Gln, X^4 is Asp or Ser, X^5 is Gly, X^6 is Ser or Gly, X^7 is Thr or Glu, and X^8 is Thr or Lys; a LCDR1 sequence of the formula $X^1-X^2-X^3-X^4-X^5-X^6-X^7-X^8-X^9-X^{10}-X^{11}-X^{12}$ (SEQ ID NO:748) wherein X^1 is Gln, X^2 is Ser, X^3 is Val or Leu, X^4 is Leu, X^5 is His or Tyr, X^6 is Arg or Ser, X^7 is Ser or Asn, X^8 is Asn or Gly, X^9 is Asn, X^{10} is Arg or Asn, X^{11} is Asn or Tyr, and X^{12} is Phe or absent; a LCDR2 sequence of the formula $X^1-X^2-X^3$ (SEQ ID NO:749) wherein X^1 is Trp or Leu, X^2 is Ala or Gly, and X^3 is Ser. FIG. 1 shows the sequence alignment of heavy and light chain variable regions for 316P and 300N mAbs.

In a fifth aspect, the invention features a human anti-PCSK9 antibody or antigen-binding fragment of an antibody comprising a heavy chain variable region (HCVR) encoded by nucleotide sequence segments derived from V_H , D_H and J_H germline sequences, and a light chain variable region (LCVR) encoded by nucleotide sequence segments derived from V_K and J_K germline sequences, wherein the germline sequences are (a) V_H gene segment 3-23, D_H gene segment 7-27, J_H gene segment 2, V_K gene segment 4-1 and J_K gene segment 2; or (b) V_H gene segment 3-7, D_H gene segment 2-8, J_H gene segment 6, V_K gene segment 2-28 and J_K gene segment 4.

In a sixth aspect, the invention features an antibody or antigen-binding fragment thereof that binds to a PCSK9 protein of SEQ ID NO:755, wherein the binding of the antibody or fragment thereof to a variant PCSK9 protein is less than

50% of the binding between the antibody or fragment thereof and the PCSK9 protein of SEQ ID NO:755. In specific embodiment, the antibody or fragment thereof binds to the variant PCSK9 protein with a binding affinity (K_D) which is less than about 50%, less than about 60%, less than about 70%, less than about 80%, less than about 90% or less than about 95% compared to the binding to PCSK9 (SEQ ID NO:755).

In one embodiment, the variant PCSK9 protein comprises at least one mutation at position 238 of SEQ ID NO:755. In a more specific embodiment, the mutation is D238R. In one embodiment, the antibody or antibody fragment binding affinity for the variant PCSK9 protein is at least 90% less relative to the wildtype protein of SEQ ID NO:755, wherein the variant protein comprises a mutation at residue 238. In one embodiment, the antibody or antibody fragment binding affinity for the variant PCSK9 protein is at least 80% less relative to the wildtype protein of SEQ ID NO:755, wherein the variant protein comprises a mutation at one or more of residue 153, 159, 238 and 343. In a more specific embodiment, the mutation is one of S153R, E159R, D238R and D343R.

In one embodiment, the variant PCSK9 protein comprises at least one mutation at position 366 of SEQ ID NO:755. In a more specific embodiment, the mutation is E366K. In one embodiment, the antibody or antibody fragment binding affinity for the variant PCSK9 protein is at least 95% less relative to the wildtype protein of SEQ ID NO:755, wherein the variant protein comprises a mutation at residue 366. In one embodiment, the antibody or antibody fragment binding affinity for the variant PCSK9 protein is at least 90% less relative to the wildtype protein of SEQ ID NO:755, wherein the variant protein comprises a mutation at one or more of residue 147, 366 and 380. In a more specific embodiment, the mutation is one of S147F, E366K and V380M. In one embodiment, the antibody or antibody fragment binding affinity for the variant PCSK9 protein is at least 80% less relative to the wildtype protein of SEQ ID NO:755, wherein the variant protein comprises a mutation at one or more of residue 147, 366 and 380. In a more specific embodiment, the mutation is one of S147F, E366K and V380M.

The invention encompasses anti-PCSK9 antibodies having a modified glycosylation pattern. In some applications, modification to remove undesirable glycosylation sites may be useful, or e.g., removal of a fucose moiety 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).

In a seventh aspect, the invention features a pharmaceutical composition comprising a recombinant human antibody or fragment thereof which specifically binds hPCSK9 and a pharmaceutically acceptable carrier. In one embodiment, the invention features a composition which is a combination of an antibody or antigen-binding fragment of an antibody of the invention, and a second therapeutic agent. The second therapeutic agent may be any agent that is advantageously combined with the antibody or fragment thereof of the invention, for example, an agent capable of inducing a cellular depletion of cholesterol synthesis by inhibiting 3-hydroxy-3-methyl-glutaryl (HMG)-coenzyme A (CoA) reductase, such as, for example, cerivastatin, atorvastatin, simvastatin, pitavastatin, rosuvastatin, fluvastatin, lovastatin, pravastatin, etc.; capable of inhibiting cholesterol uptake and or bile acid re-absorption; capable of increasing lipoprotein catabolism (such as

niacin); and/or activators of the LXR transcription factor that plays a role in cholesterol elimination such as 22-hydroxyc-
olesterol.

In an eighth aspect, the invention features methods for inhibiting hPCSK9 activity using the anti-PCSK9 antibody or antigen-binding portion of the 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 PCSK9 activity. Specific populations treatable by the therapeutic methods of the invention include subjects indicated for LDL apheresis, subjects with PCSK9-activating mutations (gain of function mutations, "GOF"), subjects with heterozygous Familial Hypercholesterolemia (heFH); subjects with primary hypercholesterolemia who are statin intolerant or statin uncontrolled; and subjects at risk for developing hypercholesterolemia who may be preventably treated. Other indications include dyslipidemia associated with secondary causes such as Type 2 diabetes mellitus, cholestatic liver diseases (primary biliary cirrhosis), nephrotic syndrome, hypothyroidism, obesity; and the prevention and treatment of atherosclerosis and cardiovascular diseases.

In specific embodiments of the method of the invention, the anti-hPCSK9 antibody or antibody fragment of the invention is useful to reduce elevated total cholesterol, non-HDL cholesterol, LDL cholesterol, and/or apolipoprotein B (apolipoprotein B100).

The antibody or antigen-binding fragment of the invention may be used alone or in combination with a second agent, for example, an HMG-CoA reductase inhibitor and/or other lipid lowering drugs.

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

BRIEF DESCRIPTION OF THE FIGURE

FIG. 1. Sequence comparison tables of heavy chain (A) and light chain (B) variable regions and CDRs of antibodies H1H316P and H1M300N.

FIG. 2. Antibody concentrations in serum over time. 316P 5 mg/kg (□); 300N 5 mg/kg (○); 316P 15 mg/kg (■); 300N 15 mg/kg (●).

FIG. 3. Serum total cholesterol level as a percentage of change over buffer control. Buffer control (*); 316P 5 mg/kg (■); 300N 5 mg/kg (▲); 316P 15 mg/kg (□); 300N 15 mg/kg (Δ).

FIG. 4. Serum LDL cholesterol level as a percentage of change over buffer control: Buffer Control (*); 316P 5 mg/kg (■); 300N 5 mg/kg (▲); 316P 15 mg/kg (□); 300N 15 mg/kg (Δ).

FIG. 5. Serum LDL cholesterol level normalized to buffer control. Buffer control (*); 316P 5 mg/kg (■); 300N 5 mg/kg (▲); 316P 15 mg/kg (□); 300N 15 mg/kg (Δ).

FIG. 6. Serum HDL cholesterol level as a percentage of change over buffer control. Buffer control (*); 316P 5 mg/kg (■); 300N 5 mg/kg (▲); 316P 15 mg/kg (□); 300N 15 mg/kg (Δ).

FIG. 7. Serum triglyceride level expressed as a percentage of change over buffer control. Buffer control (*); 316P 5 mg/kg (■); 300N 5 mg/kg (▲); 316P 15 mg/kg (□); 300N 15 mg/kg (Δ).

FIG. 8. Serum LDL cholesterol level expressed as a percentage of change over baseline following a single dose subcutaneous administration. 316P 5 mg/kg (■); 300N 5 mg/kg (●).

FIG. 9. Antibody concentrations in serum over time following a single dose subcutaneous administration. 316P 5 mg/kg (●); 300N 5 mg/kg (▲).

FIG. 10. Western blot for mouse LDL receptor of total liver homogenates. Samples were taken 24 hours after PBS (lanes 1-3), 5 mg/kg 316P (lanes 4-6), or 5 mg/kg of non-hPCSK9 specific mAb (lanes 7-8) administration and 4 hours after 1.2 mg/kg hPCSK9-mmh (all lanes).

FIG. 11. Effects of 316P on serum LDL cholesterol level in PCSK9^{hu/hu} mice. Buffer control (■); 316P 1 mg/kg (■); 316P 5 mg/kg (■); 316P 10 mg/kg (□).

FIG. 12. Anti-hPCSK9 mAb serum pharmacokinetic profile in C57BL/6 mice. Single dose of Control I mAb (●) at 10 mg/kg; 316P (▲) at 10 mg/kg and 300N (■) at 10 mg/kg.

FIG. 13. Anti-hPCSK9 mAb serum pharmacokinetic profile in hPCSK9 heterozygous mice. Single dose of Control I mAb (●) at 10 mg/kg; 316P (▲) at 10 mg/kg and 300N (■) at 10 mg/kg.

FIG. 14. Effect of 316P on serum LDL cholesterol levels in Syrian Hamster fed a normal diet. Buffer control (●); 316P 1 mg/kg (■); 316P 3 mg/kg (▲); 316P 5 mg/kg (◆).

DETAILED DESCRIPTION

Before the present methods are 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.

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. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, preferred methods and materials are now described. All publications mentioned herein are incorporated herein by reference in their entirety.

Definitions

The term "human proprotein convertase subtilisin/kexin type 9" or "hPCSK9", as used herein, refers to hPCSK9 having the nucleic acid sequence shown in SEQ ID NO:754 and the amino acid sequence of SEQ ID NO:755, or a biologically active fragment thereof.

The term "antibody", as used herein, is intended to refer to immunoglobulin molecules comprised of four polypeptide chains, two heavy (H) chains and two light (L) chains interconnected by disulfide bonds. Each heavy chain is comprised of a heavy chain variable region ("HCVR" or "VH") and a heavy chain constant region (comprised of domains CH1, CH2 and CH3). Each light chain is comprised of a light chain variable region ("LCVR" or "VL") and a light chain constant region (CL). The VH and VL regions can be further subdivided into regions of hypervariability, termed complementarity determining regions (CDR), interspersed with regions that are more conserved, termed framework regions (FR). Each VH and VL 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.

Substitution of one or more CDR residues or omission of one or more CDRs is also possible. Antibodies have been

described in the scientific literature in which one or two CDRs can be dispensed with for binding. Padlan et al. (1995 FASEB J. 9:133-139) analyzed the contact regions between antibodies and their antigens, based on published crystal structures, and concluded that only about one fifth to one third of CDR residues actually contact the antigen. Padlan also found many antibodies in which one or two CDRs had no amino acids in contact with an antigen (see also, Vajdos et al. 2002 J Mol Biol 320:415-428).

CDR residues not contacting antigen can be identified based on previous studies (for example residues H60-H65 in CDRH2 are often not required), from regions of Kabat CDRs lying outside Chothia CDRs, by molecular modeling and/or empirically. If a CDR or residue(s) thereof is omitted, it is usually substituted with an amino acid occupying the corresponding position in another human antibody sequence or a consensus of such sequences. Positions for substitution within CDRs and amino acids to substitute can also be selected empirically. Empirical substitutions can be conservative or non-conservative substitutions.

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 mAbs 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 mAbs in which CDR sequences derived from the germline of another mammalian species (e.g., mouse), have been grafted onto human FR sequences.

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 an equilibrium dissociation constant of at least about 1×10^{-6} M or less (e.g., a smaller K_D denotes a tighter binding). 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. An isolated antibody that specifically binds hPCSK9 may, however, exhibit cross-reactivity to other antigens such as PCSK9 molecules from other species. Moreover, multi-specific antibodies (e.g., bispecifics) that bind to hPCSK9 and one or more additional antigens are nonetheless considered antibodies that "specifically bind" hPCSK9, as used herein.

The term "high affinity" antibody refers to those mAbs having a binding affinity to hPCSK9 of at least 10^{-10} M; preferably 10^{-11} M; even more preferably 10^{-12} M, as measured by surface plasmon resonance, e.g., BIACORE™ or solution-affinity ELISA.

By the term "slow off rate", "Koff" or "kd" is meant an antibody that dissociates from hPCSK9 with a rate constant of 1×10^{-3} s⁻¹ or less, preferably 1×10^{-4} s⁻¹ or less, as determined by surface plasmon resonance, e.g., BIACORE™.

The term "antigen-binding portion" of an antibody (or simply "antibody fragment"), as used herein, refers to one or more fragments of an antibody that retain the ability to specifically bind to hPCSK9. An antibody fragment may include a Fab fragment, a F(ab')₂ fragment, a Fv fragment, a dAb fragment, a fragment containing a CDR, or an isolated CDR.

The specific embodiments, antibody or antibody fragments of the invention may be conjugated to a therapeutic moiety ("immunoconjugate"), such as a cytotoxin, a chemotherapeutic drug, an immunosuppressant or a radioisotope.

An "isolated antibody", as used herein, is intended to refer to an antibody that is substantially free of other mAbs having different antigenic specificities (e.g., an isolated antibody that specifically binds hPCSK9 is substantially free of mAbs that specifically bind antigens other than hPCSK9). An isolated antibody that specifically binds hPCSK9 may, however, have cross-reactivity to other antigens, such as PCSK9 molecules from other species.

A "neutralizing antibody", as used herein (or an "antibody that neutralizes PCSK9 activity"), is intended to refer to an antibody whose binding to hPCSK9 results in inhibition of at least one biological activity of PCSK9. This inhibition of the biological activity of PCSK9 can be assessed by measuring one or more indicators of PCSK9 biological activity by one or 15 more of several standard in vitro or in vivo assays known in the art (see examples below).

The term "surface plasmon resonance", as used herein, refers to an optical phenomenon that allows for the analysis of real-time biospecific interactions by detection of alterations 20 in protein concentrations within a biosensor matrix, for example using the BIACORE™ system (Pharmacia Biosensor AB, Uppsala, Sweden and Piscataway, N.J.).

The term " K_D ", as used herein, is intended to refer to the equilibrium dissociation constant of a particular antibody- 25 antigen interaction.

The term "epitope" is a region of an antigen that is bound by an antibody. Epitopes may be defined as structural or functional. Functional epitopes are generally a subset of the structural epitopes and have those residues that directly contribute to the affinity of the interaction. Epitopes may also be conformational, that is, composed of non-linear amino acids. In certain embodiments, epitopes may include determinants that are chemically active surface groupings of molecules such as amino acids, sugar side chains, phosphoryl groups, or 30 sulfonyl groups, and, in certain embodiments, may have specific three-dimensional structural characteristics, and/or specific charge characteristics.

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 90%, and more preferably at least about 95%, 96%, 97%, 98% or 99% of the nucleotide bases, as measured 45 by any well-known algorithm of sequence identity, such as FASTA, BLAST or GAP, as discussed below.

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 90% sequence identity, even more preferably at least 95%, 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 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, which is herein incorporated by reference. Examples of groups of 55 amino acids that have side chains with similar chemical prop-

erties 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: 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 45, herein incorporated by reference. A “moderately conservative” replacement is any change having a nonnegative value in the PAM250 log-likelihood matrix.

Sequence similarity for polypeptides 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 mutant thereof. See, e.g., GCG Version 6.1. Polypeptide sequences also can be compared using FASTA with 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 (1997) *Nucleic Acids Res.* 25:3389 402, each of which is herein incorporated by reference.

In specific embodiments, the antibody or antibody fragment for use in the method of the invention may be monospecific, bispecific, or multispecific. Multispecific antibodies may be specific for different epitopes of one target polypeptide or may contain antigen-binding domains specific for epitopes of more than one target polypeptide. 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) CH3 domain and a second Ig CH3 domain, wherein the first and second Ig CH3 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 CH3 domain binds Protein A and the second Ig CH3 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 CH3 may further comprise an Y96F modification (by IMGT; Y436F by EU). Further modifications that may be found within the second CH3 include: D16E, L18M, N44S, K52N, V57M, and V82I (by IMGT; D356E, L358M, N384S, K392N, V397M, and V422I by EU) in the case of IgG1 mAbs; N44S, K52N, and V82I (IMGT; N384S, K392N, and V422I by EU) in the case of IgG2 mAbs; 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 mAbs. Variations on the bi-specific antibody format described above are contemplated within the scope of the present invention.

By the phrase “therapeutically effective amount” is meant an amount that produces the desired effect for which it is administered. The exact amount will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques (see, for example, Lloyd (1999) *The Art, Science and Technology of Pharmaceutical Compounding*).

Preparation of Human Antibodies

Methods for generating human antibodies in transgenic mice are known (see for example, U.S. Pat. No. 6,596,541, Regeneron Pharmaceuticals, VELOCIMMUNE™). The VELOCIMMUNE™ technology involves generation of a transgenic mouse having a genome comprising human heavy and light chain variable regions operably linked to endogenous mouse constant region loci such that the mouse produces an antibody comprising a human variable region and a mouse constant region in response to antigenic stimulation. The DNA encoding the variable regions of the heavy and light chains of the antibody are isolated and operably linked to DNA encoding the human heavy and light chain constant regions. The DNA is then expressed in a cell capable of expressing the fully human antibody. In specific embodiment, the cell is a CHO cell.

Antibodies may be therapeutically useful in blocking a ligand-receptor interaction or inhibiting receptor component interaction, rather than by killing cells through fixation of complement and participation in complement-dependent cytotoxicity (CDC), or killing cells through antibody-dependent cell-mediated cytotoxicity (ADCC). The constant region of an antibody is thus 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.

Human antibodies can exist in two forms that are associated with hinge heterogeneity. In one form, an antibody 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.

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.

Generally, a VELOCIMMUNE™ mouse is challenged with the antigen of interest, and lymphatic cells (such as B-cells) are recovered from the mice that express antibodies. The lymphatic cells may be fused with a myeloma cell line to prepare immortal hybridoma cell lines, and such hybridoma cell lines are screened and selected to identify hybridoma cell lines that produce antibodies specific to the antigen of interest. DNA encoding the variable regions of the heavy chain

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and light chain may be isolated and linked to desirable iso-type constant regions of the heavy chain and light chain. Such an antibody protein may be produced in a cell, such as a CHO cell. Alternatively, DNA encoding the antigen-specific chimeric antibodies or the variable domains of the light and heavy chains may be isolated directly from antigen-specific lymphocytes.

Initially, high affinity chimeric antibodies are isolated having a human variable region and a mouse constant region. As described 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 (for example, SEQ ID NO:751, 752, 753). While the constant region selected may vary according to specific use, high affinity antigen-binding and target specificity characteristics reside in the variable region.

Epitope Mapping and Related Technologies

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., N.Y.) can be performed. Other methods include alanine scanning mutants, peptide blots (Reineke (2004) Methods Mol Biol 248:443-63) (herein specifically incorporated by reference in its entirety), 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) (herein specifically incorporated by reference in its entirety).

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.

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, herein specifically incorporated by reference in its entirety). 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 mAbs, such that characterization can be focused on genetically distinct mAbs. 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-PCSK9 mAbs of the invention into groups of mAbs binding different epitopes.

In various embodiments, the anti-hPCSK9 antibody or antigen-binding fragment of an antibody binds an epitope within the catalytic domain, which is about 153 to 425 of SEQ ID NO:755; more specifically, an epitope from about 153 to about 250 or from about 250 to about 425; more specifically, the antibody or antibody fragment of the invention binds an epitope within the fragment from about 153 to about 208, from about 200 to about 260, from about 250 to about 300,

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from about 275 to about 325, from about 300 to about 360, from about 350 to about 400, and/or from about 375 to about 425.

In various embodiments, the anti-hPCSK9 antibody or antigen-binding fragment of an antibody binds an epitope within the propeptide domain (residues 31 to 152 of SEQ ID NO:755); more specifically, an epitope from about residue 31 to about residue 90 or from about residue 90 to about residue 152; more specifically, the antibody or antibody fragment of the invention binds an epitope within the fragment from about residue 31 to about residue 60, from about residue 60 to about residue 90, from about residue 85 to about residue 110, from about residue 100 to about residue 130, from about residue 125 to about residue 150, from about residue 135 to about residue 152, and/or from about residue 140 to about residue 152.

In some embodiments, the anti-hPCSK9 antibody or antigen-binding fragment of an antibody binds an epitope within the C-terminal domain, (residues 426 to 692 of SEQ ID NO:755); more specifically, an epitope from about residue 426 to about residue 570 or from about residue 570 to about residue 692; more specifically, the antibody or antibody fragment of the invention binds an epitope within the fragment from about residue 450 to about residue 500, from about residue 500 to about residue 550, from about residue 550 to about residue 600, and/or from about residue 600 to about residue 692.

In some embodiments, the antibody or antibody fragment binds an epitope which includes more than one of the enumerated epitopes within the catalytic, propeptide or C-terminal domain, and/or within two or three different domains (for example, epitopes within the catalytic and C-terminal domains, or within the propeptide and catalytic domains, or within the propeptide, catalytic and C-terminal domains).

In some embodiments, the antibody or antigen-binding fragment binds an epitope on hPCSK9 comprising amino acid residue 238 of hPCSK9 (SEQ ID NO:755). Experimental results (Table 27) show that when D238 was mutated, the K_D of mAb 316P exhibited >400-fold reduction in binding affinity ($\sim 1 \times 10^{-9}$ M to $\sim 410 \times 10^{-9}$ M) and $T_{1/2}$ decreased >30-fold (from ~ 37 to ~ 1 min). In a specific embodiment, the mutation was D238R. In specific embodiments, the antibody or antigen-binding fragment of the invention binds an epitope of hPCSK9 comprising two or more of amino acid residues at positions 153, 159, 238 and 343.

As shown below, a mutation in amino acid residue 153, 159 or 343 resulted in about a 5- to 10-fold decrease in affinity or similar shortening in $T_{1/2}$. In specific embodiments, the mutation was S153R, E159R and/or D343R.

In some embodiments, the antibody or antigen-binding fragment binds an epitope on hPCSK9 comprising amino acid residue 366 of hPCSK9 (SEQ ID NO:755). Experimental results (Table 27) show that when E366 was mutated, the affinity of mAb 300N exhibited about 50-fold decrease ($\sim 0.7 \times 10^{-9}$ M to $\sim 36 \times 10^{-9}$ M) and a similar shortening in $T_{1/2}$ (from ~ 120 to ~ 2 min). In a specific embodiment, the mutation is E366K.

The present invention includes anti-PCSK9 antibodies that bind to the same epitope as any of the specific exemplary antibodies described herein. Likewise, the present invention also includes anti-PCSK9 antibodies that compete for binding to PCSK9 or a PCSK9 fragment with any of the specific exemplary antibodies described herein.

One can easily determine whether an antibody binds to the same epitope as, or competes for binding with, a reference anti-PCSK9 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-PCSK9 antibody of the invention, the reference antibody is allowed to bind to a PCSK9 protein or peptide under saturating conditions. Next, the ability of a test antibody to bind to the PCSK9 molecule is assessed. If the test antibody is able to bind to PCSK9 following saturation binding with the reference anti-PCSK9 antibody, it can be concluded that the test antibody binds to a different epitope than the reference anti-PCSK9 antibody. On the other hand, if the test antibody is not able to bind to the PCSK9 molecule following saturation binding with the reference anti-PCSK9 antibody, then the test antibody may bind to the same epitope as the epitope bound by the reference anti-PCSK9 antibody of the invention.

To determine if an antibody competes for binding with a reference anti-PCSK9 antibody, the above-described binding methodology is performed in two orientations: In a first orientation, the reference antibody is allowed to bind to a PCSK9 molecule under saturating conditions followed by assessment of binding of the test antibody to the PCSK9 molecule. In a second orientation, the test antibody is allowed to bind to a PCSK9 molecule under saturating conditions followed by assessment of binding of the reference antibody to the PCSK9 molecule. If, in both orientations, only the first (saturating) antibody is capable of binding to the PCSK9 molecule, then it is concluded that the test antibody and the reference antibody compete for binding to PCSK9. 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 identical epitope as the reference antibody, but may sterically block binding of the reference antibody by binding an overlapping or adjacent epitope.

Two antibodies bind to the same or overlapping epitope if each competitively inhibits (blocks) binding of the other to the antigen. That is, 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 have 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 have overlapping epitopes if some amino acid mutations that reduce or eliminate binding of one antibody reduce or eliminate binding of the other.

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, surface plasmon resonance, flow cytometry or any other quantitative or qualitative antibody-binding assay available in the art.

In a specific embodiment, the invention comprises an anti-PCSK9 antibody or antigen binding fragment of an antibody that binds an PCSK9 protein of SEQ ID NO:755, wherein the binding between the antibody or fragment thereof to PCSK9 and a variant PCSK9 protein is less than 50% of the binding between the antibody or fragment and the PCSK9 protein of SEQ ID NO:755. In one specific embodiment, the variant PCSK9 protein comprises at least one mutation of a residue at a position selected from the group consisting of 153, 159, 238 and 343. In a more specific embodiment, the at least one mutation is S153R, E159R, D238R, and/or D343R. In another specific embodiment, the variant PCSK9 protein comprises at least one mutation of a residue at a position selected from the group consisting of 366. In one specific

embodiment, the variant PCSK9 protein comprises at least one mutation of a residue at a position selected from the group consisting of 147, 366 and 380. In a more specific embodiment, the mutation is S147F, E366K and V380M.

5 Immunoconjugates

The invention encompasses a human anti-PCSK9 monoclonal antibody conjugated to a therapeutic moiety ("immunoconjugate"), such as a cytotoxin, a chemotherapeutic drug, an immunosuppressant or a radioisotope. Cytotoxin agents include any agent that is detrimental to cells. Examples of suitable cytotoxin agents and chemotherapeutic agents for forming immunoconjugates are known in the art, see for example, WO 05/103081.

15 Bispecifics

The antibodies of the present invention may be monospecific, bispecific, or multispecific. Multispecific mAbs 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. The human anti-PCSK9 mAbs 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 bispecific or a multispecific antibody with a second binding specificity.

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) CH3 domain and a second Ig CH3 domain, wherein the first and second Ig CH3 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 CH3 domain binds Protein A and the second Ig CH3 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 CH3 may further comprise a Y96F modification (by IMGT; Y436F by EU). Further modifications that may be found within the second CH3 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.

Bioequivalents

The anti-PCSK9 antibodies and antibody fragments of the present invention encompass proteins having amino acid sequences that vary from those of the described mAbs, but that retain the ability to bind human PCSK9. Such variant mAbs 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 mAbs. Likewise, the anti-PCSK9 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-PCSK9 antibody or antibody fragment that is essentially bioequivalent to an anti-PCSK9 antibody or antibody frag-

ment of the invention. Examples of such variant amino acid and DNA sequences are discussed above.

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

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.

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.

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.

Bioequivalent variants of anti-PCSK9 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.

Treatment Population

The invention provides therapeutic methods for treating a human patient in need of a composition of the invention. While modifications in lifestyle and conventional drug treatment are often successful in reducing cholesterol levels, not all patients are able to achieve the recommended target cholesterol levels with such approaches. Various conditions, such as familial hypercholesterolemia (FH), appear to be resistant to lowering of LDL-C levels in spite of aggressive use of conventional therapy. Homozygous and heterozygous familial hypercholesterolemia (hoFH, heFH) is a condition associated with premature atherosclerotic vascular disease. However, patients diagnosed with hoFH are largely unresponsive to conventional drug therapy and have limited treatment options. Specifically, treatment with statins, which reduce LDL-C by inhibiting cholesterol synthesis and upregulating the hepatic LDL receptor, may have little effect in patients

whose LDL receptors are non-existent or defective. A mean LDL-C reduction of only less than about 20% has been recently reported in patients with genotype-confirmed hoFH treated with the maximal dose of statins. The addition of ezetimibe 10 mg/day to this regimen resulted in a total reduction of LDL-C levels of 27%, which is still far from optimal. Likewise, many patients are statin non-responsive, poorly controlled with statin therapy, or cannot tolerate statin therapy; in general, these patients are unable to achieve cholesterol control with alternative treatments. There is a large unmet medical need for new treatments that can address the short-comings of current treatment options.

Specific populations treatable by the therapeutic methods of the invention include patients indicated for LDL apheresis, subjects with PCSK9-activating (GOF) mutations, heterozygous Familial Hypercholesterolemia (heFH); subjects with primary hypercholesterolemia who are statin intolerant or statin uncontrolled; and subjects at risk for developing hypercholesterolemia who may be preventably treated.

Therapeutic Administration and Formulations

The invention provides therapeutic compositions comprising the anti-PCSK9 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 LIPOFECTINTTM). 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.

The dose may vary depending upon the age and the size of a subject to be administered, target disease, conditions, route of administration, and the like. When the antibody of the present invention is used for treating various conditions and diseases associated with PCSK9, including hypercholesterolemia, disorders associated with LDL and apolipoprotein B, and lipid metabolism disorders, and the like, in an adult patient, it is 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.

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.

The pharmaceutical composition can be also delivered in a vesicle, in particular a liposome (see Langer (1990) *Science* 249:1527-1533; Treat et al. (1989) in *Liposomes in the Therapy of Infectious Disease and Cancer*, Lopez Berestein and Fidler (eds.), Liss, New York, pp. 353-365; Lopez-Berestein, *ibid.*, pp. 317-327; see generally *ibid.*).

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.), CRC Pres., Boca Raton, Fla. (1974). 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, in *Medical Applications of Controlled Release*, *supra*, vol. 2, pp. 115-138, 1984).

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. 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.

Numerous reusable pen and autoinjector delivery devices have applications in the subcutaneous delivery of a pharmaceutical composition of the present invention. Examples include, but certainly are not limited to AUTOPIENTM (Owen Mumford, Inc., Woodstock, UK), DISETRONIC™ pen (Disetronic Medical Systems, Burghdorf, Switzerland), HUMALOG MIX 75/25™ pen, HUMALOG™ pen, HUMALIN 70/30™ pen (Eli Lilly and Co., Indianapolis, Ind.), NOVOPEN™ I, II and III (Novo Nordisk, Copenhagen, Den-

mark), NOVOPEN JUNIOR™ (Novo Nordisk, Copenhagen, Denmark), BD™ pen (Becton Dickinson, Franklin Lakes, N.J.), 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 certainly are not limited to the SOLOSTAR™ pen (sanofi-aventis), the FLEXPENTM (Novo Nordisk), and the KWIKPENTM (Eli Lilly).

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.

The invention provides therapeutic methods in which the antibody or antibody fragment of the invention is useful to treat hypercholesterolemia associated with a variety of conditions involving hPCSK9. The anti-PCSK9 antibodies or antibody fragments of the invention are particularly useful for the treatment of hypercholesterolemia and the like. Combination therapies may include the anti-PCSK9 antibody of the invention with, for example, one or more of any agent that (1) induces a cellular depletion of cholesterol synthesis by inhibiting 3-hydroxy-3-methylglutaryl (HMG)-coenzyme A (CoA) reductase, such as cerivastatin, atorvastatin, simvastatin, pitavastatin, rosuvastatin, fluvastatin, lovastatin, pravastatin; (2) inhibits cholesterol uptake and or bile acid re-absorption; (3) increase lipoprotein catabolism (such as niacin); and activators of the LXR transcription factor that plays a role in cholesterol elimination such as 22-hydroxycholesterol or fixed combinations such as ezetimibe plus simvastatin; a statin with a bile resin (e.g., cholestyramine, colestipol, coleselvam), a fixed combination of niacin plus a statin (e.g., niacin with lovastatin); or with other lipid lowering agents such as omega-3-fatty acid ethyl esters (for example, omega-3).

EXAMPLES

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 but some experimental errors and deviations should be accounted for. Unless indicated otherwise, 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 PCSK9

VELOCIMMUNE™ mice were immunized with human PCSK9, and the antibody immune response monitored by antigen-specific immunoassay using serum obtained from these mice. Anti-hPCSK9 expressing B cells were harvested from the spleens of immunized mice shown to have elevated anti-hPCSK9 antibody titers were fused with mouse myeloma cells to form hybridomas. The hybridomas were

screened and selected to identify cell lines expressing hPCSK9-specific antibodies using assays as described below. The assays identified several cell lines that produced chimeric anti-hPCSK9 antibodies designated as H1M300, H1M504, H1M505, H1M500, H1M497, H1M498, H1M494, H1M309, H1M312, H1M499, H1M493, H1M496, H1M503, H1M502, H1M508, H1M495 and H1M492.

Human PCSK9-specific antibodies were also isolated directly from antigen-immunized B cells without fusion to myeloma cells, as described in U.S. 2007/0280945A1, hereby incorporated by reference in its entirety. Heavy and light chain variable regions were cloned to generate fully human anti-hPCSK9 antibodies designated as H1H313, H1H314, H1H315, H1H316, H1H317, H1H318, H1H320, H1H321 and H1H334. Stable recombinant antibody-expressing CHO cell lines expressing these antibodies were established.

Example 2

Gene Utilization Analysis

To analyze the structure of the mAbs produced, the nucleic acids encoding antibody variable regions were cloned and sequenced. The predicted amino acid sequences of the variable regions were confirmed by N-terminal amino acid sequencing. From the nucleic acid sequence and predicted amino acid sequence of the mAbs, gene usage was identified for each antibody chain.

TABLE 1

Antibody	Heavy Chain Variable Region		Light Chain Variable Region		35
	VH	D	JH	VK	
H313	3-13	1-26	4	3-15	3
H1H314	3-33	3-3	4	1-5	2
H1H315	3-33	3-3	4	4-1	1
H1H316	3-23	7-27	2	4-1	2
H1H317	3-13	1-26	4	1-6	1
H1H318	4-59	3-10	6	1-9	1
H1H320	1-18	2-2	6	2-30	1
H1H321	2-5	1-7	6	2-28	4
H1H334	2-5	6-6	6	2-28	4
H1M300	3-7	2-8	6	2-28	4
H1M504	3-30	2-8	6	2-28	4
H1M505	3-30	2-8	6	2-28	4
H1M500	2-5	5-5	6	2-28	4
H1M497	1-18	2-2	6	2-30	2
H1M498	3-21	2-2	4	1-5	2
H1M494	3-11	5-12	6	3-20	4
H1M309	3-21	6-13	4	1-5	1
H1M312	3-21	6-13	4	1-5	1
H1M499	3-21	6-13	4	1-5	1
H1M493	3-21	6-13	4	1-5	1
H1M496	3-13	6-19	4	3-15	3
H1M503	1-18	2-2	6	2-28	1
H1M502	3-13	6-13	4	3-15	3
H1M508	3-13	6-13	4	3-15	3
H1M495	3-9	4-17	6	1-9	3
H1M492	3-23	3-3	2	3-20	4

Example 3

Antigen Binding Affinity Determination

Equilibrium dissociation constants (K_D) for hPCSK9 binding to mAbs generated by hybridoma cell lines described above were determined by surface kinetics in a real-time biosensor surface plasmon resonance assay (BIACORE™

T100). Each antibody was captured at a flow rate of 4 μ l/min for 90 sec on a goat anti-mouse IgG polyclonal antibody surface created through direct chemical coupling to a BIACORE™ chip to form a captured antibody surface. Human PCSK9-myc-myc-his (hPCSK9-mmh) at a concentration of 50 nM or 12.5 nM was injected over the captured antibody surfaces at a flowrate of 50 μ l/min for 300 sec, and antigen-antibody dissociation was monitored for 15 min at either 25° C. or 37° C. (K_D =pM; $T_{1/2}$ =min).

TABLE 2

Antibody	25° C.		37° C.	
	K_D	$T_{1/2}$	K_D	$T_{1/2}$
H1M300	399	170	1510	32
H1M309	29.9	7461	537	326
H1M312	0.225	15568	432	392
H1M493	46.5	4921	522	341
H1M494	870	114	2350	30
H1M495	440	222	7500	19
H1M496	254	257	421	118
H1M497	20.1	5801	480	290
H1M498	6400	30	7500	14
H1M499	106	2253	582	316
H1M500	1400	91	6010	15
H1M502	78.3	958	411	151
H1M503	510	118	1880	30
H1M504	3470	35	11200	6
H1M505	2740	42	9200	6
H1M508	138	572	442	139
H1M510	1070	68	3960	10

Equilibrium dissociation constants (K_D) for hPCSK9 binding to mAbs generated via direct isolation of splenocytes were determined by surface kinetics in a real-time biosensor surface plasmon resonance assay (BIACORE™ T100). Each selected antibody was captured at a flowrate of 2 μ l/min for 6 min on a goat anti-human IgG polyclonal antibody surface created through direct chemical coupling to a BIACORE™ chip to form a captured antibody surface. Human PCSK9-mmh at a concentration of 50 nM or 12.5 nM was injected over the captured antibody surface at a flowrate of 70 μ l/min for 5 min, and antigen-antibody dissociation was monitored for 15 min at either 25° C. or 37° C. (K_D =pM; $T_{1/2}$ =min).

TABLE 3

Antibody	25° C.		37° C.	
	K_D	$T_{1/2}$	K_D	$T_{1/2}$
H1H313P	244	230	780	60
H1H314P	3990	65	3560	43
H1H315P	129	151	413	35
H1H316P	377	42	1080	11
H1H317P	30400	137	18600	70
H1H318P	972	59	1690	28
H1H320P	771	28	1930	8
H1H321P	865	106	3360	23
H1H334P	3750	46	15900	8

Dissociation rate (kd) of selected mAbs for tagged rhesus monkey (*Macaca mulata*) PCSK9 (mmPCSK9; SEQ ID NO:756) (mmPCSK9-mmh) at 25° C. was determined as described above.

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TABLE 4

Antibody	kd (1/s)	T _{1/2} (min)
H1H313P	2.92 × 10 ⁻⁵	396
H1H318P	3.69 × 10 ⁻³	3
H1H334P	8.06 × 10 ⁻³	1
H1H315P	2.29 × 10 ⁻⁴	51
H1H316P	2.29 × 10 ⁻⁴	51
H1H320P	3.17 × 10 ⁻⁴	36
H1M300	1.52 × 10 ⁻⁴	76
H1M504	5.04 × 10 ⁻⁴	23
H1M497	6.60 × 10 ⁻⁵	175
H1M503	8.73 × 10 ⁻⁵	132
H1M496	4.45 × 10 ⁻⁵	260

Example 4

Effect of pH on Antigen Binding Affinity

The effects of pH on antigen binding affinity for CHO cell-produced fully human anti-hPCSK9 mAbs was assessed as described above. The mAbs tested are fully human versions of H1H316P ("316P") (HCVR/LCVR SEQ ID NO: 90/92; CDR sequences SEQ ID NO: 76/78/80 and 84/86/88) and H1M300N ("300N") (HCVR/LCVR SEQ ID NO: 218/226; CDR sequences SEQ ID NO:220/222/224 and 228/230/232). Human PCSK9-myc-myc-his (hPCSK9-mmh) was captured on an anti-myc mAb surface either at a high density (about 35 to 45 resonance units) (RU) or at a low density (about 5 to 14 RU). Each antibody, at 50 nM in HBST (pH 7.4 or pH 5.5) was injected over the captured hPCSK9 surface at a flow rate of 100 µl/ml for 1.5 min at 25° C. and antigen-antibody dissociation was monitored for 10 min. Control I: anti-hPCSK9 mAb SEQ ID NO:79/101 (WO 2008/063382) (K_D=pM; T_{1/2}=min).

TABLE 5

Antibody	High hPCSK9 Density Surface				Low hPCSK9 Density Surface			
	pH 7.4		pH 5.5		pH 7.4		pH 5.5	
	K _D	T _{1/2}	K _D	T _{1/2}	K _D	T _{1/2}	K _D	T _{1/2}
316P	191	74	144	83	339	45	188	58
300N	65	507	1180	26	310	119	1380	13
Control I	20000	29	ND	ND	ND	ND	ND	ND

The antigen binding properties of 316P and 300N at pH 7.4 or pH 5.5 were determined by a modified BIACORE™ assay as described above. Briefly, mAbs were immobilized onto BIACORE™CM5 sensor chips via amine coupling. Varying concentrations of myc-myc-his tagged hPCSK9, mouse PCSK9 (mPCSK9, SEQ ID NO:757), hPCSK9 with a gain of function (GOF) point mutation of D374Y (hPCSK9(D374Y), cynomolgus monkey (*Macaca fascicularis*) PCSK9 (mf-PCSK9, SEQ ID NO:761) (mfPCSK9), rat (*Rattus norvegicus*) PCSK9 (rPCSK9, SEQ ID NO:763), and his-tagged Syrian golden hamster (*Mesocricetus auratus*) PCSK9 (maPCSK9, SEQ ID NO:762) (maPCSK9), ranging from 11 to 100 nM, were injected over the antibody surface at the flow rate of 100 µl/ml for 1.5 min and antigen-antibody dissociation was monitored in real time for 5 min at either 25° C. (Table 6) or 37° C. (Table 7). Control II: anti-hPCSK9 mAbs SEQ ID NO:67/12 (WO 2009/026558) (NB: no binding was observed under the experimental condition) (K_D=pM; T_{1/2}=min).

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TABLE 6

Antigen	pH Effect at 25° C.			
	pH 7.4		pH 5.5	
	K _D	T _{1/2}	K _D	T _{1/2}
316P				
hPCSK9-mmh	1260	36	22	39
mPCSK9-mmh	4460	10	63	11
hPCSK9(D347Y)-mmh	2490	15	166	13
mfPCSK9-mmh	1420	42	8	23
maPCSK9-h	8350	8	87	8
rPCSK9-mmh	24100	2	349	5
300N				
hPCSK9-mmh	1100	76	3100	5
mPCSK9-mmh	NB	NB	NB	NB
hPCSK9(D347Y)-mmh	1310	46	9030	3
mfPCSK9-mmh	2170	31	38500	0.4
maPCSK9-h	NB	NB	NB	NB
rPCSK9-mmh	NB	NB	NB	NB
Control I				
hPCSK9-mmh	33100	14	1740	31
mPCSK9-mmh	NB	NB	NB	NB
hPCSK9(D347Y)-mmh	71000	11	7320	30
mfPCSK9-mmh	362000	0.2	67200	3
maPCSK9-h	NB	NB	NB	NB
rPCSK9-mmh	NB	NB	NB	NB
Control II				
hPCSK9-mmh	143	266	2	212
mPCSK9-mmh	3500	11	33	12
hPCSK9(D347Y)-mmh	191	155	49	56
mfPCSK9-mmh	102	262	12	63
maPCSK9-h	6500	3	ND	ND
rPCSK9-mmh	22400	2	106	5

TABLE 7

Antigen	pH Effect at 37° C.			
	pH 7.4		pH 5.5	
	K _D	T _{1/2}	K _D	T _{1/2}
316P				
hPCSK9-mmh	4000	9	142	11
mPCSK9-mmh	12200	3	13600	3
hPCSK9(D347Y)-mmh	6660	4	1560	5
mfPCSK9-mmh	3770	11	44	5
maPCSK9-h	21700	2	ND	ND
rPCSK9-mmh	55100	2	399	1
300N				
hPCSK9-mmh	2470	20	11900	1
mPCSK9-mmh	NB	NB	NB	NB
hPCSK9(D347Y)-mmh	2610	14	28000	1
mfPCSK9-mmh	4810	8	65200	0.1
maPCSK9-h	NB	NB	NB	NB
rPCSK9-mmh	NB	NB	NB	NB
Control I				
hPCSK9-mmh	45900	0.1	11300	3
mPCSK9-mmh	NB	NB	NB	NB
hPCSK9(D347Y)-mmh	169000	0.4	27000	3
mfPCSK9-mmh	500000	0.6	5360	0.3
maPCSK9-h	NB	NB	NB	NB
rPCSK9	NB	NB	NB	NB
Control II				
hPCSK9-mmh	284	87	20	44
mPCSK9-mmh	8680	3	89	3
hPCSK9(D347Y)-mmh	251	57	483	26
mfPCSK9-mmh	180	127	214	65

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TABLE 7-continued

pH Effect at 37° C.			
pH 7.4		pH 5.5	
K _D	T _{1/2}	K _D	T _{1/2}
maPCSK9-h	8830	0.5	ND
rPCSK9p-mmh	30200	1	233
			1

Example 5

Anti-hPCSK9 mAbs Binding to hPCSK9 with Point Mutation D374Y

The binding affinity of selected anti-hPCSK9 mAbs to hPCSK9 with a gain of function (GOF) point mutation of D374Y (hPCSK9(D374Y)-mmh) was determined as described above. Each antibody was captured at a flowrate of 40 μ l/min for 8-30 sec on a goat anti-human IgG polyclonal antibody surface created through direct chemical coupling to a BIACORE™ chip to form a captured antibody surface. hPCSK9(D374Y)-mmh at varying concentrations of 1.78 nM to 100 nM was injected over the captured antibody surface at a flowrate of 50 μ l/min for 5 min, and the dissociation of hPCSK9(D374Y)-mmh and antibody was monitored for 15 min at 25° C. Control III: anti-hPCSK9 mAbs SEQ ID NO:49/23 (WO 2009/026558) (K_D=pM; T_{1/2}=min).

TABLE 8

Antibody	K _D	T _{1/2}
316P	1780	14
300N	1060	49
Control I	23600	25
Control II	66	216
Control III	1020	126

Example 6

Binding Specificity of Anti-hPCSK9 mAbs

316P, 300N, and Control I anti-hPCSK9 mAbs were captured on an amine-coupled anti-hFc CM5 chip on BIACORE™2000. Tagged (myc-myc-his) human PCSK9, human PCSK1 (hPCSK1) (SEQ ID NO:759), human PCSK7 (hPCSK7) (SEQ ID NO:760), or mouse PCSK9 were injected (100 nM) over the captured mAb surface and allowed to bind at 25° C. for 5 min. Changes in RU were recorded. Results: 300N and Control I bound only to hPCSK9, and 316P bound both hPCSK9 and mPCSK9.

The binding specificities of anti-hPCSK9 mAbs were determined by ELISA. Briefly, anti-hPCSK9 antibody was coated on a 96-well plate. Human PCSK9-mmh, mPCSK9-mmh, maPCSK9-h, hPCSK1-mmh, or hPCSK7-mmh, at 1.2 nM, were added to antibody-coated plates and incubated at RT for 1 hr. Plate-bound PCSK protein was then detected by HRP-conjugated anti-His antibody. Results show that 316P binds human, mouse, and hamster PCSK9, whereas 300N and Control I only bound hPCSK9. None of the anti-hPCSK9 mAbs exhibited significant binding to hPCSK1 or hPCSK7.

Example 7

Cross-Reactivity of Anti-hPCSK9 mAbs

Cross-reactivity of anti-hPCSK9 mAbs with mmPCSK9, mfPCSK9, mPCSK9, maPCSK9, or rPCSK9 was determined

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using BIACORE™3000. Briefly, anti-hPCSK9 mAbs were captured on an anti-hFc surface created through direct chemical coupling to a BIACORE™ chip. Purified tagged hPCSK9, hPCSK9(D374Y), mmPCSK9, mfPCSK9, mPCSK9, maPCSK9, or rPCSK9, each at 1.56 nM to 50 nM, was injected over the antibody surface at either 25° C. or 37° C. Binding between 316P, 300N, Control I, Control II, or Control III and the PCSK9 proteins was determined (K_D=pM; T_{1/2}=min) (ND=not determined).

TABLE 9

Antigen	316P mAb	
	37° C.	25° C.
hPCSK9-mmh	1800	9
hPCSK9(D374Y)-mmh	4200	4
mmPCSK9-mmh	1800	21
mfPCSK9-mmh	1800	11
mPCSK9-mmh	4700	3
maPCSK9-h	19000	1
rPCSK9-mmh	37500	1

TABLE 10

Antigen	300N mAb	
	37° C.	25° C.
hPCSK9-mmh	2400	22
hPCSK9(D374Y)-mmh	2200	14
mmPCSK9-mmh	1600	26
mfPCSK9-mmh	3800	11
mPCSK9-mmh	NB	NB
maPCSK9-h	NB	NB
rPCSK9-mmh	NB	NB

TABLE 11

Antigen	Control I mAb	
	37° C.	25° C.
hPCSK9-mmh	226000	2
hPCSK9(D374Y)-mmh	ND	ND
mmPCSK9-mmh	420000	3
mfPCSK9-mmh	14300	10
mPCSK9-mmh	NB	NB
maPCSK9-h	NB	NB
rPCSK9-mmh	NB	NB

TABLE 12

Antigen	Control II mAb	
	37° C.	25° C.
hPCSK9-mmh	91	162
hPCSK9(D374Y)-mmh	93	90
mfPCSK9-mmh	33	252
mPCSK9-mmh	4700	3
maPCSK9-h	60800	0.4
rPCSK9-mmh	14100	1

TABLE 13

Antigen	37° C.		25° C.	
	K _D	T _{1/2}	K _D	T _{1/2}
hPCSK9-mmh	380	378	490	450
hPCSK9(D374Y)-mmh	130	660	1000	126
mfPCSK9-mmh	110	750	340	396
mPCSK9-mmh	33500	1	10900	4
maPCSK9-h	780	107	2100	67
rPCSK9-mmh	NB	NB	33200	2

pre-mixed with varied amounts of antibody, ranging from 0 to ~50 nM in serial dilutions, followed by 1 hr incubation at room temperature (RT) to allow antibody-antigen binding to reach equilibrium. The equilibrated sample solutions were transferred to receptor or receptor fragment coated plates. After 1 hour of binding, the plates were washed and bound hPCSK9-mmh detected using HRP conjugated anti-myc antibody. IC₅₀ values (in pM) were determined as the amount of antibody required to achieve 50% reduction of hPCSK9-mmh bound to the plate-coated receptor or receptor fragment. The results show that specific mAbs functionally block PCSK9 from binding the three receptors at both neutral pH (7.2) and acidic pH (5.5).

TABLE 14

Ab	pH 7.2			pH 5.5		
	Plate Coating Surface					
hLDLR-ecto	hLDLR-ecto	EGF-A	EGF-AB	hLDLR-ecto	EGF-A	EGF-AB
316P	<125	<125	<125	<125	<125	<125
300N	144	146	<125	1492	538	447
Control I	—	>100,000	>100,000	—	>100,000	>100,000
Control II	288	510	274	411	528	508
Control III	303	635	391	742	787	1073

Example 8

Inhibition of Binding Between hPCSK9 and hLDLR Domains

The ability of selected anti-hPCSK9 mAbs to block hPCSK9 binding to human LDLR full length extracellular domain (hLDLR-ecto SEQ ID NO:758), hLDLR EGF-A domain (amino acids 313-355 of SEQ ID NO:758), or hLDLR EGF-AB domains (amino acids of 314-393 of SEQ ID NO:758) (LDLR Genbank number NM_000527) was evaluated using BIACORE™ 3000. Briefly, hLDLR-ecto, EGF-A-hFc, or EGF-AB-hFc protein was amine-coupled on a CM5 chip to create a receptor or receptor fragment surface. Selected anti-hPCSK9 mAbs, at 62.5 nM (2.5 fold excess over antigen), were premixed with 25 nM of hPCSK9-mmh, followed by 40 min incubation at 25° C. to allow antibody-antigen binding to reach equilibrium to form equilibrated solutions. The equilibrated solutions were injected over the receptor or receptor fragment surfaces at 2 µl/min for 40 min at 25° C. Changes in RU due to the binding of the anti-hPCSK9 mAbs to hLDLR-ecto, EGF-A-hFc, or EGF-AB-hFc were determined. Results show that H1H316P and H1M300N blocked the binding of hPCSK9-mmh to hLDLR-ecto, hLDLR EGF-A domain, and hLDLR EGF-AB domains; H1H320P blocked the binding of hPCSK9-mmh to hLDLR-ecto and hLDLR EGF-A domain; and H1H321P blocked the binding of hPCSK9-mmh to hLDLR EGF-A domain.

The ability of the mAbs to block hPCSK9 binding to hLDLR-ecto, hLDLR EGF-A domain, or hLDLR EGF-AB domains was also evaluated with an ELISA-based immunoassay. Briefly, hLDLR-ecto, hLDLR EGF-A-hFc or hLDLR EGF-AB-hFc, each at 2 µg/ml, was coated on a 96-well plate in PBS buffer overnight at 4° C., and nonspecific binding sites blocked with BSA. This plate was used to measure free hPCSK9-mmh in a PCSK9-mmh solution pre-equilibrated with varying concentrations of anti-hPCSK9 mAbs. A constant amount of hPCSK9-mmh (500 pM) was

30
35
40
45
50

h
hPCSK9(D374Y)-mmh binding to hLDLR EGF-A domain or hLDLR EGF-AB domain (IC₅₀ values in pM) was also evaluated with the ELISA-based immunoassay described above using a constant amount of 0.05 nM hPCSK9(D374Y)-mmh.

TABLE 15

	pH 7.2		pH 5.5	
	Plate Coating Surface			
EGF-A	EGF-AB	EGF-A	EGF-AB	
316P	203	139	1123	1139
300N	135	142	3463	3935
Control I	>100,000	>100,000	>100,000	>100,000
Control II	72	57	129	118
Control III	537	427	803	692

45
50

The ability of the mAbs to block either mmPCSK9 or mPCSK9 binding to hLDLR-ecto domain, hLDLR EGF-A domain, or hLDLR EGF-AB domain (IC₅₀ values in pM) was evaluated at neutral pH (7.2) with the ELISA-based immunoassay described above using a constant amount of 1 nM of mmPCSK9 or 1 nM of mPCSK9.

TABLE 16

	1 nM mmPCSK9-mmh		1 nM mPCSK9-mmh	
	hLDLR-ecto	EGF-A	EGF-AB	EGF-A
316P	<250	<250	<250	<250
300N	255	256	290	>33000

60
65

The ability of the mAbs to block hPCSK9, mmPCSK9, rPCSK9, maPCSK9, mfPCSK9, or mPCSK9 binding to hLDLR EGF-A domain (IC₅₀ values in pM) was evaluated at neutral pH (7.2) (Table 17) acidic pH (5.5, Table 18) with the ELISA-based immunoassay described above using a constant amount of 0.5 nM of hPCSK9-mmh, 1 nM of mmPCSK9-mmh, 1 nM of rPCSK9-mmh, 1 nM of maPCSK9-h, 0.3 nM of mfPCSK9-mmh, or 1 nM of mPCSK9-mmh.

TABLE 17

	hPCSK9	mmPCSK9	rPCSK9	maPCSK9	mfPCSK9	mPCSK9
316P	<125	<250	2662	349	75	305
300N	182	460	>100000	>100000	473	>100000
Control I	—	>100000	>100000	>100000	>100000	>100000
Control II	146	83	2572	2038	361	855
Control III	249	293	>100000	245	572	>100000

TABLE 18

	hPCSK9	mmPCSK9	rPCSK9	maPCSK9	mPCSK9
316P	<125	<250	42880	1299	991
300N	223	3704	>100000	>100000	>100000
Control I	>10000	>100000	>100000	>100000	>100000
Control II	154	<250	11640	8339	2826
Control III	390	376	>100000	414	>100000

The ability of 316P and Control I to block hPCSK9 binding to hLDLR was also determined. Briefly, either recombinant hLDLR or hLDLR-EGFA-mFc was immobilized onto BIA-CORE™ CM5 chips via amine coupling. An antigen-antibody mixture of 100 nM hPCSK9-mmh and 316P, Control I mAb, or a non-hPCSK9 specific mAb (each at 250 nM) was incubated at RT for 1 hr, and then injected over the hLDLR or hLDLR-EGFA surface at the flow rate of 10 µl/ml for 15 min at 25° C. Changes in RU due to the binding between the free hPCSK9-mmh in the mixture to either hLDLR or hLDLR-EGFA were recorded. The binding of hPCSK9 to either hLDLR or hLDLR-EGFA was completely blocked by 316P and 300N but not by Control I mAb.

Example 9

Epitope Mapping

In order to determine epitope-binding specificity, three chimeric PCSK9-mmh proteins were generated in which specific human PCSK9 domains were substituted with mouse PCSK9 domains. Chimeric protein #1 consists of a mouse PCSK9 pro-domain (amino acid residues 1-155 of SEC ID NO:757) followed by a human PCSK9 catalytic domain (residues 153-425 of SEQ ID NO:755) and a mouse PCSK9 C-terminal domain (residues 429-694 SEQ ID NO:757) (mPro-hCat-mC-term-mmh). Chimeric protein #2 consists of a human PCSK9 pro-domain (residues 1-152 of SEQ ID NO:755) followed by a mouse PCSK9 catalytic domain (residues 156-428 of SEQ ID NO:757) and a mouse PCSK9 C-terminal (hPro-mCat-mC-term-mmh). Chimeric protein #3 consists of mouse PCSK9 pro-domain and a mouse PCSK9 catalytic domain followed by a human PCSK9 C-terminal domain (residues 426-692 of SEQ ID NO:755) (mPro-mCat-hC-term-mmh). In addition, hPCSK9 with a point mutation of D374Y (hPCSK9 (D374Y)-mmh) was generated.

Binding specificity of mAbs to test proteins hPCSK9-mmh, mouse PCSK9-mmh, chimeric proteins #1, #2, and #3, and hPCSK9 (D374Y)-mmh were tested as follows: the mAbs were coated on a 96-well plate overnight at 4° C., then each test protein (1.2 nM) was added to the plate. After 1 hr binding at RT, the plate was washed and bound test protein detected using HRP-conjugated anti-myc polyclonal antibody (++=OD>1.0; +=OD 0.4 -1.0; -=OD<0.4).

TABLE 19

Antibody	hPCSK9	mPCSK9	Chimeric Protein				hPCSK9(D374Y)
			#1	#2	#3		
H1M300	++	-	++	+	-	++	
H1M309	++	-	-	-	++	++	
H1M312	++	-	-	-	++	++	
H1M492	++	-	-	-	-	+	
H1M493	++	-	-	-	++	++	
H1M494	++	-	-	+	++	++	
H1M495	++	-	-	-	++	++	
H1M496	++	-	-	-	++	++	
H1M497	++	-	-	++	+	++	
H1M498	++	-	-	-	+	++	
H1M499	++	-	-	-	++	++	
H1M500	++	-	++	-	-	++	
H1M502	++	-	-	-	++	++	
H1M503	++	-	-	++	-	++	
H1M504	++	-	-	-	-	+	
H1M505	++	-	++	+	-	++	
H1M508	++	-	-	-	++	++	
H1H318P	++	-	++	-	-	++	
H1H334P	++	-	++	-	-	++	
H1H316P	++	++	++	++	++	++	
H1H320P	++	-	-	++	-	++	
Control I	++	-	-	-	++	++	

Binding specificity of 316P, 300N and control anti-hPCSK9 mAbs to hPCSK9-mmh, mPCSK9-mmh, mmPCSK9-mmh, mfPCSK9-mmh, rPCSK9-mmh, chimeric proteins #1, #2, and #3, and hPCSK9 (D374Y)-mmh were tested as described above except that the protein concentration is 1.7 nM (=OD<0.7; +=OD 0.7-1.5; ++=OD>1.5).

TABLE 20

	316P	300N	Control I	Control II	Control III
hPCSK9-mmh	++	++	++	++	++
mPCSK9-mmh	++	-	-	++	++
mmPCSK9-mmh	++	++	++	++	++
mfPCSK9-mmh	++	++	++	++	++
rPCSK9-mmh	++	-	-	++	+
Chimeric Protein #1	++	++	-	++	++
Chimeric Protein #2	++	++	-	++	++
Chimeric Protein #3	++	+	++	++	++
hPCSK9(D374Y)	++	++	++	++	++

Similar results for selected mAbs were obtained by BIA-CORE™ binding assay. Briefly, 316P, 300N, or Control I mAb was captured on an amine-coupled anti-hFc CM5 chip and 100 nM of each protein injected over the mAb-captured surface. Changes in RU due to the binding of each protein to the mAb surface was determined.

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TABLE 21

Antibody	Chimeric Protein				
	hPCSK9	mPCSK9	#1	#2	#3
316P	500	505	529	451	467
300N	320	13	243	76	10
Control I	65	7	4	3	69

To further assess the binding specificity of 316P, which cross-reacts with mPCSK9-mmhh, a cross-competition ELISA assay was developed to determine binding domain specificity. Briefly, mAbs specific for chimeric protein #1, #2, or #3, were first coated on a 96-well plate overnight at 1 µg/ml. Human PCSK9-mmhh (2 µg/l) was then added to each well followed by 1 hr incubation at RT. 316P (1 µg/ml) was added and incubated for another hour at RT. Plate-bound 316P was detected using HRP-conjugated anti-hFc polyclonal antibody. Although 316P binding to hPCSK9-mmhh was not affected by the presence of mAbs specific for either chimeric protein #2 or chimeric protein #3, 316P binding to hPCSK9-mmhh was greatly reduced by the presence of antibody specific for chimeric protein #1.

Example 10

BIACORE™-Based Antigen Binding Profile Assessment

Antibody binding profiles were also established for 316P, 300N, Control I, II, and III mAbs using BIACORE™1000. Briefly, hPCSK9-mmhh was captured on an anti-myc surface. A first anti-hPCSK9 mAb (50 µg/ml) was injected over the PCSK9-bound surface for 10 min, at a flow rate of 10 µl/min at 25° C. A second anti-hPCSK9 mAb (50 µg/ml) was then injected over the first mAb-bound surface for 10 min, at a flow rate of 10 µl/min at 25° C. Ability of the first mAb to block binding of the second mAb was measured and is expressed as percent inhibition.

TABLE 22

First mAb	Second mAb				
	316P	300N	Control I	Control II	Control III
316P	100	101	27	99	101
300N	77	100	12	82	-2
Control I	6	12	100	6	9
Control II	91	102	-6	100	3
Control III	73	10	-12	1	100

Example 11

Increase of LDL Uptake by Anti-hPCSK9 Antibodies

The ability of anti-hPCSK9 mAbs to increase LDL uptake in vitro was determined using a human hepatocellular liver carcinoma cell line (HepG2). HepG2 cells were seeded onto 96-well plates at 9×10⁴ cells/well in DMEM complete media and incubated at 37° C., 5% CO₂, for 6 hr to form HepG2 monolayers. Human PCSK9-mmhh, at 50 nM in lipoprotein deficient medium (LPDS), and a test mAb was added in various concentrations from 500 nM to 0.98 nM in LPDS medium. Data are expressed as IC₅₀ values for each experiment (IC₅₀=antibody concentration at which increases LDL

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uptake by 50%). In addition, the experiment also showed that both 316P and 300N were able to completely reverse the inhibitory effect of hPCSK9 on LDL uptake, while Control I mAb or H1M508 anti-hPCSK9 mAb reversed the inhibitory effect by about 50%.

TABLE 23

Antibody	IC ₅₀ (nM)
316P	21.30
300N	22.12
Control I	>250
H1M508	>250

15 The ability of anti-hPCSK9 mAbs to reverse the inhibitory effect on LDL uptake by PCSK9 protein from different mammalian species was also tested in a HepG2 cell line as described above. Briefly, HepG2 cells were incubated overnight with serial dilutions of antibody in LPDS medium (beginning with 500 nM) and 50 nM of hPCSK9-mmhh, mfPCSK9-mmhh, mPCSK9-mmhh, rPCSK9-mmhh, or maPCSK9-h. HepG2 cells were also incubated overnight with serial dilutions of antibody in LPDS (beginning with 50 nM) and 1 nM hPCSK9(D374Y). As shown in Table 24, while 20 316P was able to completely reverse the inhibitory effect on LDL by all PCSK9 proteins tested, 300N was only able to reverse the inhibitory effect on LDL uptake by hPCSK9, hPCSK9 (D374Y), and mfPCSK9. Values are expressed as nM IC₅₀.

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30 316P was able to completely reverse the inhibitory effect on LDL by all PCSK9 proteins tested, 300N was only able to reverse the inhibitory effect on LDL uptake by hPCSK9, hPCSK9 (D374Y), and mfPCSK9. Values are expressed as nM IC₅₀.

TABLE 24

	316P	300N	Control I	Control II	Control III
hPCSK9-mmhh	14.1	12.6	>500	13.4	12.4
hPCSK9(D374Y)-mmhh	2.1	1.1	>50	0.7	0.6
mfPCSK9-mmhh	14.7	13.4	>500	14.2	13.6
mPCSK9-mmhh	21.2	>500	>500	19	>500
rPCSK9-mmhh	27.7	>500	>500	21.9	>500
maPCSK9-h	14.4	>500	>500	29.5	12.7

Example 12

Neutralization of Biological Effect of hPCSK9 In Vivo

45 To assess the biological effect of neutralizing PCSK9, hPCSK9 was over-expressed in C57BL/6 mice by hydrodynamic delivery (HDD) of DNA constructs encoding full-length hPCSK9-mmhh. 4 mice (C57BL/6) were injected with empty vector/saline (control), and 16 mice were injected with a 50 µg hPCSK9-mmhh-DNA/saline mixture in the tail vein equal to 10% of their body weight. At day 7 after HDD, delivery of hPCSK9 resulted in a 1.6-fold elevation of total cholesterol, 3.4-fold elevation in LDL-cholesterol (LDL-C) and a 1.9-fold elevation in non-HDL cholesterol (relative to control). Serum hPCSK9 levels on day 7 were all greater than 1 µg/ml, as assessed by quantitative ELISA.

60 Administration of H1M300N on day 6 after HDD to 3 experimental groups (1, 5 or 10 mg/kg) (n=4 per group) via intraperitoneal (i.p.) injection resulted in a significant attenuation of serum cholesterol levels. At 18 hours after administration, total cholesterol was reduced by 9.8%, 26.3% and 26.8%, LDL-C was reduced by 5.1%, 52.3% and 56.7%, and non-HDL cholesterol was reduced by 7.4%, 33.8% and 28.6% in the 1, 5 or 10 mg/kg H1M300N treated groups, respectively.

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Example 13

Pharmacokinetic and Serum Chemistry Study in
Monkeys

A pharmacokinetic (PK) study was conducted in naïve male cynomolgus monkeys (*Macaca fascicularis*) with a body weight range between 5-7 kg and aged between 3-5 years.

Group assignments. The monkeys were assigned into 5 treatment groups: Treatment Group 1 (n=3) received control buffer (10 mM sodium phosphate, pH 6, 1 ml/kg); Treatment Group 2 (n=3) received 1 ml/kg of 316P (5 mg/ml); Treatment Group 3 (n=3) received 1 ml/kg 300N (5 mg/ml); Treatment Group 4 (n=3) received 1 ml/kg 316P (15 mg/ml); and Treatment Group 5 (n=3) received 1 ml/kg 300N (15 mg/ml). All treatments were administered by IV bolus followed by a 1 ml saline flush. Total dose volume (ml) was calculated on the most recent body weight (each animal was weighed twice during acclimation and once weekly throughout the study). A single dose of test mAb or buffer control was administered on Day 1.

Animal care. Animals were housed in a temperature- and humidity-monitored environment. The targeted range of temperature and relative humidity was between 18-29° C. and 30-70%, respectively. An automatic lighting system provided a 12-hour diurnal cycle. The dark cycle could be interrupted for study- or facility-related activities. The animals were individually housed in cages that comply with the Animal Welfare Act and recommendations set forth in The Guide for the Care and Use of Laboratory Animals (National Research Council 1996).

Diet and Feeding. Animals were fed twice per day according to SNBL USA SOPs. Animals were fasted when required by specific procedures (e.g., prior to blood draws for serum chemistry, urine collection, or when procedures involving sedation are performed). The diet was routinely analyzed for contaminants and found to be within manufacturer's specifications. No contaminants were expected to be present at levels that would interfere with the outcome of the study.

Experimental Design. An appropriate number of animals were selected from SNBL USA stock. Animals were examined for health by veterinary staff, and had undergone serum chemistry, hematology, and coagulation screening. Sixteen males, confirmed healthy, were assigned to the study. Fifteen males were assigned to specific study groups and the remaining animal was available as a spare. A stratified randomization scheme incorporating serum cholesterol level (based on the average of two draws in acclimation) was used to assign animals to study groups.

Acclimation Period. Previously quarantined animals were acclimated to the study room for a minimum of 14 days prior to initiation of dosing. Acclimation phase data was collected from all animals, including the spare. All animals were assessed for behavioral abnormalities that could affect performance on study. The spare animal was returned to stock after day 1.

Blood collection. Blood was collected by venipuncture from a peripheral vein from restrained, conscious animals. Whenever possible, blood was collected via a single draw and then divided appropriately.

PK Study. Blood samples (1.5 ml) were collected at pre-dose, 2 min, 15, min, 30 min, 1 hr, 2 hr, 4 hr, 8 hr, 12 hr, 24 hr,

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and subsequently once every 24 hr in serum separator tubes (SST). Specimen storage serum is transferred to 2 vials and stored at -60° C. or below.

Serum samples were analyzed using an optimized ELISA (enzyme-linked immunosorbent assay) procedure. Briefly, a microtiter plate was first coated with hPCSK9-mmh. Test mAb 316P or 300N was then captured on the hPCSK9-mmh plate. The captured 316P or 300N was detected using a biotinylated mouse anti-hlgG4 followed by binding to NeutrAvidin-HRP. Varying concentrations of 316P or 300N, ranging from 100 to 1.56 ng/ml, were used as standards. One percent monkey serum (assay matrix) in the absence of 316P or 300N was used as the zero (0 ng/ml) standard. The results, shown in FIG. 2, indicate a dose-dependent increase in serum 316P and 300N levels. PK parameters were analyzed using WinNonlin software (Noncompartmental analysis, Model 201-IV bolus administration).

TABLE 25

PK Parameter	316P		300N	
	5 mg/kg	15 mg/kg	5 mg/kg	15 mg/kg
T _{max} (h)	0.428	0.105	4.02	0.428
C _{max} (µg/ml)	184	527	226	1223
T _{1/2} (h)	83	184	215	366

Serum Chemistry. Blood samples were collected at pre-dose, 12 hr, 48 hr, and subsequently once every 48 hr, for clinical chemistry analysis, in particular lipid profiles (i.e. cholesterol, LDL-C, HDL-C, triglycerides). With the exception of the 12 hr post-dose sample, all animals were subject to an overnight fast prior to sample collection. The sample volume was approximately 1 ml. Chemistry parameters were determined using an Olympus automated analyzer. Parameters measured (Xybion code): Albumin (ALB); Alkaline Phosphatase (ALP); Alanine Aminotransferase (ALT); Aspartate Transaminase (AST); Total Bilirubin (TBIL); Calcium (Ca); Total Cholesterol (TChO); Creatine Kinase (CK); Creatinine (CRN); Gamma Glutamyltransaminase (GGT); Glucose (GLU); Inorganic Phosphorus (IP); Total Protein (TP); Triglyceride (TRIG); Blood Urea Nitrogen (BUN); Globulin (GLOB); Albumin/Globulin Ratio (A/G); Chloride (Cl); Potassium (K); Sodium (Na); LDL and HDL cholesterol. Residual serum was stored at -20° C. or below and disposed of no sooner than one week after analysis.

Results from samples through Day 105 post-dose time point are shown in FIGS. 3-7. There was a reduction in total cholesterol and LDL-C in animals receiving 316P and 300N, regardless of dose, within 24 hours of the first dose. Serum total cholesterol reduced rapidly and robustly (~35%, FIG. 3). A robust decrease of ~80% was seen in LDL-C (FIGS. 4-5) by day 6. In animals that received a 15 mg/kg dose of 300N, the reduction in both total cholesterol (~10-15% reduction) and LDL-C (~40% reduction) continued to at least day 80 of the study. In addition, HDL-C was elevated in animals that received 316P at 15 mg/kg (FIG. 6). Animals that received a higher dose (15 mg/kg) of either 316P or 300N also showed a reduction in triglycerides during the course of study (FIG. 7). 316P exhibited maximal suppression of LDL-C levels of up to 80% relative to baseline. The length of this suppression was dose-dependent with at least 60% suppression (relative to baseline LDL-C levels) lasting approximately 18 days (5 mg/kg dose) and approximately 45 days (15 mg/kg dose).

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300N exhibits a distinct pharmacodynamic profile from 316P. LDL-C suppression by 300N was sustained for a much longer period of time at comparable doses (50% LDL-C suppression for 28 days following a 5 mg/kg dose and 50% LDL-C suppression for approximately 90 days following a 15 mg/kg dose). There was little or no measurable change in liver function as determined by ALT and AST measurements. All animals receiving an anti-PCSK9 antibody in the study exhibited a rapid suppression of LDL-C and total cholesterol.

A similar LDL-C lowering effect of 316P and 300N was also observed in cynomolgus monkeys that received a single subcutaneous (SC) administration of either 5 mg/kg 316P or 5 mg/kg 300N (FIG. 8). Both 316P and 300N dramatically suppressed LDL-C levels and maintained an LDL-C lowering effect for approximately 15 and 30 days, respectively (FIG. 8). The pharmacodynamic effect (approximately 40% LDL-C suppression) approximately correlates with functional antibody levels in monkey serum (FIG. 9). As antibody levels decrease below 10 µg/ml, LDL-C suppression appeared to diminish as well. In addition, 300N demonstrated a substantially longer circulating half-life than 316P and hence a longer observed LDL-C suppression.

TABLE 26

PK Parameter	316P	300N
T _{max} (h)	60	84
C _{max} (µg/ml)	46	63
T _{1/2} (h)	64	286

Example 14

Attenuation of LDL Receptor Degradation by Anti-hPCSK9 Antibodies

To assess the biological effect of PCSK9 on hepatic LDL receptor levels and subsequent effects on serum LDL-C levels, hPCSK9 was administered to mice expressing hPCSK9 but not mPCSK9 (PCSK9^{hu/hu} mice) by intravenous injection. Specifically, PCSK9^{hu/hu} mice were injected with PBS (control), or 1.2 mg/kg hPCSK9-mmh via the tail vein. Six hours after delivery of hPCSK9, a 1.4-fold elevation (relative to baseline level) in total cholesterol and a 2.3-fold elevation in LDL-C in serum were observed. Analysis of hepatic LDL receptor levels in a separate cohort (n=3) of animals 4 hours after hPCSK9 administration revealed a significant reduction in detectable LDL receptor in liver homogenates.

To assess the biological effect of anti-hPCSK9 on hepatic LDL receptor levels and subsequent effects on serum LDL-C levels, 316P and a non-hPCSK9 specific mAb were administered to PCSK9^{hu/hu} mice at equivalent dose (5 mg/kg i.p.) 20 hours prior to the hPCSK9-mmh protein injection described above. Four hours after the hPCSK9 administration, mice were sacrificed and a total of eight tissues (liver, brain, lung, kidney, heart, ileum, adrenal, and pancreas) were collected and levels of LDL receptor were determined by Western blot. Changes in LDL receptor levels were only observed in liver. In comparison to PBS control dosing, administration of 316P significantly blocked the PCSK9-mediated increases in total cholesterol and LDL cholesterol (LDL-C=2.49 mg/dl at baseline and 3.1 mg/dl 6 hours after PCSK9; a 25% increase compared to 135% with vehicle). Prior administration of the non-hPCSK9 specific mAb blocked LDL-C increases by

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approximately 27% from PBS alone (LDL-C=4.1 mg/dl compared to PBS 5.6 mg/dl). Analysis of LDL receptor levels in a separate cohort of mice (n=3 per treatment group) revealed a significant reduction in LDL receptor levels with 5 PCSK9 administration, which was blocked by 316P but not by the non-hPCSK9 specific mAb (FIG. 10).

Effect of different doses of 316P was also evaluated in 10 PCSK9^{hu/hu} mice with both elevated LDL-C and elevated hPCSK9 levels. PCSK9^{hu/hu} mice were first placed on a high carbohydrate diet for 8 weeks, resulting in a ~2-fold elevation in both LDL-C and hPCSK9 levels. Either 316P or a non-hPCSK9 specific mAb, each at 1 mg/kg, 5 mg/kg, or 10 mg/kg, were administered to the mice. Sera were collected 15 20 hours later and LDL-C levels were analyzed. 316P was effective in decreasing LDL-C levels in a dose-dependent manner (FIG. 11). In addition, 316P administered at a dose of 10 mg/kg, rapidly reduced LDL-C levels back to original (pre-diet) values within 24 hours.

Example 15

Mouse PK Studies

25 A PK study was conducted in 6-week-old C57BL/6 mice and 30 11-15 week old hPCSK9 heterozygous mice. A single injection of Control I, 316P, or 300N, each at 10 mg/kg, was administered SC. Serum bleeds were measured for hIgG levels at 0 hr (pre-bleed), 6 hr, day 1, 3, 6, 10, 14, 21, 28, 35, 42 and 56, for a total of 12 time points, using an anti-hFc capture and anti-hFc detection sandwich ELISA (FIGS. 12 and 13).

35 All mAbs achieved their T_{max} at approximately 3 days with corresponding C_{max} levels of approximately 47-115 µg/ml for C57BL/6 mice and 55-196 µg/ml for hPCSK9 heterozygous mice. At Day 56, Control I mAb levels were about 12 µg/ml and 300N levels were about 11 µg/ml whereas 316P levels were about less than 0.02 µg/ml in C57BL/6 mice. At Day 56 in hPCSK9 heterozygous mice, Control I mAb levels were about 29 µg/ml, while both 300N and 316P levels were below the quantifiable limit (BQL) of 0.02 µg/ml.

Example 16

50 Anti-hPCSK9 Antibody Binding to Mutant/Variant hPCSK9

To further assess binding between hPCSK9 and anti-hPCSK9 mAbs, 21 variant hPCSK9 proteins in which each 55 variant contained a single point mutation and two variant hPCSK9 proteins each contained a double mutation were generated. Each selected antibody was captured on a F(ab')₂ anti-hlgG surface created through direct chemical coupling to a BIACORE™ chip to form a captured antibody surface. 60 Each mmh-tagged variant hPCSK9 at varying concentrations from 100 nM to 25 nM was then injected over the captured antibody surface at a flowrate of 60 µl/min for 240 sec, and the dissociation of variant hPCSK9 and antibody was monitored in real time for 20 min at 25° C. nb: no binding was observed under these experimental conditions (K_D=M×10⁻⁹; T_{1/2}=min; WT=wildtype).

TABLE 27

	316P		300N		Control I		Control II		Control III	
	K _D	T _{1/2}								
WT	1.00	37	0.69	120	30.6	16	0.10	333	0.60	481
P70A	1.42	32	1.68	80	19.0	16	0.24	168	0.90	325
S127R	2.40	36	1.87	110	25.0	18	0.26	288	0.55	550
D129G	1.27	36	1.40	88	22.9	18	0.19	257	0.75	445
S147F	1.29	32	9.07	24	21.1	15	0.22	178	0.23	1468
S153R	5.64	4	0.56	141	36.6	17	0.09	322	3.33	60
E159R	6.96	5	0.82	94	31.7	16	0.08	350	2.97	68
T162R	0.98	43	0.58	140	29.0	17	0.09	322	0.48	362
D192R	1.35	28	0.75	119	30.2	15	0.09	326	nb	nb
R194E	0.38	71	0.65	129	31.4	16	0.07	389	nb	nb
E197R	1.42	27	0.67	115	30.2	17	0.09	339	nb	nb
R215H	0.86	41	1.03	98	37.8	17	0.65	49	0.74	272
R215E	0.90	43	1.81	77	44.0	16	4.48	12	0.78	276
F216L	1.83	32	0.99	121	21.2	15	1.35	39	0.33	880
R237E	2.48	15	1.03	109	29.6	15	0.07	481	5.89	43
D238R	410	1	0.78	123	25.9	19	0.24	144	0.14	1273
A341R	1.54	21	0.34	190	28.7	18	0.08	340	0.88	200
D343R	7.88	6	1.18	89	27.0	16	0.08	402	4.13	66
R357H	6.26	30	6.53	66	26.4	13	0.63	165	1.91	896
E366K	2.92	13	36.0	2	28.8	18	0.46	69	0.38	808
D374Y	2.04	15	0.66	83	25.0	17	0.08	285	1.02	161
V380M	0.48	63	2.82	28	25.9	17	0.15	177	0.35	711
P70A, S147F	1.18	34	7.87	24	23.5	18	0.23	164	0.79	348
E366K, V380M	3.33	12	78.3	1	25.5	18	0.59	60	0.52	551

The results show that when residue D238 was mutated, the binding affinity of 316P for hPCSK9 was reduced >400-fold, from a K_D of 1×10^{-9} M to 410×10^{-9} M; and T_{1/2} shortened about 30-fold, from 37 to 1 min, indicating that 316P binds an epitope on hPCSK9 comprising D238 of hPCSK9 (SEQ ID NO:755). Additionally, BIACORE™ assays show that 316P binding affinity and T_{1/2} were reduced about 5- to 10-fold when a residue at 153, 159 or 343 was mutated. Specifically, K_D was reduced from about 1×10^{-9} M to between about $5-8 \times 10^{-9}$ M when any one of S153, E159 or D343 were mutated; while T_{1/2} was decreased from about 37 min to between about 4-6 min.

30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995 1000 1005 1010 1015 1020 1025 1030 1035 1040 1045 1050 1055 1060 1065 1070 1075 1080 1085 1090 1095 1100 1105 1110 1115 1120 1125 1130 1135 1140 1145 1150 1155 1160 1165 1170 1175 1180 1185 1190 1195 1200 1205 1210 1215 1220 1225 1230 1235 1240 1245 1250 1255 1260 1265 1270 1275 1280 1285 1290 1295 1300 1305 1310 1315 1320 1325 1330 1335 1340 1345 1350 1355 1360 1365 1370 1375 1380 1385 1390 1395 1400 1405 1410 1415 1420 1425 1430 1435 1440 1445 1450 1455 1460 1465 1470 1475 1480 1485 1490 1495 1500 1505 1510 1515 1520 1525 1530 1535 1540 1545 1550 1555 1560 1565 1570 1575 1580 1585 1590 1595 1600 1605 1610 1615 1620 1625 1630 1635 1640 1645 1650 1655 1660 1665 1670 1675 1680 1685 1690 1695 1700 1705 1710 1715 1720 1725 1730 1735 1740 1745 1750 1755 1760 1765 1770 1775 1780 1785 1790 1795 1800 1805 1810 1815 1820 1825 1830 1835 1840 1845 1850 1855 1860 1865 1870 1875 1880 1885 1890 1895 1900 1905 1910 1915 1920 1925 1930 1935 1940 1945 1950 1955 1960 1965 1970 1975 1980 1985 1990 1995 2000 2005 2010 2015 2020 2025 2030 2035 2040 2045 2050 2055 2060 2065 2070 2075 2080 2085 2090 2095 2100 2105 2110 2115 2120 2125 2130 2135 2140 2145 2150 2155 2160 2165 2170 2175 2180 2185 2190 2195 2200 2205 2210 2215 2220 2225 2230 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7235 7240 7245 7250 7255 7260 7265 7270 7275 7280 7285 7290 7295 7300 7305 7310 7315 7320 7325 7330 7335 7340 7345 7350 7355 7360 7365 7370 7375 7380 7385 7390 7395 7400 7405 7410 7415 7420 7425 7430 7435 7440 7445 7450 7455 7460 7465 7470 7475 7480 7485 7490 7495 7500 7505 7510 7515 7520 7525 7530 7535 7540 7545 7550 7555 7560 7565 7570 7575 7580 7585 7590 7595 7600 7605 7610 7615 7620 7625 7630 7635 7640 7645 7650 7655 7660 7665 7670 7675 7680 7685 7690 7695 7700 7705 7710 7715 7720 7725 7730 7735 7740 7745 7750 7755 7760 7765 7770 7775 7780 7785 7790 7795 7800 7805 7810 7815 7820 7825 7830 7835 7840 7845 7850 7855 7860 7865 7870 7875 7880 7885 7890 7895 7900 7905 7910 7915 7920 7925 7930 7935 7940 7945 7950 7955 7960 796

allowed to acclimate for a period of 7 days before entry into the study. All animals were placed on either a standard chow diet or a hyperlipemic diet of chow supplemented with 0.1% cholesterol and 10% coconut oil. The 316P mAb was delivered to hamsters by a single subcutaneous injection at doses of 1, 3, or 10 mg/kg for normolipemic hamsters and at doses of 3, 10, or 30 mg/kg for hyperlipemic hamsters. Serum samples were taken from all groups at 24 hr and 7, 14, and 22 days post injection, at which time serum lipid levels were

assessed and compared to baseline levels taken 7 days prior to the administration of the mAbs. Circulating total cholesterol and LDL-C in normolipemic hamsters was significantly reduced in a dose-dependent manner compared to vehicle injection. As shown in FIG. 14, administration of 316P effectively reduced LDL-C levels by up to 60% seven days post injection at the highest dose (10 mg/kg) tested. Similar cholesterol reducing effect of 316P was not observed in hyperlipemic hamsters.

SEQUENCE LISTING

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<210> SEQ ID NO 1
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
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acaggaaaag gtctggagtg ggtctcaggt attgggttcta ccgggtgacac atactatcca	180
ggctccgtga agggccgatt caccatcacc agagaaaaag ccaagaactc cgtgtatctt	240
caaataaca gcctgagagc cggggacacgc gctgtgtatt actgtgtaa agaggggtgg	300
gagggttaccct ttgactactg gggccaggga accttggtca ctgtctctca	351

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<210> SEQ ID NO 2
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
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<400> SEQUENCE: 2

Gln Val Gln Leu Val Gln 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 Leu Ser Ser Tyr
20 25 30

Asp Met His Trp Val Arg Gln Ser Thr Gly Lys Gly Leu Glu Trp Val
35 40 45

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

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

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

Ala Glu Gly Ile Glu Val Pro Phe Asp Tyr Ile Gln Gly Ile Leu
100 105 110

115

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<210> SEQ ID NO 3
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
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24

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 4

Gly Phe Thr Leu Ser Ser Tyr Asp
1 5

<210> SEQ ID NO 5
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 5

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21

<210> SEQ ID NO 6
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 6

Ile Gly Ser Thr Gly Asp Thr
1 5

<210> SEQ ID NO 7
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 7

gtaagagagg ggtgggaggt acccttgac tac

33

<210> SEQ ID NO 8
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 8

Val Arg Glu Gly Trp Glu Val Pro Phe Asp Tyr
1 5 10

<210> SEQ ID NO 9
<211> LENGTH: 327
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 9

gacatccaga tgaccaggc tccagccacc ctgtctgtgt ctccagggga aagagccgcc 60

ctctcctgca gggccagtca gagtgtagc agcaacttag cctggtagcca ccagaaacct 120

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ggccaggctc ccaggctcct catctatggt gcatccacca	180
gggccactgg tatcccagcc	
aggttcagtg gcattggtc tggcacagag ttcaactcta ttatcagcag cctgcagtct	240
gaagatttg catttatct ctgtcagcag tataataact ggctccatt cacttcggc	300
cctgggacca aggtggagat caaacga	327

<210> SEQ ID NO 10
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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 10

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

<210> SEQ ID NO 11
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 11

cagagtgtta gcagcaac 18

<210> SEQ ID NO 12
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 12

Gln Ser Val Ser Ser Asn 1 5

<210> SEQ ID NO 13
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 13

ggtgtcatcc 9

<210> SEQ ID NO 14
<211> LENGTH: 3

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<212> TYPE: PRT
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 14

Gly Ala Ser
1

<210> SEQ ID NO 15
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 15

cagcagtata ataaactggcc tccattcact          30

<210> SEQ ID NO 16
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 16

Gln Gln Tyr Asn Asn Trp Pro Pro Phe Thr
1           5           10

<210> SEQ ID NO 17
<211> LENGTH: 351
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 17

gagggtgcagc tgggtggagtc tggggggggc ttggtaacgc ctggggggtc cctgagactc      60
tcctgtgcag cctctggatt tactctaagt agttacgaca tgcaactgggt ccgc当地atct      120
acaggaaaag gtctggagtg ggtctcagct attgggtctt cccgtgacac atactatcca      180
ggctccgtga agggcccgatt caccatcacc agagaaaaag ccaagaactc cgtgttatctt      240
caaataaca gcctgagagc cggggacacg gctgtgtatt actgtgtaaag agaggggtgg      300
gaggtaccct ttgactactg gggccaggga accctggtaa ccgtctccctc a      351

<210> SEQ ID NO 18
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 18

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 Leu Ser Ser Tyr
20          25           30

Asp Met His Trp Val Arg Gln Ser Thr Gly Lys Gly Leu Glu Trp Val
35          40           45

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

Gly Arg Phe Thr Ile Thr Arg Glu Lys Ala Lys Asn Ser Val Tyr Leu

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65	70	75	80
Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Val Tyr Tyr Cys Val			
85	90	95	
Arg Glu Gly Trp Glu Val Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu			
100	105	110	
Val Thr Val Ser Ser			
115			

<210> SEQ ID NO 19
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 19

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccgcc	60
ctctcctgca gggccagtca gagtgtagc agcaacttag cctggatcca ccagaaacct	120
ggccaggctc ccagggctt catctatggt gcatccacca gggccactgg tatcccagcc	180
aggttcagtg gcattgggtc tgggacagag ttcaactctca ttatcagcag cctgcagtct	240
gaagattttg cattttatctt ctgtcagcag tataataact ggctccatt cacttcggc	300
cctgggacca aagtggatata caaa	324

<210> SEQ ID NO 20
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 20

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

<210> SEQ ID NO 21
<211> LENGTH: 351
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 21

gaggtgcagc tggtggagtc tgggggaggc ttggtagc cttgggggtc cctgagactc	60
tcctgtgcag cctctggatt tactctaagt agttacgaca tgcactgggt ccgccaagct	120
acaggaaaag gtctggagtg ggtctcagct attggttcta ccggtgacac atactatcca	180

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ggctccgtga	agggccgatt	caccatctcc	agagaaaatg	ccaagaactc	cttgttatctt	240
caaataaca	gcctgagac	cggggacacg	gctgtgtatt	actgtgtaa	agaggggtgg	300
gaggtaccct	ttgactactg	gggcaggga	accctggta	ccgtctccctc	a	351

<210> SEQ ID NO 22
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 22

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	Leu	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	Ser	Thr	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	Val
	85				90				95						

Arg	Glu	Gly	Trp	Glu	Val	Pro	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu
	100				105				110						

Val	Thr	Val	Ser	Ser											
				115											

<210> SEQ ID NO 23
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 23

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ctctcctgca	ggcccgatca	gaggtgttagc	agcaacttag	cctggatcca	gcagaaacct	120
ggccaggctc	ccaggctct	catctatggt	gcatccacca	ggccactgg	tatcccagcc	180
aggttcagtg	cgagtgggtc	tgggcagagag	ttcactctca	ccatcagcag	cctgcagtc	240
gaagatttg	cagtttatta	ctgtcagcag	tataataact	ggctccatt	cacttcggc	300
cctgggacca	aagtggatat	caaa				324

<210> SEQ ID NO 24
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 24

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

Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Asn
	20			25					30						

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

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Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Ser
65					70					75					80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Asn Trp Pro Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

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<210> SEQ ID NO 25
<211> LENGTH: 342
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
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<400> SEQUENCE: 25

cagggtgcagc	tgggtgcagtc	tgggggagggc	gtgggtccagc	ctgggaggtc	cctgagactc	60
tccctgtgcag	cgtctggatt	cacccatcgat	agctatggca	tgcactgggt	ccgcccaggct	120
ccaggccaagg	ggctggagtg	ggtggcggtt	ataggatttg	atggaaatgtt	tatacattat	180
ggagactccg	tgagggggccg	aatcatcata	tccagagaca	attccgagaa	cacgttgtat	240
ctggaaaatga	acagcctgag	agccgaggac	acggcaatgt	actattgtgc	gagagagaag	300
ggtttagact	ggggccagggg	aaccacggtc	acccgtctct	ca		342

<210> SEQ ID NO 26

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<211> LENGTH: 114
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

<400> SEQUENCE: 26

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 Phe Ile Gly Phe Asp Gly Ser Asn Ile His Tyr Gly Asp Ser Val
 50 55 60

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

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

Ala Arg Glu Lys Gly Leu Asp Trp Gly Gln Gly Thr Thr Val Thr Val
100 105 110

Ser Ser

```
<210> SEQ ID NO 27
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

<400> SEQUENCE: 27

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<210> SEQ ID NO 28
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 28

Gly Phe Thr Phe Ser Ser Tyr Gly
1 5

<210> SEQ ID NO 29
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 29

ataggatttg atggaagtaa tata

24

<210> SEQ ID NO 30
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 30

Ile Gly Phe Asp Gly Ser Asn Ile
1 5

<210> SEQ ID NO 31
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 31

gcgagagaga agggttttaga c

21

<210> SEQ ID NO 32
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 32

Ala Arg Glu Lys Gly Leu Asp
1 5

<210> SEQ ID NO 33
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 33

gccatccaga tgacctcgtc tccttccacc ctgtctgcat ctgttaggaga cagagtcacc	60
atcaacttgcg gggccagtca gagttagt agctgggtgg cctggtatca gcagaaaccca	120
gggaaagccc ctaagctcct gatctataag gcgtcttagtt tagaaagtgg ggtcccatca	180
aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct	240

-continued

gatgatttg caacttatta ctgccaacag tataatagtt attacactt tggccagggg 300
 accaagggtgg aaatcaaacg a 321

<210> SEQ ID NO 34
 <211> LENGTH: 107
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 34

Ala	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	Ile	Ser	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	Lys	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	Gln	Tyr	Asn	Ser	Tyr	Tyr	Thr
		85			90					95					

Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg					
		100			105										

<210> SEQ ID NO 35
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 35

cagagtatta gtagctgg 18

<210> SEQ ID NO 36
 <211> LENGTH: 6
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 36

Gln Ser Ile Ser Ser Trp
 1 5

<210> SEQ ID NO 37
 <211> LENGTH: 9
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 37

aaggcgtct 9

<210> SEQ ID NO 38
 <211> LENGTH: 3
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

-continued

<400> SEQUENCE: 38

```
Lys Ala Ser
 1
```

```
<210> SEQ ID NO 39
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

<400> SEQUENCE: 39

```
caacagtata atagttatta cact 24
```

```
<210> SEQ ID NO 40
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

<400> SEQUENCE: 40

```
Gln Gln Tyr Asn Ser Tyr Tyr Thr
 1           5
```

```
<210> SEQ ID NO 41
<211> LENGTH: 342
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

<400> SEQUENCE: 41

caggtgcagc tggtgaggc tgggggaggc gtgggtccago ctggggaggc cctgagactc	60
tcctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct	120
ccaggcaagg ggctggagtg ggtggcggtt ataggatttg atggaagtaa tatacattat	180
ggagactccg tgagggcccg aatcatcata tccagagaca attccgagaa cacgttgat	240
ctggaaatga acagcctgag agccgaggac acggcaatgt actattgtgc gagagagaag	300
ggtttagact ggggccaggg aaccctggtc accgtctcct ca	342

```
<210> SEQ ID NO 42
<211> LENGTH: 114
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

<400> SEQUENCE: 42

```
Gln Val Gln Leu Val Glu Ser 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 Phe Ile Gly Phe Asp Gly Ser Asn Ile His Tyr Gly Asp Ser Val
 50          55          60
```

```
Arg Gly Arg Ile Ile Ser Arg Asp Asn Ser Glu Asn Thr Leu Tyr
 65          70          75          80
```

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

-continued

Ala Arg Glu Lys Gly Leu Asp Trp Gly Gln Gly Thr Leu Val Thr Val
 100 105 110

Ser Ser

<210> SEQ ID NO 43
 <211> LENGTH: 318
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 43

gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc	60
atcactgcc gggccagtca gagttattgt agctgggtgg cctggtatca gcagaaaacca	120
gggaaagccc ctaagtcct gatctataag gcgtcttagtt tagaaagtgg ggtcccatca	180
aggttcagcg gcagtggatc tgggacagaa ttcaactctca ccatcagcag cctgcagect	240
gatgatttg caacttatta ctgccaacag tataatagtt attacacttt tggccagggg	300
accaagctgg agatcaaa	318

<210> SEQ ID NO 44
 <211> LENGTH: 106
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 44

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 Ile Ser 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 Lys 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 Gln Tyr Asn Ser Tyr Tyr Thr
 85 90 95

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

<210> SEQ ID NO 45
 <211> LENGTH: 342
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 45

caggtgcagc tggtggagtc tgggggaggc gtgggtccago ctgggaggc cctgagactc	60
tcctgtgcag cctctggatt caccttcagt agcttatggca tgcactgggt ccggcaggct	120
ccaggcaagg ggctggagtg ggtggcagtt ataggatttg atggaagtaa tatatactat	180
gcagactccg tgaaggcccg attcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagagagaag	300
ggtttagact gggggcaggaa aaccctggtc accgtctcct ca	342

-continued

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<210> SEQ ID NO 47
<211> LENGTH: 319
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 47

gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgttaggaga cagagtca 60
atcaattgcc gggccaggta gagtattagt agctggttgg cctggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctataag gcgtctagtt tagaaagtgg ggtcccatca 180
aggttcagcg gcagtggtatc tgggacagaa ttcaactctca ccatcagcag cctgcagct 240
gtatgttttg caacttatta ctgccaacag tataatagt attacacttt tggcagggg 300
accgaacgtgg agatcaaaaac 319
```

```

<210> SEQ ID NO 48
<211> LENGTH: 106
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 48

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 Ile Ser 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 Lys 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

```

-continued

Asp	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Tyr	Asn	Ser	Tyr	Tyr	Thr
85							90				95				

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

<210> SEQ ID NO 49
<211> LENGTH: 342
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 49

caggtgcagc	tcgaggagtc	tgggggaggc	gtgggtccago	ctggggaggc	cctgagactc	60
tcctgtgcag	cgtctggatt	caccttca	agtatggca	tgcactgggt	ccggccaggct	120
ccaggcaagg	ggctggagtg	ggtggcg	ttt	ataggatttg	atgaaagtta	180
ggagactccg	tgaggggccc	aatcatcata	tccagagaca	attccgagaa	cacgttgtat	240
ctggaaatga	acagcctgag	agccgaggac	acggcagtgt	attattgtgc	gagagagaag	300
ggtttagact	ggggccaggg	aaccctggtc	actgtctcct	ca		342

<210> SEQ ID NO 50
<211> LENGTH: 114
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 50

Gln	Val	Gln	Leu	Gln	Glu	Ser	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	Phe	Ile	Gly	Phe	Asp	Gly	Ser	Asn	Ile	Tyr	Tyr	Gly	Asp	Ser	Val
	50				55				60						

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

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

Ala	Arg	Glu	Lys	Gly	Leu	Asp	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val
		100				105					110				

Ser Ser

<210> SEQ ID NO 51
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 51

ggattcacct	tcagtagcta	tggc	24
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<210> SEQ ID NO 52
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 52

Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Gly
1							5

<210> SEQ ID NO 53

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 53

ataggatttg atggaagtaa tata

24

<210> SEQ ID NO 54

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 54

Ile	Gly	Phe	Asp	Gly	Ser	Asn	Ile
1							5

<210> SEQ ID NO 55

<211> LENGTH: 21

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 55

gcgagagaga agggttttaga c

21

<210> SEQ ID NO 56

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 56

Ala	Arg	Glu	Lys	Gly	Leu	Asp
1						5

<210> SEQ ID NO 57

<211> LENGTH: 342

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 57

gccatccaga	tgacccagtc	tccagactcc	ctggctgtgt	ctctgggcga	gaggggcacc	60
atcaactgca	agtccagcca	gagtgttttt	cacacctcca	acaataagaa	ctacttagtt	120
tggtatcagc	agaaaccagg	acagcctct	aagttgtcc	tttactgggc	ctctacccgg	180
gaatccgggg	tccctgaccg	attcagtggc	agcgggtctg	ggacagattt	cactctcacc	240
atcagcagcc	tgcaggctga	agatgtggca	aattattact	gtcaccaata	ttacagtatt	300
ccgtggacgt	tcggccaagg	gaccaaggtg	gagatcaaac	ga		342

-continued

<210> SEQ ID NO 58
<211> LENGTH: 114
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 58

Ala	Ile	Gln	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 Ser Val Phe His Thr

		20			25						30				
--	--	----	--	--	----	--	--	--	--	--	----	--	--	--	--

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Gln

		35			40						45				
--	--	----	--	--	----	--	--	--	--	--	----	--	--	--	--

Pro Pro Lys Leu Leu Leu 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 Asn Tyr Tyr Cys His Gln

		85			90						95				
--	--	----	--	--	----	--	--	--	--	--	----	--	--	--	--

Tyr Tyr Ser Ile Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile

		100			105						110				
--	--	-----	--	--	-----	--	--	--	--	--	-----	--	--	--	--

Lys Arg

<210> SEQ ID NO 59
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 59

cagagtgttt ttcacacctc caacaataag aactac

36

<210> SEQ ID NO 60
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 60

Gln	Ser	Val	Phe	His	Thr	Ser	Asn	Asn	Lys	Asn	Tyr
1						5					

<210> SEQ ID NO 61
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 61

tgggcctct

9

<210> SEQ ID NO 62
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 62

Trp Ala Ser

-continued

1

<210> SEQ ID NO 63
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 63

caccaatattt acagtttcc gtggacg 27

<210> SEQ ID NO 64
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 64

His Gln Tyr Tyr Ser Ile Pro Trp Thr
1 5

<210> SEQ ID NO 65
<211> LENGTH: 342
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 65

cagggtcagc tggtgagtc tgggggaggc gtggccagc ctgggaggtc cctgagactc	60
tccctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct	120
ccaggcaagg ggctggagtg ggtggcggtt ataggatttg atgaaagtaa tatataattat	180
ggagactccg tgaggggccc aatcatcata tccagagaca attccgagaa cacgttgat	240
ctggaaatga acagcctgag agccgaggac acggcagtgt attattgtgc gagagagaag	300
ggtttagact gggccaggg aaccctggtc accgtctcct ca	342

<210> SEQ ID NO 66
<211> LENGTH: 114
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 66

Gln Val Gln Leu Val Glu Ser 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 Phe Ile Gly Phe Asp Gly Ser Asn Ile Tyr Tyr Gly Asp Ser Val
50 55 60

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

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

Ala Arg Glu Lys Gly Leu Asp Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

-continued

Ser Ser

<210> SEQ ID NO 67
<211> LENGTH: 339
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 67

```
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctggcgca gaggggccacc      60
atcaactgca agtccagcca gagtgtttt cacacctcca acaataagaa ctacttagtt      120
tggtatcagc agaaaaccagg acagcctctt aagttgctcc tttactggc ctctacccgg      180
gaatccgggg tccctgaccg attcaagtggc agcgggtctg ggacagattt cactctcacc      240
atcagcagcc tgcaggctga agatgtggca aattattact gtcaccaata ttacagtatt      300
ccgtggacgt tcggccaagg gaccaaggtg gaaatcaaa                                339
```

<210> SEQ ID NO 68
<211> LENGTH: 113
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 68

```
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 Ser Val Phe His Thr
 20          25           30

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

Pro Pro Lys Leu Leu Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50          55           60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65          70           75           80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Asn Tyr Tyr Cys His Gln
 85          90           95

Tyr Tyr Ser Ile Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100         105          110
```

Lys

<210> SEQ ID NO 69
<211> LENGTH: 342
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 69

```
caggtgcagc tggtggagtc tgggggaggc gtggccagc ctgggaggtc cctgagactc      60
tcctgtgcag cctctggatt caccttcagt agctatggca tgcactgggt ccgccaggct      120
ccaggcaagg ggctggagtg ggtggcagtt ataggatttg atggaagtaa tatatactat      180
gcagactccg tgaaggccc attcaccatc tccagagaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagagagaag      300
ggtttagact ggggccaggg aaccctggc accgtctcct ca                                342
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<210> SEQ ID NO 70
<211> LENGTH: 114
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 70

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

Ser Ser

<210> SEQ ID NO 71
<211> LENGTH: 339
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 71

gacatcgta	tgaccaggc	tccagactc	ctggctgtgt	ctctggcgca	gagggccacc	60
atcaactgca	agtccagcca	gagtgtttt	cacacotcca	acaataagaa	ctacttagct	120
tggttaccgc	agaaaaccagg	acagcctct	aagctgctca	tttactgggc	ctctacccgg	180
gaatccgggg	tccctgaccg	attcagtggc	agcgggtctg	ggacagattt	cactctcacc	240
atcagcagcc	tgcaggctga	agatgtggca	gtttattact	gtcaccaata	ttacagtatt	300
ccgtggacgt	tcggccaagg	gaccaagggtg	gaaatcaa			339

<210> SEQ ID NO 72
<211> LENGTH: 113
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 72

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 Ser Val Phe His Thr
20 25 30

Ser Asn Asn Lys Asn 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 His Gln

-continued

85 90 95

Tyr Tyr Ser Ile Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 100 105 110

Lys

<210> SEQ ID NO 73
 <211> LENGTH: 354
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 73

gaagtgcagc	tgggtgcagtc	tgggggaggc	tgggtacago	ctggggggtc	cctgagactc	60
tcctgtgcag	cctctggatt	caccttaac	aactatgcca	tgaactgggt	ccgcaggct	120
ccagggaaagg	gactggactg	ggtctcaact	attagtggta	gcgggtggta	tacaaactac	180
gcagactccg	tgaagggccg	tttcatttatt	tcccagaca	gttccaaaca	cacgctgtat	240
ctgcaaata	tgatcgatct	ctggggccgt	ggcaccacgg	tcactgtctc	ctca	300
aactggggaa	attcgatct	ctggggccgt	ggcaccacgg	tcactgtctc	ctca	354

<210> SEQ ID NO 74
 <211> LENGTH: 118
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 74

Glu	Val	Gln	Leu	Val	Gln	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	Asn	Asn	Tyr
20				25						30					

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

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

Lys	Gly	Arg	Phe	Ile	Ile	Ser	Arg	Asp	Ser	Ser	Lys	His	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	Asp	Ser	Asn	Trp	Gly	Asn	Phe	Asp	Leu	Trp	Gly	Arg	Gly	Thr
100				105						110					

Thr	Val	Thr	Val	Ser	Ser										
				115											

<210> SEQ ID NO 75
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 75

ggattcacct	ttaacaacta	tgcc	24
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<210> SEQ ID NO 76
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 76

Gly Phe Thr Phe Asn Asn Tyr Ala
1 5

<210> SEQ ID NO 77
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 77

attagtggta gcgggtggtac taca

24

<210> SEQ ID NO 78
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 78

Ile Ser Gly Ser Gly Gly Thr Thr
1 5

<210> SEQ ID NO 79
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 79

gcgaaagatt ctaactgggg aaatttcgat ctc

33

<210> SEQ ID NO 80
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 80

Ala Lys Asp Ser Asn Trp Gly Asn Phe Asp Leu
1 5 10

<210> SEQ ID NO 81
<211> LENGTH: 342
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 81

gacatccaga tgacctcagtc tccagactcc ctggctgtgt ctctggcgaa gagggccacc 60
atcaactgca agtccagcca gagtgttta tacaggtcca acaataggaa cttcttaggt 120
tggtaccagc agaaaccagg gcagcctct aatctactca ttactgggc atctaccccg 180
gaatccgggg tccctgaccg attcagtgcc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcaggctga agatgtggca gtttattact gtcaacaata ttatactact 300
ccgtacactt ttggccaggg gaccaaggtg gaaatcaaac ga 342

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<210> SEQ ID NO 82
<211> LENGTH: 114
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 82

Asp	Ile	Gln	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 Ser Val Leu Tyr Arg
20 25 30

Ser Asn Asn Arg Asn Phe Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Asn Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly 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 Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg

<210> SEQ ID NO 83
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 83

cagagtgttt	tatacaggc	caacaatagg	aacttc	36
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<210> SEQ ID NO 84
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 84

Gln	Ser	Val	Leu	Tyr	Arg	Ser	Asn	Asn	Arg	Asn	Phe
1				5							
											10

<210> SEQ ID NO 85
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 85

tgggcacatct	9
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<210> SEQ ID NO 86
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 86

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Trp Ala Ser
1

<210> SEQ ID NO 87
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 87

caacaatatt atactactcc gtacact

27

<210> SEQ ID NO 88
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 88

Gln Gln Tyr Tyr Thr Thr Pro Tyr Thr
1 5

<210> SEQ ID NO 89
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 89

gaggtgcagc tgggtggagtc tgggggaggc ttggcacago ctggggggtc cctgagactc	60
tccctgtgcag cctctggatt caccttaac aactatgcc a tgaactgggt ccggccaggct	120
ccagggaaagg gactggactg ggtctcaact attagtggta gcgggtggta tacaaaactac	180
gcagactccg tgaagggccg tttcatttatt tcccgagaca gttccaaaca cacgctgtat	240
ctgcaa atgca acagcctgag agcggaggac acggccgtat attactgtgc gaaaggattct	300
aactgggaa atttcgatct ctggggccgt ggcaccctgg tcactgtctc ctca	354

<210> SEQ ID NO 90
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 90

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 Asn Asn Tyr	
20 25 30	

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

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

Lys Gly Arg Phe Ile Ile Ser Arg Asp Ser Ser Lys His 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 Asp Ser Asn Trp Gly Asn Phe Asp Leu Trp Gly Arg Gly Thr	
100 105 110	

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Leu Val Thr Val Ser Ser
115

<210> SEQ ID NO 91
<211> LENGTH: 339
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 91

gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctggcgaa gaggggccacc	60
atcaactgca agtccagcca gagtgttta tacaggtcca acaataggaa cttcttaggt	120
tggtaccagc agaaaaccagg gcagcctctt aatctactca ttactgggc atctaccgg	180
gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc	240
atcagcagcc tgcaggctga agatgtggca gtttattact gtcaacaata ttatactact	300
ccgtacactt ttggccaggg gaccaagctg gagatcaa	339

<210> SEQ ID NO 92
<211> LENGTH: 113
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 92

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 Ser Val Leu Tyr Arg		
20	25	30

Ser Asn Asn Arg Asn Phe Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln		
35	40	45

Pro Pro Asn 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 Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile		
100	105	110

Lys

<210> SEQ ID NO 93
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 93

gaggtgcagc tgggtggagtc tgggggaggc ttggcacagc ctggggggtc cctgagactc	60
tcctgtgcag cctctggatt caccttaac aactatgcca tgagctgggt ccggcaggct	120
ccagggaaagg ggctggagtg ggtctcagct attagtggtt gcggtggta tacatactac	180
gcagactccg tgaaggcccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagattct	300
aactggggaa atttcgatct ctggggccgt ggcaccctgg tcactgtctc ctca	354

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<210> SEQ ID NO 94
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 94

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 Asn Asn 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 Thr 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

Ala Lys Asp Ser Asn Trp Gly Asn Phe Asp Leu Trp Gly Arg Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> SEQ ID NO 95
<211> LENGTH: 339
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 95

gacatcgta	tgacccagtc	tccagactcc	ctggctgtgt	ctctggcgcga	gagggccacc	60
atcaactgca	agtccagcca	gagtgttta	tacaggtcca	acaataggaa	cttcttagct	120
tggtaccaggc	agaaaaccagg	acagcctct	aagctgctca	tttactggc	atctaccgg	180
gaatccgggg	tccctgaccg	attcagtggc	agcgggtctg	ggacagattt	cactctcacc	240
atcagcagcc	tgcaggctga	agatgtggca	gtttattact	gtcaacaata	ttatactact	300
ccgtacactt	ttggccaggg	gaccaagctg	gagatcaa			339

<210> SEQ ID NO 96
<211> LENGTH: 113
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 96

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 Ser Val Leu Tyr Arg
20 25 30

Ser Asn Asn Arg Asn Phe 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 Ser Gly Thr Asp Phe Thr Leu Thr

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65 70 75 80

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

Lys

<210> SEQ ID NO 97

<211> LENGTH: 351

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 97

caggtgcagc	tgggtgcagtc	tgggggaggc	ttgggtacago	ctggggggtc	cctgagactc	60
tcctgtgcag	tctctggatt	caccctcagt	agctacgata	tgcaactgggt	ccgcacaacct	120
acaggaaaag	gtctggagtg	ggtctcagct	attggttcta	ctgggtacac	atactatcca	180
ggctccgtga	agggccgatt	caccatctcc	agagaaaatg	ccaagaactc	cttgcatactt	240
caaataaca	gcctgagagc	cggggacacg	gctgtgtatt	actgtgcaag	agagggatgg	300
gacgtaccct	ttgacttctg	gggccaggga	accctggta	ccgtctccctc	a	351

<210> SEQ ID NO 98

<211> LENGTH: 117

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 98

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	
1																15

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Val	Ser	Gly	Phe	Thr	Leu	Ser	Ser	Tyr	
20																30

Asp	Met	His	Trp	Val	Arg	Gln	Pro	Thr	Gly	Lys	Gly	Leu	Glu	Trp	Val	
35																45

Ser	Ala	Ile	Gly	Ser	Thr	Gly	Asp	Thr	Tyr	Tyr	Pro	Gly	Ser	Val	Lys	
50																60

Gly	Arg	Phe	Thr	Ile	Ser	Arg	Glu	Asn	Ala	Lys	Asn	Ser	Leu	Tyr	Leu	
65																80

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

Arg	Glu	Gly	Trp	Asp	Val	Pro	Phe	Asp	Phe	Trp	Gly	Gln	Gly	Thr	Leu	
100																110

Val	Thr	Val	Ser	Ser
				115

<210> SEQ ID NO 99

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 99

ggattcaccc tcagtagcta cgat 24

<210> SEQ ID NO 100

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<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 100

Gly Phe Thr Leu Ser Ser Tyr Asp
1 5

<210> SEQ ID NO 101
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 101

attggttcta ctggtgacac a

21

<210> SEQ ID NO 102
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 102

Ile Gly Ser Thr Gly Asp Thr
1 5

<210> SEQ ID NO 103
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 103

gcaagagagg gatgggacgt accctttgac ttc

33

<210> SEQ ID NO 104
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 104

Ala Arg Glu Gly Trp Asp Val Pro Phe Asp Phe
1 5 10

<210> SEQ ID NO 105
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 105

gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgttaggaga cagagtcacc	60
atcacttgcc gggcaagtca ggacattaga aatgatttag gctggtatca gcagaaacca	120
gggaaaagccc ctaagctct gatctatgct gcatccagtt tacaaagtgg ggtccccatca	180
cggttcagcg gcagtggtac tggcacagat ttcaactctca ccatcagcag cctgcagcct	240
gaagattttgc caacttattat ctgtctacaa gattacaatt acccgtggac gttcggccaa	300

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gggaccaagg tggagatcaa acga

324

<210> SEQ ID NO 106
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 106

Ala	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1															

Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Asp	Ile	Arg	Asn	Asp
20															30

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

Tyr	Ala	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
50															60

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

Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Leu	Gln	Asp	Tyr	Asn	Tyr	Pro	Trp
85															95

Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg				
100															105

<210> SEQ ID NO 107

<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 107

caggacatta gaaatgtat

18

<210> SEQ ID NO 108
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 108

Gln	Asp	Ile	Arg	Asn	Asp
1					

<210> SEQ ID NO 109
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 109

gctgcattcc

9

<210> SEQ ID NO 110
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 110

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Ala Ala Ser
1

<210> SEQ ID NO 111
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 111

ctacaagatt acaattaccc gtggacg 27

<210> SEQ ID NO 112
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 112

Leu Gln Asp Tyr Asn Tyr Pro Trp Thr
1 5

<210> SEQ ID NO 113
<211> LENGTH: 351
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 113

gaggtgcaga	tggtgaggc	tgggggaggc	ttggtagcago	ctggggggtc	cctgagactc	60
tccctgtcag	tctctggatt	caccctcagt	agctacgata	tgcaactgggt	ccgccaacct	120
acaggaaaag	gtctggagt	ggtctcagct	atggttcta	ctggtagcac	atactatcca	180
ggctccgtga	agggccgatt	caccatctcc	agagaaaatg	ccaagaactc	cttgtatett	240
caaataaca	gcctgagac	cggggacacg	gtctgttatt	actgtgcaag	agagggatgg	300
gacgtaccct	ttgacttctg	ggggcaggga	accctggta	ccgtctccct	a	351

<210> SEQ ID NO 114
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 114

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

Arg Glu Gly Trp Asp Val Pro Phe Asp Phe Trp Gly Gln Gly Thr Leu

-continued

100

105

110

Val Thr Val Ser Ser
115

<210> SEQ ID NO 115
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 115

gccccatccaga	tgcacccagtc	tccatcctcc	ctgtctgcat	ctgttaggaga	cagagtcacc	60
atcaacttgcc	gggcaagtca	ggacattaga	aatgatttag	gctggtatca	gcagaaacca	120
gggaaagccc	ctaagctcct	gatctatgct	gcatccagtt	tacaaaagtgg	ggteccatca	180
cggttcagcg	gcagtggtatc	tggcacagat	ttcactctca	ccatcagcag	cctgcagecct	240
gaagattttgc	caacttattta	ctgtctacaa	gattacaatt	acccgtggac	gttcggccaa	300
gggaccaagg	tggaaatcaa	a				321

<210> SEQ ID NO 116
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 116

Ala	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1															15

Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Asp	Ile	Arg	Asn	Asp
															30
20															
25															

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

Tyr	Ala	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
50															60

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

Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Leu	Gln	Asp	Tyr	Asn	Tyr	Pro	Trp
															95
85															

Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys					
100															
105															

<210> SEQ ID NO 117
<211> LENGTH: 351
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 117

gagggtgcago	tggtgaggatc	tgggggaggc	ttgggtacago	ctggggggtc	cctgagactc	60
tccctgtgcag	cctctggatt	caccctcagt	agctacgata	tgcactgggt	ccgccaagct	120
acaggaaaag	gtctggagt	ggtctcagct	atgggttcta	ctggtgacac	atactatcca	180
ggctccgtga	agggccgatt	caccatctcc	agagaaaatg	ccaagaactc	cttgttatctt	240
caaatgaaca	gcctgagagc	cggggacacg	gctgtgtatt	actgtgcaag	agagggatgg	300
gacgtaccct	ttgacttctg	gggccaggga	accctggta	cctgtctcctc	a	351

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<210> SEQ ID NO 118
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 118

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu 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 Ser Thr 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 Glu Gly Trp Asp Val Pro Phe Asp Phe Trp Gly Gln Gly Thr Leu
100         105         110

Val Thr Val Ser Ser
115

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```
<210> SEQ ID NO 119
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 119

ggccatccaga tgacccagtc tccatcctcc ctgtctgcat ctgttaggaga cagagtacc 60
atcacttgcg gggcaagtca ggacattaga aatgatttag gctggtatca gcagaaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagg tacaaggatgg ggtccccatca 180
aggttcagcg gcagttggatc tggcacagat ttcaactctca ccatcagcg cctgcagcct 240
gaagattttg caacttatta ctgtctacaa gattacaatt acccgtggac gttcggccaa 300
gggaccaaaqg tqgaaatcaa a 321
```

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<210> SEQ ID NO 120
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 120

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 Asp 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

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-continued

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Tyr Asn Tyr Pro Trp
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> SEQ ID NO 121
<211> LENGTH: 384
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 121

caggtgcagc	tgcaggagtc	ggggccagga	ctggtaago	cttcggagac	cctgtccctc	60
acctgcactg	tctctggga	ctccatcaat	acttactact	ggagctggtt	ccggcageccc	120
ccagggaaagg	gactggagtg	gattgggtat	atcttattata	gtgaaaccac	caactacaac	180
ccctccctca	agagtcgagt	caccatatca	atagacacgc	ccaggaacca	gttctccctg	240
aagctgatct	ctgtgaccgc	agcggacacg	gccgtgtatt	actgtgcgag	agagaggatt	300
actatgattc	ggggagttac	cctctactat	tactcctacg	gtatggacgt	ctggggccaa	360
gggaccacacgg	tcaccgtctc	ctca				384

<210> SEQ ID NO 122
<211> LENGTH: 128
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 122

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

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

Tyr Trp Ser Trp Phe Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Thr Thr Asn Tyr Asn Pro Ser Leu Lys
 50 55 60

Ser Arg Val Thr Ile Ser Ile Asp Thr Pro Arg Asn Gln Phe Ser Leu
 65 70 75 80

Lys Leu Ile Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Glu Arg Ile Thr Met Ile Arg Gly Val Thr Leu Tyr Tyr Ser
 100 105 110

Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> SEQ ID NO 123
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 123

ggggactcca tcaatactta ctac

<210> SEQ ID NO 124
<211> LENGTH: 8

-continued

<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<400> SEQUENCE: 124

Gly Asp Ser Ile Asn Thr Tyr Tyr
1 5

<210> SEQ ID NO 125
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<400> SEQUENCE: 125

atcttattata gtggaaaccac c

21

<210> SEQ ID NO 126
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<400> SEQUENCE: 126

Ile Tyr Tyr Ser Gly Thr Thr
1 5

<210> SEQ ID NO 127
<211> LENGTH: 66
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<400> SEQUENCE: 127

gcgagagaga ggattactat gattcgggga gttaccctct actattactc ctacggatcg 60
gacgtc 66

<210> SEQ ID NO 128
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<400> SEQUENCE: 128

Ala Arg Glu Arg Ile Thr Met Ile Arg Gly Val Thr Leu Tyr Tyr Tyr
1 5 10 15

Ser Tyr Gly Met Asp Val
20

<210> SEQ ID NO 129
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<400> SEQUENCE: 129

gacatccaga tgacccagtc tccatcccttc ctgtctgcat ctgttaggaga cagagtcacc 60
atcacttgct gggccagtca ggacattagc agttattnag cctggatca gcaaaaacca 120
gggatagcccc ctaagtcctt gatctatgct gcatccactt tgcaaagtgg ggtcccatca 180

-continued

aggttcgccg	gcagtggatc	tggacagaa	ttcactctca	caatcagca	cctgcagcct	240
gaagattttg	caaccttatta	ctgtcaacag	cttaatagtt	accctcgac	gttcggccaa	300
gggaccaagg	tggaaatcaa	acga				324

<210> SEQ ID NO 130
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 130

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Phe	Leu	Ser	Ala	Ser	Val	Gly
1															15

Asp	Arg	Val	Thr	Ile	Thr	Cys	Trp	Ala	Ser	Gln	Asp	Ile	Ser	Ser	Tyr
	20														30

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

Tyr	Ala	Ala	Ser	Thr	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Gly	Gly
	50														60

Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
	65				70										80

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

Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg				
					100										105

<210> SEQ ID NO 131
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 131

caggacatta	gcagttat	18
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<210> SEQ ID NO 132
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 132

Gln	Asp	Ile	Ser	Ser	Tyr	5
1						

<210> SEQ ID NO 133
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 133

gctgcatcc	9
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<210> SEQ ID NO 134
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 134

Ala Ala Ser
1

<210> SEQ ID NO 135
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 135

caacagctta atagttaccc tcggacg

27

<210> SEQ ID NO 136
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 136

Gln Gln Leu Asn Ser Tyr Pro Arg Thr
1 5

<210> SEQ ID NO 137
<211> LENGTH: 384
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 137

cagggtgcagc	tgcaggagtc	ggggccagga	ctggtaago	cttcggagac	cctgtccctc	60
acctgcactg	tctctgggaa	ctccatcaat	acttactact	ggagctggtt	ccggcageccc	120
ccagggaaagg	gactggagtg	gattgggtat	atctattata	gtgaaaccac	caactacaac	180
ccctccctca	agagtcgagt	caccatatca	atagacacgc	ccaggaacca	gttctccctg	240
aagctgatct	ctgtgaccgc	agcggacacg	gccgtgtatt	actgtgcgag	agagaggatt	300
actatgattc	ggggagttac	cctctactat	tactcctacg	gtatggacgt	ctggggccaa	360
gggaccacgg	tcaccgtctc	ctca				384

<210> SEQ ID NO 138
<211> LENGTH: 128
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 138

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

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

Tyr Trp Ser Trp Phe Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Thr Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Ile Asp Thr Pro Arg Asn Gln Phe Ser Leu

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65	70	75	80
----	----	----	----

Lys Leu Ile Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala			
85	90	95	

Arg Glu Arg Ile Thr Met Ile Arg Gly Val Thr Leu Tyr Tyr Tyr Ser			
100	105	110	

Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser			
115	120	125	

<210> SEQ ID NO 139

<211> LENGTH: 321

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 139

gacatccaga tgacccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc	60
atcacttgct gggccagtca ggacattagc agttattttag cctggtatca gcaaaaacca	120
gggatagccc ctaagtcct gatctatgct gcatccactt tgcaaagtgg ggtcccatca	180
aggttcggcg gcagtggatc tgggacagaa ttcaactcta caatcagcag cctgcagcct	240
gaagatttg caacttatta ctgtcaacag cttaatagtt accctcggac gtteggcaa	300
gggaccaagg tggaaatcaa a	321

<210> SEQ ID NO 140

<211> LENGTH: 107

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 140

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

Asp Arg Val Thr Ile Thr Cys Trp Ala Ser Gln Asp Ile Ser Ser Tyr			
20	25	30	

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

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Gly 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 Gln Gln Leu Asn Ser Tyr Pro Arg			
85	90	95	

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys			
100	105		

<210> SEQ ID NO 141

<211> LENGTH: 384

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 141

caggtgcagc tgcaggagtc gggcccgagga ctgggtgaagc cttcggagac cctgtccctc	60
acctgcactg tctctgggaa ctccatcaat acttactact ggagctggat ccggcagccc	120
ccagggaaagg gactggagtg gattgggtat atctattata gtggaaccac caactacaac	180

-continued

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 Gln Gln Leu Asn Ser Tyr Pro Arg
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> SEQ ID NO 145

<211> LENGTH: 378

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 145

```
caggtgcagc tgggtcagtc tggagctgag gtgaagaagc ctggggccctc agtgaaggtc      60
tcctgcaagg cttctggta caccttacc aactatggta tcagctgggt ggcacaggcc      120
cctggacaag gacttgagtt aatgggatgg attagtgggt acaatggtaa cacaaactat      180
gcacaagaac tccaggccag agtcaccatg accacagaca catccacgag cacagcctac      240
atggagctga ggaacctgag atctgacgac acggccgtat attactgtgc gagagataga      300
gtcgttgttag cagctgctaa ttactacttt tattctatgg acgtctgggg ccaagggacc      360
acggtcaccg ttcctcta                                         378
```

<210> SEQ ID NO 146

<211> LENGTH: 126

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 146

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

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

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

Gly Trp Ile Ser Gly Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Glu Leu
 50           55           60

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

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

Ala Arg Asp Arg Val Val Ala Ala Asn Tyr Tyr Phe Tyr Ser
 100          105          110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115          120          125
```

<210> SEQ ID NO 147

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

-continued

<400> SEQUENCE: 147

ggttacacct ttaccaacta tggt

24

<210> SEQ ID NO 148

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 148

Gly Tyr Thr Phe Thr Asn Tyr Gly
1 5

<210> SEQ ID NO 149

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 149

attagtggtt acaatggtaa caca

24

<210> SEQ ID NO 150

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 150

Ile Ser Gly Tyr Asn Gly Asn Thr
1 5

<210> SEQ ID NO 151

<211> LENGTH: 57

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 151

gcgagagata gagtcgttgt agcagctgct aattactact tttattctat ggacgtc

57

<210> SEQ ID NO 152

<211> LENGTH: 19

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 152

Ala Arg Asp Arg Val Val Val Ala Ala Ala Asn Tyr Tyr Phe Tyr Ser
1 5 10 15

Met Asp Val

<210> SEQ ID NO 153

<211> LENGTH: 339

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 153

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gccatccaga tgacccagtc tccactctcc ctgtccgtca cccttggaca gccggcctcc	60
atctcctgca ggtctagtca aagcctcgta tacagtgtatc gagacaccta cttgaatttg	120
tttcagcaga ggccaggcca atctccaagg cgccataattt ataagggttc taaccggac	180
tctgggtcc cagacagatt cagccgcgtt gggtcaggca ctgcttcac actgaaaatc	240
agcgggggtgg aggccgagga tgttgggtt tactactgca tgcaagctac acactggcct	300
cggaacgttcg gccaaggac caaggtggaa atcaaacga	339

<210> SEQ ID NO 154

<211> LENGTH: 113

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 154

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

Arg

<210> SEQ ID NO 155

<211> LENGTH: 33

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 155

caaaggctcg tatacagtga tggagacacc tac	33
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<210> SEQ ID NO 156

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 156

Gln Ser Leu Val Tyr Ser Asp Gly Asp Thr Tyr		
1	5	10

<210> SEQ ID NO 157

<211> LENGTH: 9

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 157

-continued

aaggttct

9

<210> SEQ ID NO 158
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 158

Lys Val Ser
1

<210> SEQ ID NO 159
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 159

atgcaagcta cacactggcc tcggacg

27

<210> SEQ ID NO 160
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 160

Met Gln Ala Thr His Trp Pro Arg Thr
1 5

<210> SEQ ID NO 161
<211> LENGTH: 378
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 161

caggttcagc tgggtcgagtc tggagctgag gtgaagaago ctggggcctc agtgaaggtc	60
tcctgcaagg cttctgggta caccttacc aactatggta tcagctgggt gcgcacaggcc	120
cctggacaag gacttgagtt aatgggatgg attagtgggt acaatggtaa cacaactat	180
gcacaagaac tccaggccag agtcaccatg accacagaca catccacggg cacagcctac	240
atggagctga ggaacctgag atctgacgac acggccgtat attactgtgc gagagataga	300
gtcggttag cagctgctaa ttactacttt tattctatgg acgtctgggg ccaaggacc	360
acggtcaccg ttcctccat	378

<210> SEQ ID NO 162
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 162

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

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

-continued

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

Gly Trp Ile Ser Gly Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Glu Leu
 50 55 60

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

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

Ala Arg Asp Arg Val Val Ala Ala Ala Asn Tyr Tyr Phe Tyr Ser
 100 105 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> SEQ ID NO 163

<211> LENGTH: 336

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 163

gatgttgtga tgactcagtc tccactctcc ctgtccgtca cccttggaca gccggcctcc 60
 atctcctgca ggtctagtca aagcctcgta tacagtgtatg gagacaccta cttgaattgg 120
 ttcagcaga ggcaggcca atctccaagg cgccataattt ataagggttc taaccggac 180
 tctggggtcc cagacagatt cageggcagt gggtcaggca ctgcattcac actgaaaatc 240
 agcggggtgg aggccgagga tgggggttt tactactgca tgcaagctac acactggct 300
 cggacgttcg gccaaggggac caaggtggaa atcaa 336

<210> SEQ ID NO 164

<211> LENGTH: 112

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 164

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser
 20 25 30

Asp Gly Asp Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
 35 40 45

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

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

Ser Gly Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
 85 90 95

Thr His Trp Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105 110

<210> SEQ ID NO 165

<211> LENGTH: 378

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 165

-continued

caggttcagc tggtgagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc	60
tcctgcaagg cttctggta caccttacc aactatggta tcagctgggt gcgcacaggcc	120
cctggacaag ggcttgagt gatggatgg attagtggta acaatggtaa cacaactat	180
gcacagaagc tccaggcagc agtcaccatg accacagaca catccacgag cacagcctac	240
atggagctga ggagcctgag atctgacgac acggccgtgtt attactgtgc gagagataga	300
gtcgtagtgc cagctgctaa ttactacttt tattctatgg acgtctgggg ccaaggacc	360
acggtcaccg ttcctca	378

<210> SEQ ID NO 166
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 166

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala	
1 5 10 15	
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr	
20 25 30	
Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met	
35 40 45	
Gly Trp Ile Ser Gly Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu	
50 55 60	
Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr	
65 70 75 80	
Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
Ala Arg Asp Arg Val Val Ala Ala Asn Tyr Tyr Phe Tyr Ser	
100 105 110	
Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser	
115 120 125	

<210> SEQ ID NO 167
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 167

gatgttgta tgactcagtc tccactctcc ctgccccgtca cccttggaca gccggcctcc	60
atctcctgca ggtctagtca aagcctcgta tacagtgtatc gagacaccta cttgaattgg	120
tttcagcaga ggccaggcca atctccaagg cgccataattt ataaggtttc taaccggac	180
tctggggtcc cagacagatt cageggcagt gggtcaggca ctgatccac actgaaaatc	240
agcagggtgg aggctgagga tgggggtt tattactgca tgcaagctac acactggcct	300
cggacgttcg gccaaggggac caagggtggaa atcaaa	336

<210> SEQ ID NO 168
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 168

-continued

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser
 20 25 30

Asp Gly Asp Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
 35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Arg Asp 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

Thr His Trp Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105 110

<210> SEQ ID NO 169

<211> LENGTH: 375

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 169

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cagggtccact tgaaggagtc tgggtcctacg ctgggtgaaac ccacacagac cctcacgctg     60
acctgcacct tctctggatt ctcactcatc actagtggag tgggtgtggg ctggatcg     120
cagccccccg gaaaggccct ggagtggctt gcactcattt attggatgg tgataagcgc     180
tacagcccat ctctgaagag caggctcacc atcaccaagg acacctccaa aaaccaggtg     240
gtccttacaa tgaccaacat ggaccctgtg gacacagcca catattactg tgcacacagg     300
ataactgaaa ctatgttacta cttctactac ggtatggacg tctggggcca agggaccacg     360
gtcacccgtct cctca                                                                    375
```

<210> SEQ ID NO 170

<211> LENGTH: 125

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 170

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ile Thr Ser
 20 25 30

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

Trp Leu Ala Leu Ile Tyr Trp Asn Gly Asp Lys Arg Tyr Ser Pro Ser
 50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
 85 90 95

Cys Ala His Arg Ile Thr Glu Thr Ser Tyr Tyr Phe Tyr Tyr Gly Met
 100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

-continued

<210> SEQ ID NO 171
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 171

ggattctcac tcatcactag tggagtgggt

30

<210> SEQ ID NO 172
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 172

Gly Phe Ser Leu Ile Thr Ser Gly Val Gly
1 5 10

<210> SEQ ID NO 173
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 173

atttatttggaa atgggtataa g

21

<210> SEQ ID NO 174
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 174

Ile Tyr Trp Asn Gly Asp Lys
1 5

<210> SEQ ID NO 175
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 175

gcacacagga taactgaaac tagttactac ttctactacg gtatggacgt c

51

<210> SEQ ID NO 176
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 176

Ala His Arg Ile Thr Glu Thr Ser Tyr Tyr Phe Tyr Tyr Gly Met Asp
1 5 10 15

Val

<210> SEQ ID NO 177
<211> LENGTH: 339

-continued

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 177

```

gacatccaga tgacccagtc tccactctcc ctgcccgtca cccctggaga gccggcctcc      60
atcttctgca ggtcttagtca gagecctcctg catagtcatg gatacgacta tttggattgg      120
tacctgcaga agccaggggca gtctccacag ctccatgtatct atttgggttc taatcgggcc      180
tccgggggtcc ctgacagggtt cagtggcagt ggatcaggca cagatttac actgaaaatc      240
agcagagtgaa aggctgagga tgttgggtt tattactgca tgcaagctct acaaaactccg      300
ctcaatttcg gcggaggggac caagggtggaa atcaaacgaa                                339

```

<210> SEQ ID NO 178
<211> LENGTH: 113
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 178

```

Asp Ile Gln 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 His Ser
 20          25           30

His Gly Tyr Asp 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 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 Leu Thr Phe Gly Gly Thr Lys Val Glu Ile Lys
100         105          110

Arg

```

<210> SEQ ID NO 179
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 179

```

cagagcctcc tgcatagtca tggatacgac tat                                33

```

<210> SEQ ID NO 180
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 180

```

Gln Ser Leu Leu His Ser His Gly Tyr Asp Tyr
 1           5           10

```

<210> SEQ ID NO 181
<211> LENGTH: 9

-continued

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 181

ttgggttct

9

<210> SEQ ID NO 182
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 182

Leu Gly Ser
1

<210> SEQ ID NO 183
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 183

atgcgaagctc tacaaaactcc gctcaact

27

<210> SEQ ID NO 184
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 184

Met Gln Ala Leu Gln Thr Pro Leu Thr
1 5

<210> SEQ ID NO 185
<211> LENGTH: 375
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 185

cagatcacct tgaaggagtc tggcctacg ctgggtaaac ccacacagac cctcacgtcg 60
acctgcaccc tctctggatt ctcactcatc actagtggag tgggtgtggg ctggattcg 120
cagccccccg gaaaggccct ggagtggatt gcactcattt attggaatgg tgataagcgc 180
tacagcccat ctctgaagag caggctcacc atcaccaagg acacctccaa aaaccagg 240
gtccttacaa tgaccaacat ggacctgtg gacacagcca catattactg tgcacacagg 300
ataactgaaa cttagttacta cttctactac ggttatggacg tctggggcca agggaccacg 360
gtcaccgtct cctca 375

<210> SEQ ID NO 186
<211> LENGTH: 125
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 186

-continued

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ile Thr Ser
 20 25 30

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

Trp Leu Ala Leu Ile Tyr Trp Asn Gly Asp Lys Arg Tyr Ser Pro Ser
 50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
 85 90 95

Cys Ala His Arg Ile Thr Glu Thr Ser Tyr Tyr Phe Tyr Gly Met
 100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> SEQ ID NO 187

<211> LENGTH: 336

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 187

```

gatattgtga tgactcagtc tccactctcc ctgccccgtca cccctggaga gccggcctcc     60
atctccttgca ggtctagtca gagectccctg catagtcatg gatacgacta tttggattgg   120
tacctgcaga agccaggggca gtctccacag ctcctgatct atttgggttc taatcgggccc   180
tccgggggtcc ctgacaggtt cagtggcagt ggatcaggca cagatttac actgaaaatc   240
agcagagtggtt aggctgagga tttttttttt tattactgca tgcaagctct acaaactccg   300
ctcaactttcg gcggaggggac caagggtggag atcaaaa                           336

```

<210> SEQ ID NO 188

<211> LENGTH: 112

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 188

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 His Ser
 20 25 30

His Gly Tyr Asp 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 Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105 110

<210> SEQ ID NO 189

-continued

```
<211> LENGTH: 375
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 189

cagatcacct tgaaggagtc tggtcctacg ctgggtaaac ccacacagac cctcacgctg 60
acctgcacct tctctggatt ctcactcatc actagtggag tgggtgtggg ctggatccgt 120
cagccccca gaaaggccct ggagtggtt gcactcattt attggaatgg tgataagcgc 180
tacagcccat ctctgaagag caggctcacc atcaccaagg acacaccttcaa aaaccaggtg 240
gtccttacaa tgacccaat ggaccctgtg gacacagcca catattactg tgcacacagg 300
ataactgaaa ctagttacta cttctactac ggtatggacg tctggggcca agggaccacg 360
gtcacccgtct cctca 375
```

```

<210> SEQ ID NO 190
<211> LENGTH: 125
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 190

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ile Thr Ser
20          25          30

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

Trp Leu Ala Leu Ile Tyr Trp Asn Gly Asp Lys Arg Tyr Ser Pro Ser
50          55          60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val
65          70          75          80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85          90          95

Cys Ala His Arg Ile Thr Glu Thr Ser Tyr Tyr Phe Tyr Tyr Gly Met
100         105         110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115         120         125

```

```
<210> SEQ ID NO 191
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 191

gatattgtga tgactctagtc tccactctcc ctgcggcgta cccctggaga gccggcctcc 60
atctcctgcga ggtcttagtca gagcctcctgtc catatgtatgc gatacgtacta ttggatgg 120
tacacctgcaga agccaggggca gtctccacag ctccgtatct atttgggttc taatcgggcc 180
tccgggggttc ctgacagagtt cagtggcagt ggatcaggca cagatttac actgaaaatc 240
agcagagtggtgg aggctgagga ttttttttttattactgca tgcaagctct acaaactccg 300
ctcaacttttca gggggggggaaac caaagggtggag atcaaa 336
```

<210> SEQ ID NO 192

-continued

<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 192

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

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

His Gly Tyr Asp 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 Leu Thr Phe Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> SEQ ID NO 193
<211> LENGTH: 375
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 193

cagatcacct	tgaaggagtc	tggcctact	ctgggtgaaac	cctcacagac	cctcacgctg	60
acctgcaccc	tctctgggtt	ctcaactcagc	actagtggag	tgggtgtggg	ctggatccgt	120
cagccccccag	gaaaggccct	ggagtggttt	gcactcattt	atttggaaattt	tgataagcgc	180
tacagcccat	ctctgaagag	caggctcacc	atcaccaagg	acacctccaa	aaaccaggta	240
gtccttacaa	tgaccaacat	ggaccctgtg	gacacagcca	catattactg	tgcacacaga	300
catgacagct	cgtcctacta	cttctactac	ggtatggacg	tctggggcca	agggatcact	360
gtcaccgtct	cctca					375

<210> SEQ ID NO 194
<211> LENGTH: 125
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 194

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

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

Trp Leu Ala Leu Ile Tyr Trp Asn Ser Asp Lys Arg Tyr Ser Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

-continued

Cys Ala His Arg His Asp Ser Ser Ser Tyr Tyr Phe Tyr Tyr Gly Met
 100 105 110

Asp Val Trp Gly Gln Gly Ile Thr Val Thr Val Ser Ser
 115 120 125

<210> SEQ ID NO 195
 <211> LENGTH: 30
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 195

gggttctcac tcagcactag tggagtggtt 30

<210> SEQ ID NO 196
 <211> LENGTH: 10
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 196

Gly Phe Ser Leu Ser Thr Ser Gly Val Gly
 1 5 10

<210> SEQ ID NO 197
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 197

atttatttggaa attctgataaa g 21

<210> SEQ ID NO 198
 <211> LENGTH: 7
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 198

Ile Tyr Trp Asn Ser Asp Lys
 1 5

<210> SEQ ID NO 199
 <211> LENGTH: 51
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 199

gcacacagac atgacagctc gtcctactac ttctactacg gtatggacgt c 51

<210> SEQ ID NO 200
 <211> LENGTH: 17
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 200

Ala His Arg His Asp Ser Ser Ser Tyr Tyr Phe Tyr Tyr Gly Met Asp

-continued

1	5	10	15
---	---	----	----

Val

```

<210> SEQ ID NO 201
<211> LENGTH: 339
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 201

gacatccaga tgacccagtc tccgctctcc ctggccgtca cccctggaga gccggcctcc      60
atctcctgca ggtcttagtca gagcctcctc catagtcatg gataacaacta tttggattgg      120
tacctgcaga agccaggggca gtctccacaa ctcctgatct atttgggttc taatcgggcc      180
tccggggtcc ctgacaggtt cagtggcggt ggatcaggca cagattttac actgaaaatc      240
agcagagtgg aggctgagga tggttggatt tattactgca tgcaagctct acagactcct      300
ctcactttcg gcggagggac caaggtggag atcaaacga                         339

```

```

<210> SEQ ID NO 202
<211> LENGTH: 113
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 202

Asp Ile Gln 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 His Ser
 20          25           30

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

Pro Gln Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
 50          55           60

Asp Arg Phe Ser Gly 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 Leu Thr Phe Gly Gly Thr Lys Val Glu Ile Lys
100         105          110

Arg

```

```

<210> SEQ ID NO 203
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 203

cagagcctcc tccatagtc tggataacaac tat                         33

<210> SEQ ID NO 204
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 204

```

-continued

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

```
<210> SEQ ID NO 205
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

<400> SEQUENCE: 205

6

```
<210> SEQ ID NO 206
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

<400> SEQUENCE: 206

Leu Gly Ser
1

```
<210> SEQ ID NO 207
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

<400> SEQUENCE: 207

atgcaagctc tacagactcc tctcact

27

```
<210> SEQ ID NO 208
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

<400> SEQUENCE: 208

Met Gln Ala Leu Gln Thr Pro Leu Thr
1 5

```
<210> SEQ ID NO 209
<211> LENGTH: 375
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

<400> SEQUENCE: 209

cagatcacacct tgaaggagtc tggtcctact ctgggtgaaac cctcacagac cctcacgctg 60

acctgcaccc tctctgggtt ctcactcagc actagtggag tgggtgtggg ctggatccgt 120

cagcccccaag gaaaggccct ggagtggctt gcactcattt attggaattc tgataagcgc 180

tacagccccat ctctgaagag caggctcacc atcaccaagg acacctccaa aaaccaggtt 240

gtccttacaa tgaccaacat ggaccctgtg gacacagcca catattactg tgcacacaga 300

catgacagct cgtcctacta cttctactac ggtatggacg tctggggcca agggaccacg 360

gtcaccgtct cctca 375

<210> SEQ ID NO 210

-continued

<211> LENGTH: 125
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 210

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

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

Trp Leu Ala Leu Ile Tyr Trp Asn Ser Asp Lys Arg Tyr Ser Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala His Arg His Asp Ser Ser Ser Tyr Tyr Phe Tyr Tyr Gly Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> SEQ ID NO 211
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 211

gatattgtga	tgactcagtc	tccgctctcc	ctgccccgtca	cccctggaga	gccggcctcc	60
atctcctgca	ggtctagtca	gagccctcctc	catagtcatg	gataacaacta	tttggattgg	120
tacctgcaga	agccaggggca	gtctccacaa	ctcctgatct	atttgggttc	taatcgggccc	180
tccgggggtcc	ctgacaggtt	cagtggcggt	ggatcaggca	cagattttac	actgaaaatc	240
agcagagtgg	aggctgagga	tgttgggatt	tattactgca	tgcaagctct	acagactcct	300
ctcactttcg	gcggaggggac	caagggtggag	atcaaa			336

<210> SEQ ID NO 212
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 212

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 His Ser
20 25 30

His 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 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

-continued

85

90

95

Leu Gln Thr Pro Leu Thr Phe Gly Gly Thr Lys Val Glu Ile Lys
 100 105 110

<210> SEQ ID NO 213
 <211> LENGTH: 375
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 213

cagatcacct tgaaggagtc tggcctacg ctgggtgaaac ccacacagac cctcacgctg	60
acacctgcacct tctctgggtt ctcactcagc actagtggag tgggtgtggg ctggatccgt	120
cagccccccag gaaaggccct ggagtggattt gcactcattt atttggaaattt tgataagcg	180
tacagcccat ctctgaagag caggctcacc atcacaagg acacactccaa aaaccaggta	240
gtccttacaa tgaccaacat ggaccctgtg gacacagcca catattactg tgcacacaga	300
catgacagct cgtcctacta cttctactac ggtatggacg tctggggcca agggaccacg	360
gtcacccgtct cctca	375

<210> SEQ ID NO 214
 <211> LENGTH: 125
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 214

Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln	
1 5 10 15	
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser	
20 25 30	
Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu	
35 40 45	
Trp Leu Ala Leu Ile Tyr Trp Asn Ser Asp Lys Arg Tyr Ser Pro Ser	
50 55 60	
Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val	
65 70 75 80	
Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr	
85 90 95	
Cys Ala His Arg His Asp Ser Ser Ser Tyr Tyr Phe Tyr Tyr Gly Met	
100 105 110	
Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser	
115 120 125	

<210> SEQ ID NO 215
 <211> LENGTH: 336
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 215

gatattgtga tgactcagtc tccactctcc ctgcccgtca cccctggaga gccggccctcc	60
atctcttgca ggtctagtca gagecttcctc catagtcatg gataacaactt tttggattgg	120
tacctgcaga agccaggcgtca gtctccacag ctcctgtatct atttgggttc taatcgggcc	180
tccggggtcc ctgacaggtt cagtgccagt ggatcaggca cagatttac actgaaaatc	240

-continued

```
agcagagtgg aggctgagga tttttgggtt tattactgca tgcaagctct acagactcct      300
ctcacttcg cgccggggac caagggtggag atcaaaa                           336
```

<210> SEQ ID NO 216
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 216

```
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 His Ser
 20          25          30
```

```
His 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 Leu Thr Phe Gly Gly Thr Lys Val Glu Ile Lys
100         105         110
```

<210> SEQ ID NO 217
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 217

```
gagatgcaac tggtgaggc ttggggaggc ttgggtccago ctggggggtc cctgagactc      60
tcctgtgcag cctctggatt caccttagt agtcactgga tgaagtgggt ccgccaggct    120
ccagggagg ggctggagtg ggtggccaac ataaaccaag atggaagtga gaaatactat    180
gtggactctg tgaaggcccg attcaccatc tccagagaca acgccaagaa ctcactgttt    240
ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagatatt    300
gtactaatgg tctatgatat ggactactac tactacggta tggacgtctg gggccaaggg    360
accacggta ccgtctcctc a                                         381
```

<210> SEQ ID NO 218
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 218

```
Glu Met Gln Leu Val Glu Ser 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 His
 20          25          30
```

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

```
Ala Asn Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
```

-continued

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 Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Ile Val Leu Met Val Tyr Asp Met Asp Tyr Tyr Tyr Tyr
 100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> SEQ ID NO 219
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 219

ggattcacct ttagtagtca ctgg 24

<210> SEQ ID NO 220
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 220

Gly Phe Thr Phe Ser Ser His Trp
 1 5

<210> SEQ ID NO 221
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 221

ataaaccaag atggaagtga gaaa 24

<210> SEQ ID NO 222
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 222

Ile Asn Gln Asp Gly Ser Glu Lys
 1 5

<210> SEQ ID NO 223
 <211> LENGTH: 60
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 223

gcgagagata ttgtactaat ggtctatgtat atggactact actactacgg tatggacgtc 60

<210> SEQ ID NO 224
 <211> LENGTH: 20
 <212> TYPE: PRT

-continued

<213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 224

Ala	Arg	Asp	Ile	Val	Leu	Met	Val	Tyr	Asp	Met	Asp	Tyr	Tyr	Tyr	Tyr
1				5			10			15					

Gly	Met	Asp	Val
		20	

<210> SEQ ID NO 225
 <211> LENGTH: 336
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 225

gatattgtga	tgactcagtc	tccactctcc	ctggccgtca	ccccctggaga	gccgggcctcc	60
atctcctgca	ggtctagtca	gagccctcctg	catacataatg	gaaacaacta	tttggattgg	120
tacctgcaga	agccaggggca	gtctccacag	ctcctgatct	atttgggttc	taatcgggccc	180
tccgggggtcc	ctgacagggtt	cagtggcagt	ggatcaggca	caagatttac	actgaaaatc	240
agcagagtg	aggctgagga	tgttgggtt	tattactgca	tgcaaactct	acaaaactccg	300
ctcactttcg	gcccggggac	caagggtggag	atcaaaa			336

<210> SEQ ID NO 226
 <211> LENGTH: 112
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 226

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	His	Ser
				20			25			30					

Asn	Gly	Asn	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	Thr
				85			90			95					

Leu	Gln	Thr	Pro	Leu	Thr	Phe	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys
				100			105			110				

<210> SEQ ID NO 227
 <211> LENGTH: 33
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 227

cagagcctcc	tgcatagtaa	tggaaacaac	tat
------------	------------	------------	-----

33

<210> SEQ ID NO 228
 <211> LENGTH: 11

-continued

<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 228

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

<210> SEQ ID NO 229
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 229

ttgggttct

9

<210> SEQ ID NO 230
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 230

Leu Gly Ser
1

<210> SEQ ID NO 231
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 231

atgcaaactc tacaaaactcc gctca

27

<210> SEQ ID NO 232
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 232

Met Gln Thr Leu Gln Thr Pro Leu Thr
1 5

<210> SEQ ID NO 233
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 233

gaggtgcagc tggtgaggc tgggggaggc ttgggtccago ctggggggtc cctgagactc 60
tcctgtgcag cctctggatt caccttagt agtcaactgga tgaagtgggt ccggcaggct 120
ccagggagg ggctggagtg ggtggccaac ataaaccaag atggaagtga gaaatactat 180
gtggactctg tgaaggcccg attcaccatc tccagagaca acgccaaagaa ctcactgttt 240
ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagatatt 300

-continued

gtactaatgg tctatgatat ggactactac tactacggta tggacgtctg gggccaagggg	360
accacggtca ccgtctcctc a	381

<210> SEQ ID NO 234
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 234

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 His			
20	25	30	
Trp Met Lys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val			
35	40	45	
Ala Asn Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val 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 Val Tyr Tyr Cys			
85	90	95	
Ala Arg Asp Ile Val Leu Met Val Tyr Asp Met Asp Tyr Tyr Tyr Tyr			
100	105	110	
Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser			
115	120	125	

<210> SEQ ID NO 235
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 235

gatattgtga tgactcagtc tccactctcc ctgcccgtca cccctggaga gccggcctcc	60
atctcctgca ggtctagtca gagcctcctg catagtaatg gaaacaacta tttggattgg	120
tacctgcaga agccaggcga gtctccacag ctcctgatct atttgggttc taatcgggccc	180
tccggggtcc ctgacagggtt cagtgccagt ggatcaggca cagattttac actgaaaatc	240
agcagagtggtt aggctgagga tgttgggtt tattactgca tgcaaactct acaaaactccg	300
ctcaacttccg gcggagggac caaggtggag atcaaa	336

<210> SEQ ID NO 236
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 236

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 His Ser			
20	25	30	
Asn Gly Asn 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			

-continued

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 Thr
 85 90 95

Leu Gln Thr Pro Leu Thr Phe Gly Gly Thr Lys Val Glu Ile Lys
 100 105 110

<210> SEQ ID NO 237

<211> LENGTH: 381

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 237

```

gagggtcagc tgggtggagtc tgggggaggc ttgggtccagc ctggggggtc cctgagactc      60
tcctgtgcag cctctggatt cacctttagt agtcactgga tgagctgggt ccgccaggct      120
ccagggaaagg ggctggagtg ggtggccaac ataaaccaag atggaagtga gaaatactat      180
gtggactctg tgaaggcccg attcaccatc tccagagaca acgccaagaa ctcactgtat      240
ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagatatt      300
gtactaatgg tctatgatat ggactactac tactacggta tggacgtctg gggcaaggg      360
accacggtca ccgtctcctc a                                         381

```

<210> SEQ ID NO 238

<211> LENGTH: 127

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 238

Glu Val Gln Leu Val Glu Ser 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 His
 20 25 30

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

Ala Asn Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val 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 Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Ile Val Leu Met Val Tyr Asp Met Asp Tyr Tyr Tyr
 100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> SEQ ID NO 239

<211> LENGTH: 336

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 239

gatattgtga tgactcagtc tccactctcc ctgccccgtca cccctggaga gccggcctcc 60

-continued

atctcctgca ggtcttagtca gagcctcctg catagtaatg gaaaacaacta tttggattgg	120
tacctgcaga agccaggcga gtctccacag ctccctgatct atttgggttc taatcgcc	180
tccggggtcc ctgacagggtt cagtggcagt ggcgcaggca cagatttac actgaaaatc	240
agcagagtgg aggctgagga tggtgggtt tattactgca tgcaaactct acaaactccg	300
ctcaacttcg gcggaggagc caaggtggag atcaaa	336

<210> SEQ ID NO 240
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 240

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 His Ser			
20	25	30	
Asn Gly Asn 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 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 Thr			
85	90	95	
Leu Gln Thr Pro Leu Thr Phe Gly Gly Thr Lys Val Glu Ile Lys			
100	105	110	

<210> SEQ ID NO 241
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 241

caggtgcagc tgggtggagtc tgggggaggc gtggccago ctggggaggc cctgagactc	60
tcctgtgcag tctctggatt caccttcagt agctatggca tgcactgggt ccgcaggct	120
ccaggcaagg ggctggagtg ggtggcagct atatcatatg atggaaagtaa taaaactat	180
gtagactccg tgaaggcccg attcaccatc tccagagaca attccaagaa aacgctgtat	240
ctgcaaatga acagcctgag agctgaggac acggctgtgt ataattgtgc gaaaaatatt	300
gtactagtga tgtatgatat agactatcac tactatggta tggacgtctg gggccaagg	360
accacggta ccgtctccctc a	381

<210> SEQ ID NO 242
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 242

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

-continued

20

25

30

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

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

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

Ala Lys Asn Ile Val Leu Val Met Tyr Asp Ile Asp Tyr His Tyr Tyr
 100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> SEQ ID NO 243
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 243

ggattcacct tcagtagcta tggc 24

<210> SEQ ID NO 244
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 244

Gly Phe Thr Phe Ser Ser Tyr Gly
 1 5

<210> SEQ ID NO 245
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 245

atatcatatg atggaagtaa taaa 24

<210> SEQ ID NO 246
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 246

Ile Ser Tyr Asp Gly Ser Asn Lys
 1 5

<210> SEQ ID NO 247
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 247

165

166

-continued

gcgaaaaata ttgtactagt gatgtatgt atagactatc actactatgg gatggacgtc 60

```
<210> SEQ ID NO 248
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

<400> SEQUENCE: 248

Ala Lys Asn Ile Val Leu Val Met Tyr Asp Ile Asp Tyr His Tyr Tyr
1 5 10 15

Gly Met Asp Val
20

<210> SEQ ID NO 249

```
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

<400> SEQUENCE: 249

gatattgtga tgacttcggc tccactctcc ctggccgtca cccctggaga gccggccctcc	60
atctcctgca ggtcttagtca gagcctcctg catagtaaatg gataacaacta ttggattttgg	120
tacctgcaga agccaggggca gtctccacaaa ctccgtatct atttgggttt taatcgggcc	180
tccggggtcc ctgacagagtt cagtgccagt ggatcaggca cagattttac actgaaaatc	240
agcagagtggg aggctgagga tgttgggtt tattactgca tgcaagctct acaaactcct	300
ctcacatccq qcqqaqqqdca caaqqtggqaq atcaqa	336

<210> SEQ ID NO 250

```
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

<400> SEQUENCE: 250

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 His 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 Phe 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 Gin Ala
85 90 95

Leu Gln Thr Pro Leu Thr Phe Gly Gly Thr Lys Val Glu Ile Arg
100 105 110

<210> SEQ ID NO 251
<211> LENGTH: 33

<211> LENGTH: 33
<212> TYPE: DNA

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 351

-continued

cagaggctcc tgcatagtaa tggataacaac tat

33

<210> SEQ ID NO 252
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 252

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

<210> SEQ ID NO 253
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 253

ttggggtttt

9

<210> SEQ ID NO 254
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 254

Leu	Gly	Phe
1		

<210> SEQ ID NO 255
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 255

atgcagaactc tacaaaactcc tctcaact

27

<210> SEQ ID NO 256
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 256

Met	Gln	Ala	Leu	Gln	Thr	Pro	Leu	Thr
1				5				

<210> SEQ ID NO 257
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 257

caggtgcagc	tggtgagtc	tgggggaggc	gtgggtccago	ctgggaggtc	cctgagactc	60
tcctgtgcag	tctctggatt	caccttcagt	agcttatggca	tgcactgggt	ccgcaggct	120

-continued

ccaggcaagg ggctggagt ggtggcagct atatcatatg atgaaagtaa taaatactat	180
gttagactccg tgaagggccg attcaccatc tccagagaca attccaagaa aacgctgtat	240
ctgcaaatga acagcctgag agctgaggac acggctgtgt ataattgtgc gaaaaatatt	300
gtactagtga tgtatgatat agactatcac tactatggg tggacgtctg gggccaagg	360
accacggtca ccgtctcc tc a	381

<210> SEQ ID NO 258
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 258

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 Val 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 Ala Ile Ser 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 Lys Thr Leu Tyr	
65 70 75 80	
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Asn Cys	
85 90 95	
Ala Lys Asn Ile Val Leu Val Met Tyr Asp Ile Asp Tyr His Tyr Tyr	
100 105 110	
Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser	
115 120 125	

<210> SEQ ID NO 259
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 259

gatattgtga tgactcagtc tccactctcc ctgccccgtca cccctggaga gccggccctcc	60
atctcctgca ggtctagtca gagectcctg catactaactg gataacaacta tttggattgg	120
tacctgcaga agccagggca gtctccacaa ctcctgatct atttgggttt taatcgccc	180
tccggggtcc ctgacaggtt cagtgccagt ggatcaggca cagatttac actgaaaatc	240
agcagagtggtt aggctgagga tttttttttt tattactgca tgcaagctct acaaactct	300
ctcactttcg gcggagggac caaggtggag atcaaa	336

<210> SEQ ID NO 260
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 260

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 His Ser

-continued

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 Phe Asn Arg Ala Ser Gly Val Pro
 50 55 60

Asp Arg Phe 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 Leu Thr Phe Gly Gly Thr Lys Val Glu Ile Lys
 100 105 110

<210> SEQ ID NO 261

<211> LENGTH: 381

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 261

```
caggtgcagc tggtgaggc tgggggaggc gtgggtccago ctgggagggt cctgagactc 60
tcctgtgcag cctctggatt cacttcagt agctatggca tgcaactgggt ccgccaggct 120
ccaggcaagg ggctggaggc ggtggcagtt atatcatatg atgaaagttaaaaactat 180
gcagactccg tgaaggggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gaaaaatatt 300
gtactagtga tgtatgatat agactatcac tactatggta tggacgtctg gggcaagg 360
accacggtca ccgtctcctc a 381
```

<210> SEQ ID NO 262

<211> LENGTH: 127

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 262

Gln Val Gln Leu Val Glu Ser 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 Ser 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 Lys Asn Ile Val Leu Val Met Tyr Asp Ile Asp Tyr His Tyr Tyr
 100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> SEQ ID NO 263

<211> LENGTH: 336

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

-continued

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 263

gatattgtga tgactcagtc tccactctcc ctgcccgtca cccctggaga gccggcctcc	60
atctcttgca ggtcttagtca gagecttcgtc catactaactg gataacaacta tttggattgg	120
tacctgcaga agccaggggca gtctccacag ctcctgatct atttgggttt taatcgcc	180
tccggggtcc ctgacagggtt cagtggcagt ggatcaggca cagatttac actgaaaatc	240
agcagagtgaa aggctgagga tgttgggtt tattactgca tgcaagctct acaaactcct	300
ctcaacttcg gcggaggac caaggtggag atcaaa	336

<210> SEQ ID NO 264

<211> LENGTH: 112

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 264

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 His 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 Phe 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 Leu Thr Phe Gly Gly Thr Lys Val Glu Ile Lys			
100	105	110	

<210> SEQ ID NO 265

<211> LENGTH: 381

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 265

caggtgcagc tgggtggagtc tggggggagc gtgggtccago ctggggaggc cctgagactc	60
tcctgtgcag tctctggatt cacttcagt agctatggca tgcactgggt ccggccaggct	120
ccaggcaagg ggctggagtg ggtggcagct atatcatatg atggaagtaa taaaactat	180
gtagactccg tgaaggcccg attcaccatc tccagagaca attccaagaa aacgctgtat	240
ctgcaaattga acagcctgag agctgaggac acggctgtgt ataattgtgc gaaaaatatt	300
gtactagtga tgtatgatag actatcac tactatggc tggacgtctg gggccaagg	360
accacggta ccgtcttc a	381

<210> SEQ ID NO 266

<211> LENGTH: 127

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

-continued

<400> SEQUENCE: 266

```

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 Val 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 Ala Ile Ser 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 Lys Thr Leu Tyr
 65          70          75          80

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

Ala Lys Asn Ile Val Leu Val Met Tyr Asp Ile Asp Tyr His Tyr Tyr
100         105         110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115         120         125

```

<210> SEQ ID NO 267

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 267

ggattcacct tcagtagcta tggc

24

<210> SEQ ID NO 268

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 268

```

Gly Phe Thr Phe Ser Ser Tyr Gly
 1           5

```

<210> SEQ ID NO 269

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 269

atatcatatg atggaagtaa taaa

24

<210> SEQ ID NO 270

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 270

```

Ile Ser Tyr Asp Gly Ser Asn Lys
 1           5

```

<210> SEQ ID NO 271

<211> LENGTH: 60

<212> TYPE: DNA

-continued

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 271

gcgaaaaata ttgtactagt gatgtatgt atagactatc actactatgg gatggacgtc 60

<210> SEQ ID NO 272
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 272

Ala Lys Asn Ile Val Leu Val Met Tyr Asp Ile Asp Tyr His Tyr Tyr
1 5 10 15

Gly Met Asp Val
20

<210> SEQ ID NO 273
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 273

gatattgtga tgactcagtc tccactctcc ctgcccgtca cccctggaga gccggcctcc 60
atctcctgca ggtcttagtca gagecctcctg catactaatt qataacaacta tttggattgg 120
tacctgcaga agccagggca gtctccacaa ctcctgatct atttgggttt taatcgggcc 180
tccggggtcc ctgacagggtt cagtgccagt ggatcaggca cagattttac actgaaaatc 240
agcagagtgaa aggctgagga tgttgggtt tattactgca tgcaagctct acaaaactcct 300
ctcaacttcg gcggagggac caaggtggag atcaga 336

<210> SEQ ID NO 274
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 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 His 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 Phe 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 Leu Thr Phe Gly Gly Thr Lys Val Glu Ile Arg
100 105 110

<210> SEQ ID NO 275
<211> LENGTH: 33

-continued

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 275

cagagcctcc tgcatagtaa tggatacaac tat

33

<210> SEQ ID NO 276
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 276

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

<210> SEQ ID NO 277
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 277

ttgggtttt

9

<210> SEQ ID NO 278
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 278

Leu Gly Phe
1

<210> SEQ ID NO 279
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 279

atgcaagctc tacaaaactcc tctcact

27

<210> SEQ ID NO 280
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 280

Met Gln Ala Leu Gln Thr Pro Leu Thr
1 5

<210> SEQ ID NO 281
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

-continued

<400> SEQUENCE: 281

```
caggtgcagc tggtggagtc tgggggaggc gtgggtccago ctggggaggc cctgagactc      60
tcctgtgcag tctctggatt caccttcagt agctatggca tgcactgggt ccggccaggct     120
ccaggcaagg ggctggagtg ggtggcagct atatcatatg atgaaagttaaaaactat      180
gttagactccg tgaaggcccg attcaccatc tccagagaca attccaagaa aacgctgtat     240
ctgcaaataatga acagcctgag agctgaggac acggctgtgt ataattgtgc gaaaaatatt   300
gtactagtga tgtatgatat agactatcac tactatggta tggacgtctg gggccaaggg     360
accacggtca ccgtctcctc a                                              381
```

<210> SEQ ID NO 282

<211> LENGTH: 127

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 282

Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg
1														

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Val	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr
20															

Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
35															

Ala	Ala	Ile	Ser	Tyr	Asp	Gly	Ser	Asn	Lys	Tyr	Tyr	Val	Asp	Ser	Val
50															

Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Lys	Thr	Leu	Tyr
65															

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

Ala	Lys	Asn	Ile	Val	Leu	Val	Met	Tyr	Asp	Ile	Asp	Tyr	His	Tyr	Tyr
100															

Gly	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	
115															

<210> SEQ ID NO 283

<211> LENGTH: 336

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 283

```
gatatttgta tgactcagtc tccactctcc ctggccgtca cccctggaga gccggcctcc      60
atctcttgca ggtctagtca gagcctctcg catactaactt gataacaactt tttggattgg     120
tacctgcaga agccaggggca gtctccacaa ctcctgtatct atttgggttt taatcggggc     180
tccgggggtcc ctgacagggtt cagtgccagt ggatcaggca cagatttac actgaaaatc     240
agcagagtggtt aggctgagga tgttggggtt tattactgca tgcaagctct acaaaactcct   300
ctcactttcg gcggaggggac caaggtggag atcaaa                                              336
```

<210> SEQ ID NO 284

<211> LENGTH: 112

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

-continued

<400> SEQUENCE: 284

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

Glu	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Leu	His	Ser
								25						30	

Asn	Gly	Tyr	Asn	Tyr	Leu	Asp	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser
								40						45	

Pro	Gln	Leu	Leu	Ile	Tyr	Leu	Gly	Phe	Asn	Arg	Ala	Ser	Gly	Val	Pro
									55					60	

Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile
65									75					80	

Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys	Met	Gln	Ala
									90					95	

Leu	Gln	Thr	Pro	Leu	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys
									105					110	

<210> SEQ ID NO 285

<211> LENGTH: 381

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 285

caggtgcagc	tggtggagtc	tgggggaggc	gtgggtccagc	ctggggaggc	cctgagactc	60
tcctgtgcag	cctctggatt	caccttcagt	agctatggca	tgcactgggt	ccgccaggct	120
ccaggcaagg	ggctggagtg	ggtggcagtt	atatcatatg	atggaaagtaa	taataactat	180
gcagactccg	tgaaggggccg	attcaccatc	tccagagaca	attccaagaa	cacgctgtat	240
ctgcaaatga	acagcctgag	agctgaggac	acggctgtgt	attactgtgc	aaaaaatatt	300
gtactagtga	tgtatgatat	agactatcac	tactatggta	tggacgtctg	ggggcaagg	360
accacggtca	ccgtctccctc	a				381

<210> SEQ ID NO 286

<211> LENGTH: 127

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 286

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

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

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

Ala	Val	Ile	Ser	Tyr	Asp	Gly	Ser	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val
									50					60	

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

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

Ala	Lys	Asn	Ile	Val	Leu	Val	Met	Tyr	Asp	Ile	Asp	Tyr	His	Tyr	Tyr
									100					110	

Gly	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	
									115					125	

-continued

<210> SEQ ID NO 287
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 287

```

gatattgtga tgactcagtc tccactctcc ctgccccgtca cccctggaga gccggcctcc      60
atctcctgca ggtctagtca gagectcctg catagttaatg gataacaacta tttggattgg      120
tacctgcaga agccaggggca gtctccacag ctcctgatct atttggggtt taatcgcc          180
tccggggtcc ctgacagggtt cagtggcagt ggatcaggca cagatttac actgaaaatc      240
agcagagtgg aggctgagga ttttttttattactgca tgcaagctct acaaactcct      300
ctcacttccg gcggaggggac caagggtggag atcaaaa      336

```

<210> SEQ ID NO 288
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 288

```

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 His 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 Phe 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 Leu Thr Phe Gly Gly Thr Lys Val Glu Ile Lys
 100         105          110

```

<210> SEQ ID NO 289
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 289

```

cagatcacct tgaaggagtc tggtcctacg ctggtaaaac ccacacagac cctcacgctg      60
acctgcacct tctctgggtt ctcactcagc gctagtggag tgggtgtggg ctggttccgt      120
cagccccccag gaaaggccct ggagtggctt gcactcattt attggaatga tgataagcgt      180
tacagcccat ctctaaagaa cagccctacc atcacaagg acacctccaa aaaccaggtg      240
gtccttacaa tgaccaaactat ggaccctgtg gacacagca catattactg tgcacacaga      300
atacatctat ggtcctactt ctactacggt atggacgtct ggggccaagg gaccacggtc      360
accgtctccct ca      372

```

<210> SEQ ID NO 290

-continued

<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 290

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Ala Ser
20 25 30

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

Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
50 55 60

Leu Lys Asn Ser Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala His Arg Ile His Leu Trp Ser Tyr Phe Tyr Tyr Gly Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 291
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 291

gggttctcac tcagcgctag tggagtgggt 30

<210> SEQ ID NO 292
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 292

Gly Phe Ser Leu Ser Ala Ser Gly Val Gly
1 5 10

<210> SEQ ID NO 293
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 293

atttattgga atgatgataa g 21

<210> SEQ ID NO 294
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 294

Ile Tyr Trp Asn Asp Asp Lys

-continued

1 5

<210> SEQ ID NO 295
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 295

gcacacagaa tacatctatg gtcctacttc tactacggta tggacgtc 48

<210> SEQ ID NO 296
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 296

Ala His Arg Ile His Leu Trp Ser Tyr Phe Tyr Tyr Gly Met Asp Val
1 5 10 15

<210> SEQ ID NO 297
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 297

gatattgtga tgactcagtc tccactctcc ctgcccgtca cccctggaga gccggcctcc 60
atctcctgca ggtctagtca gactctcctg catagtaatg gataacaacta tttcgattgg 120
tacctgcaga agccaggggca gtctccacag ctcctgatct atttgggttc taatcgggcc 180
tccgggggtcc ctgacagatt cagtggcagt ggatcaggca cagattttac actgaaaatc 240
agcagagtg 300
aggctgagga tggttggatt tattactgca tgcaagctct acaaactct
ctcactttcg gcggaggac caaggtggag atcaga 336

<210> SEQ ID NO 298
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 298

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

-continued

<210> SEQ ID NO 299
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 299

cagactctcc tgcatagtaa tggatacaac tat

33

<210> SEQ ID NO 300
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 300

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

<210> SEQ ID NO 301
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 301

ttgggttct

9

<210> SEQ ID NO 302
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 302

Leu Gly Ser
1

<210> SEQ ID NO 303
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 303

atgcaagctc tacaaactcc tctcact

27

<210> SEQ ID NO 304
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 304

Met Gln Ala Leu Gln Thr Pro Leu Thr
1 5

<210> SEQ ID NO 305
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

-continued

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 305

cagatcacct tgaaggagtc tggcctacg ctggtaaaac ccacacagac cctcacgtg	60
acctgcacct tctctgggtt ctcactcagc gctagtggag tgggtgtggg ctggttccgt	120
cagccccca gaaaggccct ggagtggcatt gcactcattt attggaatga tgataagcgt	180
tacagcccat ctctaaagaa cagcctcacc atcaccaagg acacctccaa aaaccaggtg	240
gtccttacaa tgaccaacat ggaccctgtg gacacagcca catattactg tgcacacaga	300
atacatctat ggtcctactt ctactacggt atggacgtct gggccaagg gaccacggtc	360
accgtctccca	372

<210> SEQ ID NO 306

<211> LENGTH: 124

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 306

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

<210> SEQ ID NO 307

<211> LENGTH: 336

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 307

gatattgtga tgactcagtc tccactctcc ctgccgtca cccctggaga gccggcctcc	60
atctcctgca ggtctagtca gactctcctg catactaattgatacaactt ttctcgatttg	120
tacctgcaga agccaggcgtc gtctccacag ctcctgtatctt atttgggttc taatcgggccc	180
tccggggtcc ctgacagatt cagttggcagt ggatcaggca cagatttac actgaaaatc	240
agcagagtggttgg aggctgagga tggatggatttattactgca tgcaagctctt acaaactcctt	300
ctcactttcg gccggaggac caaggtggag atcaaa	336

<210> SEQ ID NO 308

<211> LENGTH: 112

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

-continued

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 308

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 Thr Leu Leu His Ser															
			20			25						30			
Asn Gly Tyr Asn Tyr Phe 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 Leu Thr Phe Gly Gly Thr Lys Val Glu Ile Lys															
			100			105						110			

<210> SEQ ID NO 309

<211> LENGTH: 372

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 309

cagatcacct	tgaaggagtc	tggcctacg	ctgggtgaaac	ccacacagac	cctcacgctg	60
acctgcacct	tctctgggtt	ctcaactcagc	gctagtgagg	tgggtgtggg	ctggatccgt	120
cagccccccag	gaaaggccct	ggagtggctt	gcactcattt	atttggaaatga	tgataagcgc	180
tacagcccat	ctctgaagag	caggttcacc	atcaccaagg	acacctccaa	aaaccagggt	240
gtccttacaa	tgaccaacat	ggaccctgtg	gacacagcca	catattactg	tgcacacaga	300
atacatctat	ggcctactt	ctactacggt	atggacgtct	gggggcaagg	gaccacggtc	360
accgtctcct	ca					372

<210> SEQ ID NO 310

<211> LENGTH: 124

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 310

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

-continued

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 311
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 311

gatattgtga tgactcagtc tccactctcc ctggccgtca cccctggaga gccggccctcc	60
atctcctgca ggtcttagtca gactctcctg catactaattgatacaacta tttggattgg	120
tacctgcaga agccaggcga gtctccacag ctcctgatct atttgggttc taatcgggcc	180
tccggggtcc ctgacaggtt cagtgccagt ggatcaggca cagatttac actgaaaatc	240
agcagagtgg aggctgagga tgggggtt tattactgca tgcaagtc acaaactcct	300
ctcaacttcg gcgaggagggac caaggtggag atcaaa	336

<210> SEQ ID NO 312
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 312

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 Thr Leu Leu His 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 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 Leu Thr Phe Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> SEQ ID NO 313
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 313

caggttcagtc tggtgcagtc tggacctgag gtgaagaacc ctggggctc agtgaaggtc	60
tcctgcaagg cttctggta caccttacc acctatggta tcagttgggt acgacaggcc	120
cctggacaag ggcttggatgt gatggggatgg atcagcggta aacaatggtaa aacaacgat	180
gcacagaagt tccaggacag agtcgcccatt accacagaca catccacgag cacagcctac	240
atggagctga ggagcctgag atctgacgac acggccattt attactgttc gagagatcg	300
ttagtagtac cacctgcct taattattcc tactacgtta tggacgtctg gggccaagg	360
accacggtaa ccgtctccctc a	381

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<210> SEQ ID NO 314
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 314

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

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

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

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

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

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

Ser	Arg	Asp	Arg	Leu	Val	Val	Pro	Pro	Ala	Leu	Asn	Tyr	Ser	Tyr	Tyr
	100				105										110

Val	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	
115				120											125

<210> SEQ ID NO 315
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 315

ggttacacctt ttaccaccta tggt

24

<210> SEQ ID NO 316
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 316

Gly	Tyr	Thr	Phe	Thr	Thr	Tyr	Gly
1			5				

<210> SEQ ID NO 317
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 317

atcagcggtt acaatggtaa aaca

24

<210> SEQ ID NO 318
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

-continued

<400> SEQUENCE: 318

```
Ile Ser Gly Tyr Asn Gly Lys Thr
 1           5
```

<210> SEQ ID NO 319

```
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

<400> SEQUENCE: 319

```
tcgagagatc gtttagtagt accacctgcc cttaattatt cctactacgt tatggacgtc      60
```

<210> SEQ ID NO 320

```
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

<400> SEQUENCE: 320

```
Ser Arg Asp Arg Leu Val Val Pro Pro Ala Leu Asn Tyr Ser Tyr Tyr
 1           5           10          15
```

Val Met Asp Val

20

<210> SEQ ID NO 321

```
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

<400> SEQUENCE: 321

```
gatgttgtga tgactcagtc tccactctcc ctgcccgtca cccttggaca gccggcctcc      60
atctcttgca ggtctagtca aagcctcgta tacagtgtatg gaaacaccta cttgaattgg     120
tctcagcaga gcccagggtca atctccaagg cgccataattt ataagggttc taaccgggac     180
tctggggtcc cagacagatt cageggcagt gggtcaggca ctgatttcac actgaaaatc     240
agcagggtgg aggctgagga tgggggtt tattactgca tgcaagggtac acactggccg     300
tacacttttg gccaggggac caagctggag atcaaa                           336
```

<210> SEQ ID NO 322

```
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

<400> SEQUENCE: 322

```
Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
 1           5           10          15
```

```
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser
 20          25           30
```

```
Asp Gly Asn Thr Tyr Leu Asn Trp Ser Gln Gln Arg Pro Gly Gln Ser
 35          40           45
```

```
Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Arg Asp 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
```

-continued

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

Thr His Trp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> SEQ ID NO 323
 <211> LENGTH: 33
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 323

caaaggctcg tatacagtga tggaaacacc tac 33

<210> SEQ ID NO 324
 <211> LENGTH: 11
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 324

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

<210> SEQ ID NO 325
 <211> LENGTH: 9
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 325

aaggtttct 9

<210> SEQ ID NO 326
 <211> LENGTH: 3
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 326

Lys Val Ser
 1

<210> SEQ ID NO 327
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 327

atgcaaggta cacactggcc gtacact 27

<210> SEQ ID NO 328
 <211> LENGTH: 9
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 328

Met Gln Gly Thr His Trp Pro Tyr Thr
 1 5

-continued

<210> SEQ ID NO 329
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 329

```
caggttcagc tgggtgcagtc tggacctgag gtgaagaacc ctggggcctc agtgaaggc 60
tcctgcaagg cttctggta caccttacc acctatggta tcagttgggt acgacaggcc 120
cctggacaag ggcttgagtg gatgggatgg atcagcggtt acaaatacgat 180
gcacagaagt tccaggacag agtgcgcatt accacagaca catccacgag cacagcctac 240
atggagctga ggagcctgag atctgacgac acggccattt attactgttc gagagatcg 300
tttagtagtac cacctgccct taattattcc tactacgtta tggacgtctg gggccaagg 360
accacggtca ccgtctccctc a 381
```

<210> SEQ ID NO 330
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 330

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

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

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

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

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

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

Ser	Arg	Asp	Arg	Leu	Val	Val	Pro	Pro	Ala	Leu	Asn	Tyr	Ser	Tyr	Tyr
	100			105					110						

Val	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	
	115				120					125					

<210> SEQ ID NO 331
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 331

```
gatgttgta tgactcagtc tccactctcc ctgccccgtca cccttggaca gcccggctcc 60
atctcctgca ggtctagtca aagcctcgta tacagtgtatc gaaacaccta cttgaattgg 120
tctcagcaga ggccagggtca atctccaagg cgccctaattt ataaggtttc taaccggac 180
tctggggtcc cagacagatt cageggcagt gggtcaggca ctgatccac actgaaaatc 240
agcagggtgg aggctgagga tgggggtt tattactgca tgcaaggatc acactggccg 300
tacacttttg gccaggggac caagctggag atcaaa 336
```

-continued

```

<210> SEQ ID NO 332
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 332

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser
20 25 30

Asp Gly Asn Thr Tyr Leu Asn Trp Ser Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Arg Asp 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 Gly
85 90 95

Thr His Trp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

```

```
<210> SEQ ID NO 333
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 333

caggttcagg tggtgcaagt tggagctgag gtgaagaaga ctggggcata agtgaaggta 60
tcctgcagg cttctggta cacccttacc acctatggta tcagctgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatggatgg atcagcggtt acaatggtaa aacaaactat 180
gcacagaago tccagggcag agtcaccatg accacagaca catccacgag cacagcctac 240
atggagctga ggagcctgag atctgacgac acggccgtgt attactgttc gagagatcgt 300
tttagtagtac cacctgcctt taattattcc tactacgtta tggacgtctg ggggcaagg 360
accacacgtca ccgttccctc a 381
```

```

<210> SEQ ID NO 334
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 334

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

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

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

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

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

```

-continued

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

Ser Arg Asp Arg Leu Val Val Pro Pro Ala Leu Asn Tyr Ser Tyr Tyr
100 105 110

Val Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> SEQ ID NO 335

<211> LENGTH: 336

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 335

gatgttgtga	tgactcagtc	tccactctcc	ctgcccgtca	cccttggaca	gccggcctcc	60
atctcctgca	ggctctagtca	aagecctcgta	tacagtgtat	gaaacacacta	cttgaatttg	120
tttcagcaga	ggccaggcca	atctccaagg	cgcctaattt	ataaggtttc	taaccggac	180
tctggggtcc	cagacagatt	cagcggcagt	gggtcaggca	ctgatttcac	actgaaaatc	240
agcagggtgg	aggctgagga	tgttggggtt	tattactgca	tgcaaggtac	acactggccg	300
tacacttttgc	ccaggggac	caagctggag	atcaaa			336

<210> SEQ ID NO 336

<211> LENGTH: 112

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 336

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

<210> SEQ ID NO 337

<211> LENGTH: 354

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 337

gaggtgcagc	tggggaggc	ctggtaagc	ctgggggtc	cctgagactc	60
tccctgtgcag	cctctggatt	caccttcagt	agctatagca	tggactgggt	120
ccagggaaagg	ggctggagt	ggctcatcc	attagtagta	gtagtagtta	cataatactac
gcagactctg	tgaaggccg	attcaccatc	tccagagaca	ccggcaagaa	ctcactgtat
					240

-continued

```
ctgcaaatga acagcctgag agacgaggac acggctgttt attactgtgc gagagagggc      300
agttagcagac ttttgacta ctggggccag ggaaccctgg tcaccgtctc ctca            354
```

<210> SEQ ID NO 338
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 338

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

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

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

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

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

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

Ala Arg Glu Gly Ser Ser Arg Leu Phe Asp Tyr Trp Gly Gln Gly Thr
100         105          110

Leu Val Thr Val Ser Ser
115
```

<210> SEQ ID NO 339
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 339

```
ggattcacct tcagtagcta tagc          24
```

<210> SEQ ID NO 340
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 340

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

<210> SEQ ID NO 341
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 341

```
attagtagta gtagtagtta cata          24
```

<210> SEQ ID NO 342
<211> LENGTH: 8
<212> TYPE: PRT

-continued

<213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 342

Ile Ser Ser Ser Ser Ser Tyr Ile
 1 5

<210> SEQ ID NO 343
 <211> LENGTH: 33
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 343

gcgagagagg gcagtagcag acttttgac tac 33

<210> SEQ ID NO 344
 <211> LENGTH: 11
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 344

Ala Arg Glu Gly Ser Ser Arg Leu Phe Asp Tyr
 1 5 10

<210> SEQ ID NO 345
 <211> LENGTH: 321
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 345

gacatccaga tgacctcagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc	60
atcaactgcc gggccagtca gagtattagt agctgggtgg cctggtatca gcagagacca	120
gggaaagccc ctaagctcct gatctataag gcgtctagtt tagaagggtgg agtccccatca	180
aggttcagcg gcagtggtatc tgggacagaa ttcaactctca ccatcagcag cctgcagecct	240
gaggattttg caacttatta ctgccaacag tataatagtt attggcacac ttttggccag	300
gggaccaagc tggagatcaa a	321

<210> SEQ ID NO 346
 <211> LENGTH: 107
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 346

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 Ile Ser Ser Trp
 20 25 30

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

Tyr Lys Ala Ser Ser Leu Glu Gly 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

-continued

1 5

<210> SEQ ID NO 353
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 353

```

gaggtgcagc tggtgaggc tgggggaggc ctggcaagc ctggggggc cctgagactc      60
tcctgtgcag cctctggatt caccttcagt agctatagca tggactgggt ccgcaggct     120
ccagggaaagg ggctggaggc ggtctcatcc attagtagta gttagtgcataactac      180
gcagactctg tgaaggggccg attcaccatc tccagagaca ccgccaagaa ctcactgtat    240
ctgcaaatga acagcctgag agacgaggac acggctgttt attactgtgc gagagaggc      300
agtagcagac tttttacta ctggggccag ggaacctgg tcaccgtctc ctca            354

```

<210> SEQ ID NO 354
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 354

```

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

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

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

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

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

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

Ala Arg Glu Gly Ser Ser Arg Leu Phe Asp Tyr Trp Gly Gln Gly Thr
100         105          110

Leu Val Thr Val Ser Ser
115

```

<210> SEQ ID NO 355
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 355

```

gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgttaggaga cagagtcacc      60
atcaactgcc gggccagtca gagttagt agctgggtgg cctggtatca gcagagacca     120
gggaaagccc ctaagctcct gatctataag gcgtcttagtt tagaagggtgg agtcccatca    180
aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagect    240
gaggattttg caacttatta ctgccaacag tataatagtt attggcacac ttttggccag      300
gggaccaagc tggagatcaa a                                         321

```

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219

220

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```

<210> SEQ ID NO 356
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 356

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 Ile Ser Ser Trp
20 25 30

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

Tyr Lys Ala Ser Ser Leu Glu Gly 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 Gln Gln Tyr Asn Ser Tyr Trp Tyr
85 90 95

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

```

```
<210> SEQ ID NO 357
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 357

gagggtgcagc tgggtggagtgc tggggggaggc ctgggtcaagc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt cacccttcagt agctatagca tgaactgggt ccgccaggct 120
ccagggaaagg ggctggagtg ggtctcatcc attagtagta gttagtagtta catatactac 180
gcagacttcag tgaaggggccg attcaccatc tccagagaca acggcaagaa ctcactgtat 240
ctgcaaatga acagcctgag agccgaggac acggctgtgtt attactgtgc gagagaggc 300
acttagcagac tttttgacta ctggggccaa qqaacccctgg tcaccatctc ctca 354
```

```

<210> SEQ ID NO 358
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 358

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

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

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

Ser Ser Ile Ser Ser Ser Tyr Ile Tyr 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 Val Tyr Tyr Cys
      85          90          95

```

-continued

Ala Arg Glu Gly Ser Ser Arg Leu Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> SEQ ID NO 359
 <211> LENGTH: 321
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 359

gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc	60
atcaattgcc gggccagtca gagtattagt agctggttgg cctggtatca gcagaaacca	120
gggaaagccc ctaagtcctt gatctataag ggcgtctatgg tagaaagtgg ggtccccatca	180
agggtcagcg gcagtggatc tgggacagaa ttcaactctca ccatcagcag cctgcagcct	240
gatgattttg caacttatta ctgccaacag tataatagtt attggcacac ttttggccag	300
gggaccaagc tggagatcaa a	321

<210> SEQ ID NO 360
 <211> LENGTH: 107
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 360

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 Ile Ser 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 Lys 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 Gln Tyr Asn Ser Tyr Trp Tyr
 85 90 95

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

<210> SEQ ID NO 361
 <211> LENGTH: 384
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 361

caggtgcacc tggtgaggc tgggggaggc ttggtcaagc ctggagggtc cctgagactc	60
tcctgtgcag cctctggatt caccttcagt gaccactaca tgagctggat ccggcaggct	120
ccagggagg ggctggaggc gatttcatac attagtaatg atgggtggat caaatactat	180
gtggactctg tggaggggccg attcatcatt tccaggacac acggccaagaa ctcattgtat	240
ctacatatga acagcctcag agccgacgac acggccgtgt attactgtgc gagagatcag	300

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ggatataattg gctacgactc gtattattac tattcctacg gtagggacgt ctggggccaa	360
gggaccacgg tcaccgtcgc ctca	384

<210> SEQ ID NO 362
<211> LENGTH: 128
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 362

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

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

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

Ser	Tyr	Ile	Ser	Asn	Asp	Gly	Gly	Thr	Lys	Tyr	Tyr	Val	Asp	Ser	Val
	50			55				60							

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

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

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

Tyr	Gly	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ala	Ser
	115				120						125				

<210> SEQ ID NO 363
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 363

ggattcacct tcagtgacca ctac	24
----------------------------	----

<210> SEQ ID NO 364
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 364

Gly	Phe	Thr	Phe	Ser	Asp	His	Tyr
1			5				

<210> SEQ ID NO 365
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 365

attagtaatg atgggtggta caaa	24
----------------------------	----

<210> SEQ ID NO 366
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

-continued

<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 366

Ile Ser Asn Asp Gly Gly Thr Lys
1 5

<210> SEQ ID NO 367
<211> LENGTH: 63
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 367

gcgagagatc	aggatataat	tggctacgac	tcgtattatt	actattccta	cggtatggac	60
gtc						63

<210> SEQ ID NO 368
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 368

Ala Arg Asp Gln Gly Tyr Ile Gly Tyr Asp Ser Tyr Tyr Tyr Ser						
1	5	10	15			

Tyr Gly Met Asp Val
20

<210> SEQ ID NO 369
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 369

aaaattgtgt	tgacgcagtc	tccaggcacc	ctgcctttgt	ttccagggga	aagagccacc	60
ctctcctgta	ggccagtc	gagtgttaac	aacaaattct	tagcctggta	ccagcagaaa	120
tctggccagg	ctcccaggct	cctcatctat	ggtgtcatcca	gcagggccac	tggcatccca	180
gacaggttca	gtggcagtgg	gtctgggacc	gacttcactc	tcaccatcag	cggactggag	240
cctgaagatt	ttgaagtgtta	ttattgtcaa	gtatatggta	actcaactcac	tctcggcggaa	300
gggaccaagg	tggagatcaa	g				321

<210> SEQ ID NO 370
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 370

Lys Ile Val Leu Thr Gln Ser Pro Gly	Thr Leu Pro Leu Phe Pro Gly					
1	5	10	15			

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Asn Asn Lys						
20	25	30				

Phe Leu Ala Trp Tyr Gln Gln Lys Ser 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

-continued

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Gly Leu Glu
 65 70 75 80

Pro Glu Asp Phe Glu Val Tyr Tyr Cys Gln Val Tyr Gly Asn Ser Leu
 85 90 95

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

<210> SEQ ID NO 371
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 371

cagagtgtta acaacaaatt c 21

<210> SEQ ID NO 372
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 372

Gln Ser Val Asn Asn Lys Phe
 1 5

<210> SEQ ID NO 373
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 373

ggtgcatcc 9

<210> SEQ ID NO 374
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 374

Gly Ala Ser
 1

<210> SEQ ID NO 375
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 375

caagtatatg gtaactcact cact 24

<210> SEQ ID NO 376
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

-continued

<400> SEQUENCE: 376

```
Gln Val Tyr Gly Asn Ser Leu Thr
 1           5
```

<210> SEQ ID NO 377

<211> LENGTH: 384

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 377

```
caggtgcagc tggtgaggc tgggggaggc ttggtaaagc ctggagggtc cctgagactc      60
tcctgtgcag cctctggatt caccttcaat gaccactaca tgagctggat ccgcaggct      120
ccagggaaagg ggctggagtg gatttcatac attagtaatg atgggtggtaa caaatactat      180
gtggactctg tggaggcccg attcatcatt tccaggaca acgccaagaa ctcatgtat      240
ctacatatga acagccttag agccgacgac acggccgtgt attactgtgc gagagatcag      300
ggatataattg gctacgactc gtattttac tattccttagt gtatggacgt ctggggccaa      360
gggaccacgg tcaccgtctc ctca                                         384
```

<210> SEQ ID NO 378

<211> LENGTH: 128

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 378

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

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

```
Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
 35          40          45
```

```
Ser Tyr Ile Ser Asn Asp Gly Gly Thr Lys Tyr Tyr Val Asp Ser Val
 50          55          60
```

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

```
Leu His Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys
 85          90          95
```

```
Ala Arg Asp Gln Gly Tyr Ile Gly Tyr Asp Ser Tyr Tyr Tyr Ser
 100         105         110
```

```
Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115         120         125
```

<210> SEQ ID NO 379

<211> LENGTH: 321

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 379

```
gaaatttgtt tgacgcagtc tccaggcacc ctgcctttgt ttccaggaga aagagccacc      60
ctctctgtta gggccagtca gagtgttaac aacaaattct tagcctggta ccagcagaaa      120
tctggccagg ctcccaggct cctcatctat ggtgcattca gcaggccac tggcatcccc      180
```

-continued

```
gacagggttca gtggcagtgg gtctgggacc gacttcactc tcaccatcg cggaactggag 240  
cctgaagatt ttgaagtgtt ttattgtcaa gtatatggta actcactcac tctcgccgga 300  
gggaccaagg tggagatcaa a 321
```

```

<210> SEQ ID NO 380
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 380

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Asn Asn Lys
20 25 30

Phe Leu Ala Trp Tyr Gln Gln Lys Ser 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 Gly Leu Glu
65 70 75 80

Pro Glu Asp Phe Glu Val Tyr Tyr Cys Gln Val Tyr Gly Asn Ser Leu
85 90 95

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

```

```
<210> SEQ ID NO 381
<211> LENGTH: 384
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 381

cagggtgcagc tggtggagtc tgggggaggc ttggtaaagc ctggagggtc cctgagactc 60
tccctgtcgac cctctggatt caccttcagt gaccactaca tgagctggat ccgccaggct 120
ccagggaaagg ggctggagtg ggtttcatac attagtaatg atggtggtac caaatactac 180
gcagactctg tgaagggccc attcaccatc tccaggacca acgccaagaa ctcactgttat 240
ctgc当地atga acagcctgag agccgaggac acggccgtgtt attactgtgc gagagatcg 300
ggatatattt gctacgactc gtatttattac tattcctacg gtatggaejt ctggggccaa 360
ggggcacccgg tcaccgtctc ctca 384
```

```

<210> SEQ ID NO 382
<211> LENGTH: 128
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 382

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

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

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

```

-continued

Ser Tyr Ile Ser Asn Asp Gly Gly Thr Lys 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 Val Tyr Tyr Cys
 85 90 95

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

Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> SEQ ID NO 383

<211> LENGTH: 321

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 383

```

gaaattgtgt tgacgcagtc tccaggcacc ctgtcttgc ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttaac aacaaattct tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatacc gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtt ttactgtcaa gtatatggta actcactcac ttccggcgg 300
gggaccaagg tggagatcaa a 321

```

<210> SEQ ID NO 384

<211> LENGTH: 107

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 384

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 Asn Asn Lys
 20 25 30

Phe 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 Val Tyr Gly Asn Ser Leu
 85 90 95

Thr Phe Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> SEQ ID NO 385

<211> LENGTH: 360

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 385

```

gaggtgcaga aggtggagtc tgggggaggc ctggtaago cgggggggtc cctgagactc 60

```

-continued

```

tcctgtacag cctctggatt cacttcagt acttataaca tgaattgggt ccggcaggct    120
ccagggaaagg gactggagtg ggtctcatcc attaggagta gtagtaatta cataatactac    180
gcagactcg tgaagggccg attcaccatc tccagagaca acgccaagaa ttcaactgtat    240
ctgcaaatga acagcctgag agccgatgac acggctgtgt attactgtgc gagagatggc    300
agcagtttgt acgactactc tgactactgg ggccaggaa ccctggcac cgttcctca    360

```

<210> SEQ ID NO 386
<211> LENGTH: 120
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 386

```

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

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

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

Ser Ser Ile Arg Ser Ser Asn Tyr Ile Tyr 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 Asp Asp Thr Ala Val Tyr Tyr Cys
 85          90           95

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

Gly Thr Leu Val Thr Val Ser Ser
115          120

```

<210> SEQ ID NO 387
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 387

```
ggattcacct tcagtaactta taac           24
```

<210> SEQ ID NO 388
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 388

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

<210> SEQ ID NO 389
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 389

```
attaggagta gtagtaatta cata           24
```

-continued

<210> SEQ ID NO 390
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 390

Ile Arg Ser Ser Ser Asn Tyr Ile
1 5

<210> SEQ ID NO 391
<211> LENGTH: 39
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 391

gcgagagatg gcagcagttg gtacgactac tctgactac 39

<210> SEQ ID NO 392
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 392

Ala Arg Asp Gly Ser Ser Trp Tyr Asp Tyr Ser Asp Tyr
1 5 10

<210> SEQ ID NO 393
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 393

gacatccaga tgacctcgtc	tccttccacc ctgtctgcat	ctgtaggaga cagagtcacc	60
atcaactgcc gggccagtca	gagttattgt agctgggtgg	cctggtatca acagatacca	120
ggaaagccc ctaaactcct	gatctataag gcgtcttagtt	tagaaaatgg ggtcccatca	180
aggttcagcg gcagtggtatc	tgggacagaa ttcaactctca	tcatcagcag cctgcagecct	240
gatgatttttgc acaacttatta	ctgccaacag tatatttagtt	attctcgac gttcggccaa	300
gggaccaagg tggaaatcaa a			321

<210> SEQ ID NO 394
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 394

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 Ile Ser Ser Trp
20 25 30

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

-continued

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

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

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ile Ser Tyr Ser Arg
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> SEQ ID NO 395
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 395

cagagtattatgtactgg 18

<210> SEQ ID NO 396
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 396

Gln Ser Ile Ser Ser Trp
 1 5

<210> SEQ ID NO 397
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 397

aaggcgtct 9

<210> SEQ ID NO 398
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 398

Lys Ala Ser
 1

<210> SEQ ID NO 399
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 399

caacagttataatgttttcgcgacg 27

<210> SEQ ID NO 400
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

-continued

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 400

Gln	Gln	Tyr	Ile	Ser	Tyr	Ser	Arg	Thr
1								5

<210> SEQ ID NO 401

<211> LENGTH: 360

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 401

gaggtgcagc	tggtgaggc	tgggggaggc	ctggtaago	cgggggggtc	cctgagactc	60
tcctgtacag	cctctggatt	cacccatcgat	acctataaca	tgaattgggt	ccgcaggct	120
ccagggaaagg	gactggagtg	ggtctcatcc	attaggagta	gtagtaatta	cataactac	180
gcagactca	gtaagggccg	attcaccatc	tccagagaca	acgccaagaa	ttcactgtat	240
ctgcaaatga	acagcctgag	agccgatgac	acggctgtgt	attactgtgc	gagagatggc	300
agcagtttgt	acgactactc	tgactactgg	ggccaggaa	ccctggcac	cgtctccat	360

<210> SEQ ID NO 402

<211> LENGTH: 120

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 402

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

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

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

Ser	Ser	Ile	Arg	Ser	Ser	Asn	Tyr	Ile	Tyr	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	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
						85		90		95					

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

Gly	Thr	Leu	Val	Thr	Val	Ser	Ser
					115		120

<210> SEQ ID NO 403

<211> LENGTH: 321

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 403

gacatccaga	tgacccagtc	tccttccacc	ctgtctgcat	ctgttaggaga	cagagtccacc	60
atcaactgcc	ggggccagtca	gagttttagt	agctgggtgg	cctggtatca	acagataccca	120
gggaaagccc	ctaaactcct	gatctataag	gcgtcttagtt	tagaaaatgg	ggtcccatca	180
aggttcagcg	gcagtggatc	tgggacagaa	ttcactctca	tcatcagcag	cctgcagcct	240

-continued

gatgattttg caacttatta ctgccaacag tatatttagtt attctcgac gttcggccaa 300
qqqaccaaqq tqqaatcaa a 321

```
<210> SEQ ID NO 404
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

<400> SEQUENCE: 404

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 Ile Ser Ser Trp
20 25 30

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

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

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

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ile Ser Tyr Ser Arg
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

```
<210> SEQ ID NO 405
<211> LENGTH: 360
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

<400> SEQUENCE: 405

gagggtgcagc tgggtggagtc tggggggaggc ctgggtcaagc ctgggggggtc cctgagactc 60

tccctgtgcag cctctggatt caccttcagt acttataaca tgaactgggt ccgcccaggct 120

ccagggaagg ggctggagtg ggtctcatcc attagtaggta gtatgttattt catataactac 180

gcagacttcg tgaaggggccg attcaccatc tccagagaca acgccaagaa ctcactgtat 240

ctgcaa atga acaggc ttagag agcc gaggac acgg ctgtgtt attact gtgc gagaga tggc 300

agcagtttgt acgactactc tgactactgg ggccaaaggaa ccctggtcac cgtctccca 360

<210> SEQ ID NO 406

<211> LENGTH: 120

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence
<220> FEATURE

<220> FEATURE:
-221: OTHER INFORMATION: Synthetic

<223> OTHER IN

(400) SEQUENCE 406

G3 - H3 G3 - R3 H3

1 5 10 15

20 25 30

35 40 45
Ser Ser Ile Arg Ser Ser Asn Tyr Ile Tyr Tyr Ala Asp Ser Val

-continued

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 Val Tyr Tyr Cys
85 90 95

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 407

<211> LENGTH: 321

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 407

gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc	60
atcaattgcc gggccagtca gagtattagt agctggttgg cctggtatca gcagaaacca	120
gggaaagccc ctaagtcctt gatctataag gcgtcttagtt tagaaagtgg ggtccccatca	180
aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct	240
gatgattttg caacttatta ctgccaacag tatattagtt attctcgac gttcggccaa	300
gggaccaagg tggaaatcaa a	321

<210> SEQ ID NO 408

<211> LENGTH: 107

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 408

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 Ile Ser 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 Lys 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 Gln Tyr Ile Ser Tyr Ser Arg
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> SEQ ID NO 409

<211> LENGTH: 360

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 409

gaggtgcagc tggtgaggc tgggggaggc ctggtaago cgggggggtc cctgagactc	60
tcctgtacag cctctggatt caccttcagt acttataaca tgaattgggt ccgccaggct	120
ccagggaaagg gactggagtg ggtctcatcc attaggagta gtagtaatta catatactac	180

-continued

```
gcagactcg tgaaggccg attcaccatc tccagagaca acgccaagaa ttcaactgtat    240
ctgcaaatga acagcctgag agccgatgac acggctgtgt attactgtgc gagagatggc    300
agcagtttgtt acgactactc tgactactgg ggcagggaa ccctggcac cgttcctca    360
```

```
<210> SEQ ID NO 410
<211> LENGTH: 120
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 410

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

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

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

Ser Ser Ile Arg Ser Ser Asn Tyr Ile Tyr 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 Asp Asp Thr Ala Val Tyr Tyr Cys
 85          90          95

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

Gly Thr Leu Val Thr Val Ser Ser
115         120
```

```
<210> SEQ ID NO 411
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 411

ggattcacct tcagtaactta taac
```

24

```
<210> SEQ ID NO 412
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

```
<400> SEQUENCE: 412
```

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

```
<210> SEQ ID NO 413
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

```
<400> SEQUENCE: 413
```

```
attaggagta gtatgtatata cata
```

24

```
<210> SEQ ID NO 414
```

-continued

<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 414

Ile Arg Ser Ser Ser Asn Tyr Ile
1 5

<210> SEQ ID NO 415
<211> LENGTH: 39
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 415

gcgagagatg gcagcagttg gtacgactac tctgactac 39

<210> SEQ ID NO 416
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 416

Ala Arg Asp Gly Ser Ser Trp Tyr Asp Tyr Ser Asp Tyr
1 5 10

<210> SEQ ID NO 417
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 417

gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgttaggaga cagagtcacc 60
atcaattgcc gggccagtca gagtattagt agctggttgg cctggtatca acagatacca 120
gggaaagccc ctaaactcct gatctataag ggcgtctatgg tagaaaaatgg ggtccccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcaactctca tcatcagcag cctgcagcct 240
gatgattttg caacttatta ctgccaacag tatattatgtt attctcgac gttcggccaa 300
gggaccaagg tggaaatcaa a 321

<210> SEQ ID NO 418
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 418

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 Ile Ser Ser Trp
20 25 30

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

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

-continued

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

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ile Ser Tyr Ser Arg
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> SEQ ID NO 419
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 419

cagagtattatgtagctgg 18

<210> SEQ ID NO 420
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 420

Gln Ser Ile Ser Ser Trp
1 5

<210> SEQ ID NO 421
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 421

aaggcgtct 9

<210> SEQ ID NO 422
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 422

Lys Ala Ser
1

<210> SEQ ID NO 423
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 423

caacagtata ttagttatttc tcggacg 27

<210> SEQ ID NO 424
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 424

-continued

Gln Gln Tyr Ile Ser Tyr Ser Arg Thr
1 5

```
<210> SEQ ID NO 425
<211> LENGTH: 360
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 425

gaggtgcagc tgggtggagtc tggggggaggc ctggtaagc cgggggggtc cctgagactc 60
tcctgtacag cctctggatt caccttca gtttataaca tgaattgggt ccgcaggct 120
ccagggaaagg gactggagtg ggtctcatcc attaggagta gtagtaatataactac 180
gcagactcag tgaagggccg attcaccatc tccagagaca acgccaagaa ttcaactgtat 240
ctgcaa atga acaggctgag agccgatgac acggctgtgt attactgtgc gagagatggc 300
agcagtttgtt acgactactc tgactactgg ggccaggaa ccctggcac cgttcctca 360
```

```
<210> SEQ ID NO 426
<211> LENGTH: 120
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

```
<400> SEQUENCE: 426

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

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

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

```
Ser Ser Ile Arg Ser Ser Asn Tyr Ile Tyr 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 Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95
```

```
Ala Arg Asp Gly Ser Ser Trp Tyr Asp Tyr Ser Asp Tyr Trp Gly Gln
100 105 110
```

```
Gly Thr Leu Val Thr Val Ser Ser
115 120
```

```
<210> SEQ ID NO 427
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

```
<400> SEQUENCE: 427

gacatccaga tgaccttgcacc ctgtctgcat ctgttaggaga cagagtccacc 60
atcacttgcc gggccagtca gagtattagt agctgggtgg cctggtatca acagatacca 120
gggaaagccc ctaaaactcct gatctataag gcgcttagtt tagaaaaatgg ggtccccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcaactctca tcatcagcag cctgcagcct 240
gatgattttg caacttatta ctgccaacag tatatttagtt attctcgac gttcgccaa 300
```

-continued

gggaccaagg tggaaatcaa a

321

<210> SEQ ID NO 428
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 428

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 Ile Ser Ser Trp
20 25 30

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

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

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

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ile Ser Tyr Ser Arg
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> SEQ ID NO 429
<211> LENGTH: 360
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 429

gaggtgcagc	tgggtggagtc	tgggggaggc	ctggtaago	ctggggggtc	cctgagactc	60
tccctgtgcag	cctctggatt	caccttcaagt	acttataaca	tgaactgggt	ccgcaggct	120
ccagggaaagg	ggctggagtg	ggtctcatcc	attaggagta	gttagtaatta	cataatactac	180
gcagactcag	tgaagggccg	attcaccatc	tccagagaca	acgccaagaa	ctcaactgtat	240
ctgcaaatga	acagcctgag	agccgaggac	acggctgtgt	attactgtgc	gagagatggc	300
agcagtttgt	acgactactc	tgactactgg	ggccaaggaa	ccctggcac	cgttcctca	360

<210> SEQ ID NO 430
<211> LENGTH: 120
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 430

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

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

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

Ser Ser Ile Arg Ser Ser Asn Tyr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

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

-continued

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

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

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> SEQ ID NO 431
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 431

gacatccaga tgacccagtc tccttccacc ctgtctgcatt	ctgttaggaga cagagtcacc	60
atcaacttgcc gggccagtca gagttattgt agctgggtgg	cctggtatca gcagaaacca	120
gggaaaagcccc ctaagtcct gatctataag gcgtcttagtt	tagaaagtgg ggtcccatca	180
aggttcagcg gcagtggatc tgggacagaa ttcaactctca	ccatcagcag cctgcagecct	240
gatgattttg caacttatta ctgccaacag tatattagtt attctcgac	gttcggccaa	300
gggaccaagg tggaaatcaa a		321

<210> SEQ ID NO 432
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 432

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 Ile Ser 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 Lys 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 Gln Tyr Ile Ser Tyr Ser Arg
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> SEQ ID NO 433
<211> LENGTH: 360
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 433

gaggtgcagc tggtggagtc tgggggaggc ctggtaagc cgggggggtc cctgagactc	60
tccctgtacag cctctggatt caccttcagt acttataaca tgaattgggt ccgccaggct	120
ccagggaaagg gactggagtg ggtctcatcc attaggagta gtagtaatta catataactac	180
gcagactcag tgaaggcccg attcaccatc tccagagaca acgccaagag ttcaactgtat	240

259**260**

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ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagatggc 300
 agcagtttgtt acgactactc tgactactgg ggccaggaa ccctggcac cgttcctca 360

<210> SEQ ID NO 434
<211> LENGTH: 120
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<400> SEQUENCE: 434

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

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

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

Ser	Ser	Ile	Arg	Ser	Ser	Asn	Tyr	Ile	Tyr	Tyr	Ala	Asp	Ser	Val	
	50				55					60					

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

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

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

Gly	Thr	Leu	Val	Thr	Val	Ser	Ser								
	115				120										

<210> SEQ ID NO 435
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<400> SEQUENCE: 435

ggattcacct tcagtagtta taac 24

<210> SEQ ID NO 436
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<400> SEQUENCE: 436

Gly Phe Thr Phe Ser Thr Tyr Asn
 1 5

<210> SEQ ID NO 437
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<400> SEQUENCE: 437

attagagta gtagtaatta cata 24

<210> SEQ ID NO 438
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

-continued

<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 438

Ile Arg Ser Ser Ser Asn Tyr Ile
1 5

<210> SEQ ID NO 439
<211> LENGTH: 39
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 439

gcgagagatg gcagcagttg gtacgactac tctgactac 39

<210> SEQ ID NO 440
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 440

Ala Arg Asp Gly Ser Ser Trp Tyr Asp Tyr Ser Asp Tyr
1 5 10

<210> SEQ ID NO 441
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 441

gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgttaggaga cagagtcacc 60
atcaattgcc gggccagtca gagtattagt agctgggtgg cctggtatca acaggatcca 120
gggaaagccc ctaaactcct gatctataag gcgtctagtt tagaaaatgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca tcatcagcag cctgcagect 240
gatgattttg caacttatta ctgccaacag tatattagtt attctcgac gttcggccaa 300
gggaccaagg tggaaatcaa a 321

<210> SEQ ID NO 442
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 442

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 Ile Ser Ser Trp
20 25 30

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

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

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

-continued

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ile Ser Tyr Ser Arg
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> SEQ ID NO 443
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 443

cagagtat_a gtagctgg

18

<210> SEQ ID NO 444
 <211> LENGTH: 6
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 444

Gln Ser Ile Ser Ser Trp
 1 5

<210> SEQ ID NO 445
 <211> LENGTH: 9
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 445

aaggcgtct

9

<210> SEQ ID NO 446
 <211> LENGTH: 3
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 446

Lys Ala Ser
 1

<210> SEQ ID NO 447
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 447

caacagtata ttatatttc tcggacg

27

<210> SEQ ID NO 448
 <211> LENGTH: 9
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 448

Gln Gln Tyr Ile Ser Tyr Ser Arg Thr
 1 5

-continued

<210> SEQ ID NO 449
<211> LENGTH: 360
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 449

```

gaggtgcagc tggtggagtc tgggggaggc ctggtaagc cgggggggtc cctgagactc      60
tcctgtacag cctctggatt caccttcaacttataaca tgaattgggt ccgcaggct      120
ccagggaaagg gactggagtg ggtctcatcc attaggagta gtagtaatta cataactac      180
gcagactcag tgaaggcccg attcaccatc tccagagaca acgccaagag ttcaactgtat      240
ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagatggc      300
agcagtttgtt acgactactc tgactactgg ggccaggaa ccctggtcac cgctccctca      360

```

<210> SEQ ID NO 450
<211> LENGTH: 120
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 450

```

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

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

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

Ser Ser Ile Arg Ser Ser Asn Tyr Ile Tyr Tyr Ala Asp Ser Val
 50          55           60

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
 115         120

```

<210> SEQ ID NO 451
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 451

```

gacatccaga tgacccagtc tcctccacc ctgtctgcat ctgtaggaga cagagtacc      60
atcaactgcc gggccagtca gagtattagt agctgggtgg cctggtatca acaggtacca      120
gggaaagccc ctaaactcct gatctataag gcgtctagtt tagaaaatgg ggtcccatca      180
aggttcagcg gcagtggatc tgggacagaa ttcactctca tcatcagcag cctgcagecct      240
gatgattttg caacttatta ctgccaacag tatattagtt attctcgac gtteggccaa      300
gggaccaagg tggaaatcaa a                                         321

```

-continued

<210> SEQ ID NO 452
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 452

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 Ile Ser Ser Trp
20 25 30

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

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

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

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ile Ser Tyr Ser Arg
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> SEQ ID NO 453
<211> LENGTH: 360
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 453

gaggtgcagc	tggtgaggc	tgggggaggc	ctggtaagc	ctggggggtc	cctgagactc	60
tcctgtgcag	cctctggatt	cacccatcgat	acttataaca	tgaactgggt	ccgcaggct	120
ccagggaaagg	ggctggagtg	ggtctcatcc	attaggagta	gttagtaatta	cataactac	180
gcagactcag	tgaaggcccg	attaccatc	tccagagaca	acgccaagaa	ctcactgtat	240
ctgcaaatga	acagcctgag	agccgaggac	acggctgtgt	attactgtgc	gagagatggc	300
agcagtttgt	acgactactc	tgactactgg	ggccaggaa	ccctggcac	cgttcctca	360

<210> SEQ ID NO 454
<211> LENGTH: 120
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 454

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

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

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

Ser Ser Ile Arg Ser Ser Ser Asn Tyr Ile Tyr 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 Val Tyr Tyr Cys
85 90 95

-continued

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

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> SEQ ID NO 455
 <211> LENGTH: 321
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 455

gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc	60
atcactgcc gggccagtca gagttattgt agctgggtgg cctggtatca gcagaaaacca	120
gggaaagccc ctaagctcct gatctataag gcgtcttagtt tagaaaagtgg ggtcccatca	180
aggttcagcg gcagtggatc tgggacagaa ttcaactctca ccatcagcag cctgcagect	240
gatgattttg caacttatta ctgccaacag tatattagtt attctcggac gtteggccaa	300
gggaccaagg tggaaatcaa a	321

<210> SEQ ID NO 456
 <211> LENGTH: 107
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 456

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 Ile Ser 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 Lys 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 Gln Tyr Ile Ser Tyr Ser Arg
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> SEQ ID NO 457
 <211> LENGTH: 360
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 457

gaggtgcagc tggtgaggc tgggggaggc ctggtaagc cgggggggtc cctgagactc	60
tcctgtacag cctctggatt caccttcaacttataaca tgaattgggt ccgcaggct	120
ccagggagg gactggagtg ggtctcatcc attaggagta gtagtaatta cataactac	180
gcagactcag tgaaggcccg attcaccatc tccagagaca acgccaagaa ttcaactgtat	240
ctgcaaatga acagcctgag agccgatgac acggctgtgt attactgtgc gagagatggc	300
agcagtttgt acgactactc tgactactgg ggccaggaa ccctggtcac cgttcctca	360

-continued

<210> SEQ ID NO 458
<211> LENGTH: 120
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 458

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Lys	Pro	Gly	Gly
1															15

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

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

Ser	Ser	Ile	Arg	Ser	Ser	Asn	Tyr	Ile	Tyr	Tyr	Ala	Asp	Ser	Val	
	50														60

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

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

Ala	Arg	Asp	Gly	Ser	Ser	Trp	Tyr	Asp	Tyr	Ser	Asp	Tyr	Trp	Gly	Gln
															110

Gly	Thr	Leu	Val	Thr	Val	Ser	Ser								
	115														120

<210> SEQ ID NO 459
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 459

ggattcacct tcagtagtactta taac 24

<210> SEQ ID NO 460
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 460

Gly Phe Thr Phe Ser Thr Tyr Asn
1 5

<210> SEQ ID NO 461
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 461

attaggagta gtagtaatta cata 24

<210> SEQ ID NO 462
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

-continued

<400> SEQUENCE: 462

Ile Arg Ser Ser Ser Asn Tyr Ile
1 5

<210> SEQ ID NO 463

```
<211> LENGTH: 39
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

<400> SEQUENCE: 463

gcgagagatg gcagcagttg gtacgactac tctgactac

39

<210> SEQ ID NO 464

```
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

<400> SEQUENCE: 464

Ala Arg Asp Gly Ser Ser Trp Tyr Asp Tyr Ser Asp Tyr
 1 5 10

<210> SEQ ID NO 465

```
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

<400> SEQUENCE: 465

gacatccaga tgacctcagtc tccctccacc cttgtctgcattt	60
atcacttgcc gggccagtc gagtattagt agctggttgg cctggtatca acagatacca	120
ggaaaagccc ctaaaactcct gatctataag gcgtctagtt tagaaaatgg ggtcccatca	180
aggttcagcg gcagtggatc tgggacagaa ttcaactctca tcatcagcag cctgcagcct	240
gtatgttttgc caacttatta ctgccaacag tatatttagttt attctcgac gttcgccaa	300
ggggaccaagg tggaaatcaa a	321

<210> SEQ ID NO 466

```
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

<400> SEQUENCE: 466

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 Ile Ser Ser Trp
20 25 30

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

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

Ser Gly Ser Gly Thr Glu Phe Thr Leu Ile Ile Ser Ser Ser Leu Gln Phe
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ile Ser Tyr Ser Arg
85 90 95

-continued

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> SEQ ID NO 467
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 467

cagagtattatgtacgtgg

18

<210> SEQ ID NO 468
 <211> LENGTH: 6
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 468

Gln Ser Ile Ser Ser Trp
 1 5

<210> SEQ ID NO 469
 <211> LENGTH: 9
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 469

aaggcgtct

9

<210> SEQ ID NO 470
 <211> LENGTH: 3
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 470

Lys Ala Ser
 1

<210> SEQ ID NO 471
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 471

caacagtata ttagtttcc tcggacg

27

<210> SEQ ID NO 472
 <211> LENGTH: 9
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 472

Gln Gln Tyr Ile Ser Tyr Ser Arg Thr
 1 5

<210> SEQ ID NO 473

-continued

<211> LENGTH: 360
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 473

```

gaggtgcagc tggtgaggc tgggggagc ctggtaago cgggggggtc cctgagactc      60
tcctgtacag cctctggatt caccttca gttataaca tgaattgggt ccgcaggct      120
ccagggaaagg gactggagtg ggtctcatcc attaggagta gtagtaatta cataactac      180
gcagactcag tgaagggccg attcaccatc tccagagaca acgccaagaa ttcaactgtat      240
ctgcaaatga acagcctgag agccgatgac acggctgtgt attactgtgc gagagatggc      300
agcagtttgt acgactactc tgactactgg ggccaggaa ccctggcac cgtctcccta      360

```

<210> SEQ ID NO 474
<211> LENGTH: 120
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 474

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Lys	Pro	Gly	Gly
1															
Ser	Leu	Arg	Leu	Ser	Cys	Thr	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Thr	Tyr
Asn	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
Ser	Ser	Ile	Arg	Ser	Ser	Ser	Asn	Tyr	Ile	Tyr	Tyr	Ala	Asp	Ser	Val
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr
65															
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
Ala	Arg	Asp	Gly	Ser	Ser	Trp	Tyr	Asp	Tyr	Ser	Asp	Tyr	Trp	Gly	Gln
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser								
115															

<210> SEQ ID NO 475
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 475

```

gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgttaggaga cagagtcacc      60
atcacttgcc gggccagtca gaggattagt agctgggtgg cctggtatca acagatacca      120
gggaaaagccc ctaaaactcct gatctataag gogtctagtt tagaaaaatgg ggtccccatca      180
aggttcagcg gcagtggatc tgggacagaa ttcaactctca tcatcagcag cctgcagecct      240
gatgattttg caacttattt ctgccaacag tatatttagtt attctcgac gttcggccaa      300
gggaccaagg tggaaatcaa a                                         321

```

<210> SEQ ID NO 476
<211> LENGTH: 107
<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 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 Ile Ser Ser Trp
 20          25           30

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

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

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

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ile Ser Tyr Ser Arg
 85          90           95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100         105

```

<210> SEQ ID NO 477
 <211> LENGTH: 360
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 477

```

gagggtcagc tggtgaggc tgggggagc ctggtaagc ctgggggtc cctgagactc      60
tcctgtgcag cctctggatt caccttcagt acttataaca tgaactgggt ccgccaggct    120
ccagggaaagg ggctggagtg ggtctcatcc attaggagta gtagtaatta cataatactac   180
gcagactcag tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat   240
ctgcaaatga acagcctgag agccgaggac acggctgtgtt attactgtgc gagagatggc   300
agcagtttgt acgactactc tgactactgg ggccaaggaa ccctggcac cgttcctca      360

```

<210> SEQ ID NO 478
 <211> LENGTH: 120
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 478

```

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

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

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

Ser Ser Ile Arg Ser Ser Asn Tyr Ile Tyr 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 Val Tyr Tyr Cys
 85          90           95

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

```

-continued

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 479
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 479

gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc	60
atcaacttgcc gggccagtca gagtattagt agctggttgg cctggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctataag gcgcttagtt tagaaagtgg ggteccatca	180
aggttcagecg gcagtggtatc tgggacagaa ttcaactctca ccatcagcag cctgcagect	240
gatgattttg caacttatta ctgccaacag tatattagtt attctcgac gttcgccaa	300
gggaccaagg tggaaatcaa a	321

<210> SEQ ID NO 480
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 480

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp			
20	25	30	
30			

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

Tyr Lys Ala Ser Ser Leu 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 Gln Tyr Ile Ser Tyr Ser Arg		
85	90	95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
100	105

<210> SEQ ID NO 481
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 481

gaggtgcaac tagtggagtc tgggggaggc ttggcacgc ctgggggtc cctgagactc	60
tctctggatt caccttcggt gactacgaca tgcactgggt ccgtcaagct	120
acaggaagag gtctggagtg ggtctcgat attgtccctg ctgggtacac atcctataca	180
ggctccgtga agggccgatt caccatctcc agagagaatg ccaagaactc cttgcacat	240
caaataaca gcctgacaac cggggacacg gctatataatt attgtgttag agaggatata	300
gcagtgctg ttttggatca ctggggccag ggaaccctgg tcaccgtctc ctca	354

<210> SEQ ID NO 482

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<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 482

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 Val Val Ser Gly Phe Thr Phe Gly Asp Tyr
 20          25          30

Asp Met His Trp Val Arg Gln Ala Thr Gly Arg Gly Leu Glu Trp Val
 35          40          45

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

Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn Ser Leu His Leu
 65          70          75          80

Gln Met Asn Ser Leu Thr Thr Gly Asp Thr Ala Ile Tyr Tyr Cys Ala
 85          90          95

Arg Glu Asp Ile Ala Val Pro Gly Phe Asp Tyr Trp Gly Gln Gly Thr
100          105         110

Leu Val Thr Val Ser Ser
115

```

```

<210> SEQ ID NO 483
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

```

<400> SEQUENCE: 483

ggattcacct tcgggtgacta cgac

24

```

<210> SEQ ID NO 484
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

```

<400> SEQUENCE: 484

Gly Phe Thr Phe Gly Asp Tyr Asp
 1 5

```

<210> SEQ ID NO 485
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 485

attgctcctg ctgggtgacac a

21

```

<210> SEQ ID NO 486
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 486

Ile Ala Pro Ala Gly Asp Thr

-continued

1 5

<210> SEQ ID NO 487
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 487

gctagagagg atatagcagt gcctgggtt gattac 36

<210> SEQ ID NO 488
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 488

Ala Arg Glu Asp Ile Ala Val Pro Gly Phe Asp Tyr
1 5 10

<210> SEQ ID NO 489
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 489

gaaatatgta tgacgcagtc tccagccacc ctgtctgtgt ctccagggga acgaggcacc 60
ctctcctgca gggccagtca gagtgtagc agcaacttag cctggtagcca gcagaaacct 120
ggccaggctc ccagactcct catctatggt gcatccacga gggccactgg cttcccagcc 180
aggttcagtg gcagtgggtc tgggacagag ttcaactctca ccatcagcag cctgcagtct 240
gaagattttg cagtttattta ctgtcagcag tataataagt ggctccgtt cacttcggc 300
cctgggacca aagtggattt caaa 324

<210> SEQ ID NO 490
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 490

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

-continued

<210> SEQ ID NO 491
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 491

cagagtgtta gcagcaac

18

<210> SEQ ID NO 492
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 492

Gln Ser Val Ser Ser Asn
1 5

<210> SEQ ID NO 493
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 493

ggtgcatcc

9

<210> SEQ ID NO 494
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 494

Gly Ala Ser
1

<210> SEQ ID NO 495
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 495

cagcagtata ataagtggcc tccgttcact

30

<210> SEQ ID NO 496
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 496

Gln Gln Tyr Asn Lys Trp Pro Pro Phe Thr
1 5 10

<210> SEQ ID NO 497
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

-continued

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 497

gaggtgcaac	tagtggagtc	tgggggaggc	ttggtagcago	ctggggggtc	cctgagactc	60
tcctgtgtag	tctctggatt	caccccggt	gactacgaca	tgcaactgggt	ccgtcaagct	120
acaggaagag	gtctggagt	ggtctcggt	attgctccctg	ctgggtgacac	atccataaca	180
ggctccgtga	agggccgatt	caccatctcc	agagagaatg	ccaagaactc	cttgcacatctt	240
caaatatgaca	gcctgacaac	cggggacacg	gctatataatt	attgtgctag	agaggatata	300
gcagtgcctg	gttttgatta	ctggggccag	ggaaccctgg	tcaccgtctc	ctca	354

<210> SEQ ID NO 498

<211> LENGTH: 118

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 498

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

<210> SEQ ID NO 499

<211> LENGTH: 324

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 499

gaaatagtga	tgacgcagtc	tccagccacc	ctgtctgtgt	ctccagggga	acgaggcacc	60
ctctctgtca	gggccagtca	gagtgttagc	agcaacttag	cctggtagca	gcagaaacct	120
ggccaggctc	ccagactcct	catctatggt	gcatccacga	gggccactgg	cttcccagcc	180
aggttcagt	gcagtggttc	tgggacagag	ttcactctca	ccatcagcag	cctgcagtct	240
gaagattttgc	cagttttattta	ctgtcagcag	tataataagt	ggcctccgtt	cactttcgcc	300
cctgggacca	aagtggatata	caaaa				324

<210> SEQ ID NO 500

<211> LENGTH: 108

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

-continued

<210> SEQ ID NO 503
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 503

```

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc      60
ctctcctgca gggccagtca gagtgtagc agcaacttag cctggtagcca gcagaaacct      120
ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc      180
aggttcagtg gcagtgggtc tgggacagag ttcaactctca ccatcagcag cctgcagtct      240
gaagattttg cagtttatta ctgtcagcag tataataagt ggctccgtt cacttcggc      300
cctggacca aagtggatat caaa                                         324

```

<210> SEQ ID NO 504
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 504

```

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
 20          25           30

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

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50           55           60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
 65           70           75           80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Lys Trp Pro Pro
 85           90           95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
 100          105

```

<210> SEQ ID NO 505
<211> LENGTH: 378
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 505

```

caaattctgc tggtgcaatc tggacctgag gtgaaggago ctggggctc agtgaaggta      60
tcctgcaagg cttctggta caccttacc aactacgcta tcagctgggt gcgcacaggta      120
cctggacaag ggctttagtg gatgggatgg gtcagcgctt acaatggta cacaactat      180
gcacatgaag tccaggccag agtcaccatg accacagaca catccacgac cacagcctac      240
atggagctga ggagcctgag atctgacgac acggccatgt attactgtgc gagaggggt      300
gtagtcgtgc cagttgtcc ccacttctac aacggtatgg acgtctgggg ccaaggacc      360
acggtcaccc tctcctca                                         378

```

<210> SEQ ID NO 506
<211> LENGTH: 126

-continued

<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 506

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

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

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

Gly Trp Val Ser Ala Tyr Asn Gly His Thr Asn Tyr Ala His Glu Val
 50          55          60

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

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

Ala Arg Gly Gly Val Val Val Pro Val Ala Pro His Phe Tyr Asn Gly
100         105         110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115         120         125
```

<210> SEQ ID NO 507
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 507

```
ggttacacct ttaccaacta cgct
```

<210> SEQ ID NO 508
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 508

```
Gly Tyr Thr Phe Thr Asn Tyr Ala
 1           5

<210> SEQ ID NO 509  

<211> LENGTH: 24  

<212> TYPE: DNA  

<213> ORGANISM: Artificial Sequence  

<220> FEATURE:  

<223> OTHER INFORMATION: Synthetic
```

<400> SEQUENCE: 509

```
gtcagcgctt acaatggtca caca
```

<210> SEQ ID NO 510
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 510

```
Val Ser Ala Tyr Asn Gly His Thr
 1           5
```

-continued

<210> SEQ ID NO 511
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 511

gcgagagggg gtgttagtcgt gccagttgct cccacttct acaacggtat ggacgta 57

<210> SEQ ID NO 512
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 512

Ala Arg Gly Gly Val Val Val Pro Val Ala Pro His Phe Tyr Asn Gly
1 5 10 15

Met Asp Val

<210> SEQ ID NO 513
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 513

gatattgtga tgactcagtt tccactctcc ctgcccgtca cccctggaga gccggcctcc 60
atctcctgca ggtctagtca gagcctcctg catattaatg aataacaacta tttggattgg 120
tacctaaaga agccaggcga gtctccacag ctcctgatct atttgggtt taatcgggcc 180
tccggggtcc ctgacaggtt cagtgccagt ggatcaggca cagattttac actgaaaatc 240
agcagagtgg aggctgagga tgggggttc tattactgca tgcaagctct tcaaactccg 300
tggacgttag gccaaggcac caaggtggaa atcaaa 336

<210> SEQ ID NO 514
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 514

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

-continued

<210> SEQ ID NO 515
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 515

cagagcctcc tgcataattaa tgaataacaac tat

33

<210> SEQ ID NO 516
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 516

Gln Ser Leu Leu His Ile Asn Glu Tyr Asn Tyr
1 5 10

<210> SEQ ID NO 517
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 517

ttgggtttt

9

<210> SEQ ID NO 518
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 518

Leu Gly Phe
1

<210> SEQ ID NO 519
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 519

atgcaagctc ttcaaactcc gtggacg

27

<210> SEQ ID NO 520
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 520

Met Gln Ala Leu Gln Thr Pro Trp Thr
1 5

<210> SEQ ID NO 521
<211> LENGTH: 378
<212> TYPE: DNA

-continued

<213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 521

caggttcagc tgggtcagtc tggacctgag gtgaaggagc ctggggcctc agtgaaggtc	60
tcctgcagg cttctggta caccttacc aactacgcta tcagctgggt gcgcacaggc	120
cctggacaag ggcttgagt gatggatgg gtcagcgctt acaatggtca cacaactat	180
gcacatgaag tccaggcagc agtccccatg accacagaca catccacgac cacagcctac	240
atggagctga ggagcctgag atctgacgac acggccatgt attactgtgc gagaggggt	300
gtagtcgtgc cagttgtcc ccacttctac aacggtatgg acgtctgggg ccaagggacc	360
acggtcaccg ttccttca	378

<210> SEQ ID NO 522
 <211> LENGTH: 126
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 522

Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Glu Pro Gly Ala	
1 5 10 15	
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr	
20 25 30	
Ala Ile Ser Trp Val Arg Gln Val Pro Gly Gln Gly Leu Glu Trp Met	
35 40 45	
Gly Trp Val Ser Ala Tyr Asn Gly His Thr Asn Tyr Ala His Glu Val	
50 55 60	
Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Thr Ala Tyr	
65 70 75 80	
Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Met Tyr Tyr Cys	
85 90 95	
Ala Arg Gly Gly Val Val Val Pro Val Ala Pro His Phe Tyr Asn Gly	
100 105 110	
Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser	
115 120 125	

<210> SEQ ID NO 523
 <211> LENGTH: 336
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 523

gatattgtga tgactcagtc tccactctcc ctgcccgtca cccctggaga gccggcctcc	60
atctcctgca ggtctagtca gagectcctg catattaatg aataacaacta ttggattgg	120
tacctaaaga agccaggcgtca gtctccacag ctcctgatct atttgggttt taatcggcc	180
tccggggtcc ctgacagggtt cagtggcagt ggatcaggca cagatttac actgaaaatc	240
agcagagtggtt aggctgagga ttttgggttc tattactgca tgcaagctct tc当地actccg	300
tggacgttag gccaaggcgtca caagggtggaa atcaaa	336

<210> SEQ ID NO 524
 <211> LENGTH: 112
 <212> TYPE: PRT

-continued

<213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 524

```

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 His Ile
 20          25          30

Asn Glu Tyr Asn Tyr Leu Asp Trp Tyr Leu Lys Lys Pro Gly Gln Ser
 35          40          45

Pro Gln Leu Leu Ile Tyr Leu Gly Phe 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 Leu Gly Gln Gly Thr Lys Val Glu Ile Lys
100         105         110

```

<210> SEQ ID NO 525
 <211> LENGTH: 378
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 525

```

caggttcagc tggtgcaagg tggagctgag gtgaagaagc ctggggcctc agtgaaggtc      60
tcctgcagg cttctggta caccttacc aactacgcta tcagctgggt gcgacaggcc      120
cctggacaag ggcttgagtg gatgggatgg gtcagcgctt acaaattgtca cacaactat      180
gcacagaagc tccagggcag agtcaccatg accacagaca catccacgag cacagcctac      240
atggagctga ggagcctgag atctgacgac acggccgtgt attactgtgc gagagggggt      300
gtatgcgtgc cagttgctcc ccacttctac aacggtatgg acgtctgggg gcaagggacc      360
acggtcaccc ttcctctca                                         378

```

<210> SEQ ID NO 526
 <211> LENGTH: 126
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 526

```

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

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

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

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

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

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

Ala Arg Gly Gly Val Val Val Pro Val Ala Pro His Phe Tyr Asn Gly

```

-continued

100 105 110

```
<210> SEQ ID NO 527
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

<400> SEQUENCE: 527

gatattgtga tgactcagtc tccactctcc ctggccgtca cccctggaga gccggcctcc	60
atctccgtca ggtcttagtca gagcctcctg cataattaatg aataacaacta ttggattttgg	120
tacctgcaga agccaggcca gtctccacag ctctgtatct atttgggttc taatcgggcc	180
tccggggtcc ctgacaggtt cagtggcagt ggatcaggca cagattttac actgaaaatc	240
agcagagtggg aggctgagga tgggggtt tattactgca tgcaagctct tc当地actccg	300
ttggacattcg qccaaqqdca caaqgtqaaa atcaaa	336

<210> SEO ID NO 528

```
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

<400> SEQUENCE: 528

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 His Ile
 20 25 30

Asn Glu 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

```
<210> SEQ ID NO 529
<211> LENGTH: 351
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

<400> SEQUENCE: 529

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```

<210> SEQ ID NO 530
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 530

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 Leu 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 Ser Thr Gly Asp Thr Tyr Tyr Thr Gly Ser Val Met
 50          55           60

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

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

Arg Glu Gly Ile Arg Thr Pro Tyr Asp Tyr Trp Gly Gln Gly Ala Arg
100         105          110

Val Thr Val Ser Ser
 115

```

```

<210> SEQ ID NO 531
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

```

<400> SEQUENCE: 531

ggattcaccc taagtagcta cgac 24

```

<210> SEQ ID NO 532
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

```

<400> SEQUENCE: 532

Gly Phe Thr Leu Ser Ser Tyr Asp
 1 5

```

<210> SEQ ID NO 533
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

```

<400> SEQUENCE: 533

atggcagta ctggtgacac a 21

```

<210> SEQ ID NO 534
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

```

<400> SEQUENCE: 534

-continued

Ile Gly Ser Thr Gly Asp Thr
1 5

<210> SEQ ID NO 535
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 535

gcaagagagg gaataagaac accctatgtat 33

<210> SEQ ID NO 536
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 536

Ala Arg Glu Gly Ile Arg Thr Pro Tyr Asp Tyr
1 5 10

<210> SEQ ID NO 537
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 537

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc	60
ctctcctgca gggccagtca gagtgtagc agcaatgttag cctggtagcca gcagaaaacct	120
ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc	180
aggttcagtg gcagtggttc tgggacagaa ttcaactctca ccatcagcag cctgcagttct	240
gaagatttttgc agttttatata ctgtcagcag tataataatt ggcctccatt cactttcgcc	300
cctgggacca aagtggatat caaa	324

<210> SEQ ID NO 538
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 538

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
20 25 30

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

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Asn Trp Pro Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys

-continued

100 105

<210> SEQ ID NO 539
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 539

cagagtgtta gcagcaat

18

<210> SEQ ID NO 540
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 540

Gln Ser Val Ser Ser Asn
1 5

<210> SEQ ID NO 541
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 541

ggtgcatcc

9

<210> SEQ ID NO 542
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 542

Gly Ala Ser
1

<210> SEQ ID NO 543
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 543

cagcagtata ataattggcc tccattcaact

30

<210> SEQ ID NO 544
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 544

Gln Gln Tyr Asn Asn Trp Pro Pro Phe Thr
1 5 10

<210> SEQ ID NO 545
<211> LENGTH: 351

-continued

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 545

```

gaggtgcagc tggtggagtc tgggggaggc ttggtagc ctgggggtc cctgagactc   60
tcctgtgcag cctctggatt caccctaagt agctacgaca tgcaactgggt ccgccaagca 120
acaggaaaag gtctggagtg ggtctcagct attggcagta ctggtgacac atactataca 180
ggctccgtga tgggccgatt caccatctcc agagacgctg ccaaaaactc cttcttatctt 240
gaaatgaaca gcctgagagt cggggacacg gctgtatatt actgtgcaag agagggataa 300
agaacacct atgattattt gggccaggga accctggta ccgtctccctc a           351

```

<210> SEQ ID NO 546
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 546

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1															
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Leu	Ser	Ser	Tyr
20															
Asp	Met	His	Trp	Val	Arg	Gln	Ala	Thr	Gly	Lys	Gly	Leu	Glu	Trp	Val
35															
Ser	Ala	Ile	Gly	Ser	Thr	Gly	Asp	Thr	Tyr	Tyr	Thr	Gly	Ser	Val	Met
50															
Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Ala	Ala	Lys	Asn	Ser	Phe	Tyr	Leu
65															
Glu	Met	Asn	Ser	Leu	Arg	Val	Gly	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala
85															
Arg	Glu	Gly	Ile	Arg	Thr	Pro	Tyr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu
100															
Val	Thr	Val	Ser	Ser											
115															

<210> SEQ ID NO 547
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 547

```

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttagc agcaatgttag cctggtagcca gcagaaacct 120
ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 180
aggttcagtgc cagtggtggtc tgggacagaa ttcactctca ccatcagcag cctgcagtct 240
gaagattttc cagtttattt ctgtcagcag tataataatt ggctccatt cactttcgcc 300
cctgggacca aagtggatat caaa                           324

```

<210> SEQ ID NO 548
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

-continued

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 548

```

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
 20          25          30

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

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50          55          60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
 65          70          75          80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Asn Trp Pro Pro
 85          90          95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
 100         105

```

<210> SEQ ID NO 549

<211> LENGTH: 351

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 549

```

gaggtgcagc tggtgaggc tgggggaggc ttggtagc cttgggggtc cctgagactc      60
tcctgtgcag cctctggatt cacccatagt agctacgaca tgcactgggt ccgccaagct    120
acaggaaaag gtctggagt ggtctcagct attggcagta ctggtgacac atactatcca    180
ggctccgtga agggccgatt caccatctcc agagaaaatg ccaagaactc cttgttatctt    240
caaatgaaca gcctgagagc cggggacacg gctgtgtatt actgtgcaag agagggaaata    300
agaacacct atgattattg gggccaagga accctggtca ccgtctcctc a            351

```

<210> SEQ ID NO 550

<211> LENGTH: 117

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 550

```

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu 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 Ser Thr 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 Glu Gly Ile Arg Thr Pro Tyr Asp Tyr Trp Gly Gln Gly Thr Leu
 100         105          110

Val Thr Val Ser Ser

```

-continued

115

```

<210> SEQ ID NO 551
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 551

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccaggaga aagagccacc      60
ctctcctgca gggccagtca gagtgtagc agcaatttag cctggtagcca gcagaaacct      120
ggccaggctc ccaggctctt catctatggt gcatccacca gggccactgg tatcccagcc      180
aggttcagtg cgactgggtc tgggacagag ttcaactctca ccatcagcag cctgcagtct      240
gaagattttg cagtttatta ctgtcagcag tataataatt ggctccatt cacttcggc      300
cctgggacca aagtggatat caaa                                         324

```

```

<210> SEQ ID NO 552
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 552

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
 20          25           30

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

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50          55           60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
 65          70           75           80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Asn Trp Pro Pro
 85          90           95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
 100         105

```

```

<210> SEQ ID NO 553
<211> LENGTH: 351
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 553

gaggtgcagc tggtgaggc tgggggaggc ttggtagc ctgggggtc cctgagactc      60
tcctgtgcag cctctggatt caccctaagt agctacgaca tgcactgggt ccgccaagca      120
acaggaaaag gtctggagt ggtctcagct attggcagta ctggtagcac atactataca      180
ggctccgtga tgggccgatt caccatctcc agagacgctg ccaaaaactc cttctatctt      240
gaaatgaaca gcctgagagt cggggacacg gctgtatatt actgtgcaag agaggaaata      300
agaacaccct atgattattg gggccaggga gcccgggtca ccgtctccctc a             351

<210> SEQ ID NO 554
<211> LENGTH: 117

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-continued

<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 554

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	
1																15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu 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 Ser Thr Gly Asp Thr Tyr Tyr Thr Gly Ser Val Met
50 55 60

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

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

Arg Glu Gly Ile Arg Thr Pro Tyr Asp Tyr Trp Gly Gln Gly Ala Arg
100 105 110

Val Thr Val Ser Ser
115

<210> SEQ ID NO 555
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 555

ggattcaccc taagtagcta cgac 24

<210> SEQ ID NO 556
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 556

Gly Phe Thr Leu Ser Ser Tyr Asp
1 5

<210> SEQ ID NO 557
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 557

atggcagta ctggtgacac a 21

<210> SEQ ID NO 558
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 558

Ile Gly Ser Thr Gly Asp Thr
1 5

-continued

<210> SEQ ID NO 559
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 559

gcaagagagg gaataagaac accctatgtat tat

33

<210> SEQ ID NO 560
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 560

Ala Arg Glu Gly Ile Arg Thr Pro Tyr Asp Tyr
1 5 10

<210> SEQ ID NO 561
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 561

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc	60
ctctcctgca gggccagtca gagtgtagc agcaatgtag cctggtagcca gcagaaacct	120
ggccaggctc ccaggctct catctatggt gcatccacca gggccactgg tatcccagcc	180
aggttcagtg gcagtgggtc tgggacagaa ttcaactctca ccatcagcag cctgcagtct	240
gaagattttg cagtttatta ctgtcagcag tataataatt ggctccatt cacttcggc	300
cctgggacca aagtggatata caaa	324

<210> SEQ ID NO 562
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 562

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

-continued

<210> SEQ ID NO 563
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 563

cagagtgtta gcagcaat

18

<210> SEQ ID NO 564
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 564

Gln Ser Val Ser Ser Asn
1 5

<210> SEQ ID NO 565
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 565

ggtgtcatcc

9

<210> SEQ ID NO 566
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 566

Gly Ala Ser
1

<210> SEQ ID NO 567
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 567

cagcagtata ataattggcc tccattcact

30

<210> SEQ ID NO 568
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 568

Gln Gln Tyr Asn Asn Trp Pro Pro Phe Thr
1 5 10

<210> SEQ ID NO 569
<211> LENGTH: 351
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

-continued

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 569

gaggtgcagc	tggtggagtc	tgggggaggc	ttggtagc	ctggggggtc	cctgagactc	60
tcctgtgcag	cctctggatt	caccctaagt	agctacgaca	tgcaactgggt	ccgccaagca	120
acagggaaag	gtctggagtg	ggtctcagct	atggcagta	ctggtgacac	atactataca	180
ggctccgtga	tgggccgatt	caccatctcc	agagacgctg	ccaaaaactc	cttcttatctt	240
gaaatgaaca	gcctgaggt	cggggacacg	gctgtatatt	actgtcaag	agaggaaata	300
agaacaccct	atgattattg	gggcaggga	accctggta	ccgtctcc	a	351

<210> SEQ ID NO 570

<211> LENGTH: 117

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 570

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	Leu	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	Ser	Thr	Gly	Asp	Thr	Tyr	Tyr	Thr	Gly	Ser	Val	Met
	50									55		60			

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

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

Arg	Glu	Gly	Ile	Arg	Thr	Pro	Tyr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu
										100		105		110	

Val	Thr	Val	Ser	Ser											
					115										

<210> SEQ ID NO 571

<211> LENGTH: 324

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 571

gaaatagtga	tgacgcagtc	tccagccacc	ctgtctgtgt	ctccagggg	aagagccacc	60
ctctcttgca	ggccagtc	gaggttgtac	agcaatgtac	cctggtagca	gcagaaaacct	120
ggccaggctc	ccaggctct	catctatgg	gcatccacca	ggccactgg	tatcccagcc	180
aggttcagtg	cgactgggtc	tggcacagaa	ttcaactctca	ccatcagcag	cctgcagtc	240
gaagatttg	cagtttatta	ctgtcagcag	tataataatt	ggcctccatt	cacttcggc	300
cctgggacca	aagtggat	aaaa				324

<210> SEQ ID NO 572

<211> LENGTH: 108

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

-continued

```

<210> SEQ ID NO 575
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 575

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccaggggaa aagagccacc      60
ctctcctgca gggccagtca gagtgtagc agcaatttag cctggtagcca gcagaaaacct      120
ggccaggctc ccaggctct catctatggt gcatccacca gggccactgg tatcccagcc      180
aggttcagtg gcagtggttc tgggacagag ttcaactctca ccatcagcag cctgcagtt      240
gaagatttttgcagtttataatctgtcagcag tataataatt ggctccatt cacttcggc      300
cctggacca aagtggatataaaa                                         324

```

```

<210> SEQ ID NO 576
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 576

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
 20          25           30

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

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50          55           60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
 65          70           75           80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Asn Trp Pro Pro
 85          90           95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
 100         105


```

```

<210> SEQ ID NO 577
<211> LENGTH: 363
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 577

gaagtgtcagtc tggtggagtc tgggggaggc ttggtagcactc ctggcaggtc cctgagactc      60
tcctgtgcag cctctggatt cacctttat gattatgccat tgcaactgggt ccggcaagct      120
ccagggaaagg gcctggagtg ggtctcaggat attaatggaa acagtggtag cataggctat      180
gcggactctg tgaaggcccg attcaccatc tccagagaca acgccaagca ctccctgtat      240
ctgcaaatga acagtctgag acctgaggac acggccttgtt attactgtgt aaaagaggta      300
actacggat actactacgg tatggacgtc tggggccaag ggaccacggc caccgtctcc      360
tca


```

```

<210> SEQ ID NO 578
<211> LENGTH: 121
<212> TYPE: PRT

```

-continued

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 578

```

Glu Val Gln Leu Val Glu Ser 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 Asn 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 His Ser Leu Tyr
 65          70          75          80

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

Val Lys Glu Val Thr Thr Gly Tyr Tyr Gly Met Asp Val Trp Gly
100         105         110

Gln Gly Thr Thr Val Thr Val Ser Ser
115         120

```

<210> SEQ ID NO 579
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 579

```

ggattcacct ttgatgatta tgcc

```

<210> SEQ ID NO 580
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

24

<400> SEQUENCE: 580

```

Gly Phe Thr Phe Asp Asp Tyr Ala
 1           5

```

<210> SEQ ID NO 581
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 581

```

attaatttggaa acagttggtag cata

```

<210> SEQ ID NO 582
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

24

<400> SEQUENCE: 582

```

Ile Asn Trp Asn Ser Gly Ser Ile
 1           5

```

-continued

<210> SEQ ID NO 583
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 583

gtaaaagagg tgactacggg atactactac ggtatggacg tc 42

<210> SEQ ID NO 584
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 584

Val Lys Glu Val Thr Thr Gly Tyr Tyr Tyr Gly Met Asp Val
1 5 10

<210> SEQ ID NO 585
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 585

gacatccagt tgacccagtc tccatccttc ctgtctgcat ctgttaggaga cagagtcacc	60
atcacttgct gggccagtca gggcatttgc agttattttag cctggtatca gaaaaaaacca	120
gggaaagccc ctaaccttct gatctatgtat gcatccactt tgcaaagtgg ggtcccatca	180
aggttcagcg gcagtggatc tgggacagaa ttcaactctca cactcagcag cctgcagcc	240
gaagattttgc caacttattatca ctgtcaacag cttaatattt acccattcac ttccggccct	300
gggacccaaag tggatatcaa a	321

<210> SEQ ID NO 586
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 586

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

<210> SEQ ID NO 587

-continued

<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 587

cagggcattatcgagttat

18

<210> SEQ ID NO 588
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 588

Gln Gly Ile Ser Ser Tyr
1 5

<210> SEQ ID NO 589
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 589

gatgcattcc

9

<210> SEQ ID NO 590
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 590

Asp Ala Ser
1

<210> SEQ ID NO 591
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 591

caacagctta atatttaccc attcaact

27

<210> SEQ ID NO 592
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 592

Gln Gln Leu Asn Ile Tyr Pro Phe Thr
1 5

<210> SEQ ID NO 593
<211> LENGTH: 363
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 593

gaagtgcagc	tggtgaggc	tgggggaggc	ttggtagcago	ctggcaggc	cctgagactc	60
tcctgtgcag	cctctggatt	cacctttagat	gattatgcca	tgcactgggt	ccggcaagct	120
ccagggaaagg	gcctggagtg	ggtctcaggat	attaatttgg	acagtggtag	cataggctat	180
gcggactctg	tgaagggccg	attcaccatc	tccagagaca	acgccaagca	ctccctgtat	240
ctgcaaata	acagtctgag	acctgaggac	acggccttgt	attactgtgt	aaaagaggtg	300
actacggat	actactacgg	tatggacg	tggggccaag	ggaccacgg	caccgtctcc	360
tca						363

<210> SEQ ID NO 594

<211> LENGTH: 121

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 594

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Ley	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	Ley	Glu	Trp	Val
	35				40					45					
Ser	Gly	Ile	Asn	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	His	Ser	Leu	Tyr
65			70			75					80				
Leu	Gln	Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Leu	Tyr	Tyr	Cys
	85				90				95						
Val	Lys	Glu	Val	Thr	Thr	Gly	Tyr	Tyr	Tyr	Gly	Met	Asp	Val	Trp	Gly
	100				105				110						
Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser							
	115				120										

<210> SEQ ID NO 595

<211> LENGTH: 321

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 595

gacatccagt	tgacccagtc	tccatccttc	ctgtctgcat	ctgttaggaga	cagagtcacc	60
atcaattgt	gggccagtca	gggcatttgc	agttattttg	cctggtatca	aaaaaaacca	120
gggaaagccc	ctaaccctct	gatctatgt	gcatccactt	tgc当地tgg	ggtccccatca	180
aggttcagcg	gcagtggtatc	tgggacagaa	ttcactctca	cactcagcag	cctgcagcct	240
gaagattttgc	caacttattta	ctgtcaacag	c当地atattt	accattcac	tttc当地ccct	300
gggaccataag	tggatataaa	a				321

<210> SEQ ID NO 596

<211> LENGTH: 107

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

-continued

<400> SEQUENCE: 596

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

<210> SEQ ID NO 597

<211> LENGTH: 363

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 597

gaagtgcagc	tgggtggagtc	tgggggaggc	ttgggtacago	ctggcaggc	cctgagactc	60
tccctgtgcag	cctctggatt	cacctttgat	gattatgcc	tgcactgggt	ccggcaagct	120
ccagggaaagg	gcctggagtg	ggtctcaggt	attaattgga	acagtggttag	cataggctat	180
gcggactctg	tgaaggcccg	attcaccatc	tccagagaca	acgccaagaa	ctccctgtat	240
ctgcaaatga	acagtctgag	agctgaggac	acggccttgc	attactgtgt	aaaagaggtg	300
actacggat	actactacgg	tatggacg	tgggggcaag	ggaccacgg	caccgtctcc	360
tca						363

<210> SEQ ID NO 598

<211> LENGTH: 121

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 598

Glu	Val	Gln	Leu	Val	Glu	Ser	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	Asn	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	Val	Thr	Thr	Gly	Tyr	Tyr	Gly	Met	Asp	Val	Trp	Gly	
	100					105						110			
Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser							

-continued

115

120

<210> SEQ ID NO 599
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 599

```

gacatccagt tgacccagtc tccatccttc ctgtctgcat ctgttaggaga cagagtcacc      60
atcaattgcc gggccagtca gggcattagc agttatattag cctggtatca gcaaaaacca      120
gggaaaggccc ctaagtcctt gatctatgtat gcatccactt tgcaaagtgg ggtcccatca      180
agggttcagcg cgactggatc tgggacagaa ttcaactctca caatcagcag cctgcagcct      240
gaagattttg caacttatta ctgtcaacag cttaatattt acccattcac tttcgccct      300
gggaccaaag tggatataaa a                                              321

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<210> SEQ ID NO 600
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 600

```

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

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

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

Tyr Asp Ala Ser Thr 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 Gln Gln Leu Asn Ile Tyr Pro Phe
 85          90          95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
 100         105

```

<210> SEQ ID NO 601
<211> LENGTH: 366
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 601

```

gaggtgcagt tggggggggc ttgggtacagc ctggggggtc cctgagactc      60
tcctgtgcag cctctggatt cacgttttgt agctatgcca tgaactgggt ccggcaggct      120
ccagggagg ggctggattt ggtctcaggat atcagtggta atgggtggtag cacctactac      180
gcagactccg tgaaggcccg gttcaccatc tccagagaca tttccaagaa cacgctgtat      240
gtgcaaattgc acagcctgag agtcgaggac acggccgttt actactgtgc gaaagccgt      300
tattacgatt tttggggggg gaatttcgat ctctggggcc gtggcaccca ggtcactgtc      360
tcctca                                              366

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-continued

<210> SEQ ID NO 602
<211> LENGTH: 122
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 602

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

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

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

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

Ala	Lys	Ala	Arg	Tyr	Tyr	Asp	Phe	Trp	Gly	Gly	Asn	Phe	Asp	Leu	Trp
	100					105						110			

Gly	Arg	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser						
	115					120									

<210> SEQ ID NO 603
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 603

ggattcacgt ttagtagcta tgcc 24

<210> SEQ ID NO 604
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 604

Gly Phe Thr Phe Ser Ser Tyr Ala
1 5

<210> SEQ ID NO 605
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 605

atcagtggta atgggtggtag cacc 24

<210> SEQ ID NO 606
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 606

-continued

Ile Ser Gly Asn Gly Gly Ser Thr
1 5

<210> SEQ ID NO 607
<211> LENGTH: 45
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 607

gcgaaagccc gttattacga ttttggggg gggatattcg atctc 45

<210> SEQ ID NO 608
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 608

Ala Lys Ala Arg Tyr Tyr Asp Phe Trp Gly Gly Asn Phe Asp Leu
1 5 10 15

<210> SEQ ID NO 609
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 609

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgtagc atcaggtact tagcctggta tcagcagaaa 120
cctggccagg ctcggcaggct cctcatctat ggtgcattca gcaggggcac tggcatccca 180
gacaggttca gtgtcagttgt gtctggaca gacttcactc tcaccatcac tagactggag 240
cctgaagatt ttgcagttca ttactgttag caaatggta gttcacccgt cacttcggc 300
ggagggacca aggtggagat caaa 324

<210> SEQ ID NO 610
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 610

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 Ile Arg
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

Val Ser Val Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr 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

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

-continued

<210> SEQ ID NO 611
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 611

cagagtgtta gcatacggtt c

21

<210> SEQ ID NO 612
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 612

Gln Ser Val Ser Ile Arg Tyr
1 5

<210> SEQ ID NO 613
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 613

ggtgcatcc

9

<210> SEQ ID NO 614
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 614

Gly Ala Ser
1

<210> SEQ ID NO 615
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 615

cagcaatatg gtatgttacc gctcact

27

<210> SEQ ID NO 616
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 616

Gln Gln Tyr Gly Ser Ser Pro Leu Thr
1 5

<210> SEQ ID NO 617
<211> LENGTH: 366
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 617

gagggtgcagt	tgttggagtc	tgggggaggc	ttggcacgc	ctggggggtc	cctgagactc	60
tcctgtgcag	cctctggatt	cacgttttagt	agctatgcc	tgaactgggt	ccgcaggct	120
ccagggaaagg	ggctggattt	ggtctcagg	atcagtggta	atgggttgt	cacctactac	180
gcagactccg	tgaaggcccg	gttccaccatc	tccagagaca	tttccaagaa	cacgctgtat	240
gtgcaaatgc	acagcctgag	agtcgaggac	acggccgttt	actactgtgc	gaaagcccgt	300
tattacgatt	tttggggggg	gaatttcgat	ctctggggcc	gtggcaccc	ggtactgtc	360
tcctca						366

<210> SEQ ID NO 618

<211> LENGTH: 122

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 618

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

<210> SEQ ID NO 619

<211> LENGTH: 324

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 619

gaaattgtgt	tgacgcagtc	tccaggcacc	ctgtcttgt	ctccagggg	aagagccacc	60
ctctctgc	ggccagtc	gagtgttagc	atcaggta	tagctggta	tcagcagaaa	120
cctggccagg	c	c	c	c	c	180
gacaggttca	gtgtcagtgt	gtctggaca	gacttcactc	tcaccatcac	tagactggag	240
cctgaagatt	ttgcagtc	ttactgtcag	caatatggta	gttcaccgct	cactttcggc	300
ggagggacca	aggtggagat	caaa				324

<210> SEQ ID NO 620

<211> LENGTH: 108

<212> TYPE: PRT

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100

105

110

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

<210> SEQ ID NO 623
 <211> LENGTH: 324
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 623

gaaattgtgt tgacgcagtc tccaggcacc ctgtcttgc	ctccagggga aagagccacc	60
ctctcttgca gggccagtca gagtgttagc atcaggtact tagcctggta	ccagcagaaa	120
cctggccagg ctcccaggct cctcatctat ggtgcatacca	gcagggccac tggcatccca	180
gacaggttca gtggcagtgg gtctggaca gacttcactc tcaccatcag	cagactggag	240
cctgaagatt ttgcagtgtt tactgtcag caatatggta	gttcaccgct cacttcggc	300
ggagggacca aggtggagat caaa		324

<210> SEQ ID NO 624
 <211> LENGTH: 108
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 624

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ile Arg		
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

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

<210> SEQ ID NO 625
 <211> LENGTH: 381
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 625

caggttcago tggtgcaagtc tggacctgag gtgaagaacc	ctggggcctc agtgaaggta	60
tccgtcaagg cttctggta caccttacc acctatggta	tcagttgggt acgcacaggcc	120
cctggacaag ggctttagtg gatgggatgg atcagcggtt	acaatggtaa aacaaacgat	180
gcacagaagt tccaggacag agtcgccccatg accacagaca	catccacgag cacagcctac	240
atggagctga ggagcctgag atctgacgac acggccattt	attactgttc gagagatcg	300
tttagtagtac cacctgcctt ttattattcc tactacgtta	tggacgtctg gggccaagg	360

-continued

accacggtaa ccgtcttc a

381

<210> SEQ ID NO 626
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 626

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu	Val	Lys	Asn	Pro	Gly	Ala	
1																15

Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Thr	Tyr	
																30
Gly	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	
																45
Gly	Trp	Ile	Ser	Gly	Tyr	Asn	Gly	Lys	Thr	Asn	Asp	Ala	Gln	Lys	Phe	
																60
Gln	Asp	Arg	Val	Ala	Met	Thr	Thr	Asp	Thr	Ser	Thr	Ser	Thr	Ala	Tyr	
																80
Met	Glu	Leu	Arg	Ser	Leu	Arg	Ser	Asp	Asp	Thr	Ala	Ile	Tyr	Tyr	Cys	
																95
Ser	Arg	Asp	Arg	Leu	Val	Val	Pro	Pro	Ala	Leu	Tyr	Tyr	Ser	Tyr	Tyr	
																110
Val	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser		
																125

<210> SEQ ID NO 627
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 627

ggttacacctt ttaccaccta tgg

24

<210> SEQ ID NO 628
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 628

Gly	Tyr	Thr	Phe	Thr	Thr	Tyr	Gly
1							5

<210> SEQ ID NO 629
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 629

atcagcggtt acaatggtaa aaca

24

<210> SEQ ID NO 630
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

-continued

<400> SEQUENCE: 630

```
Ile Ser Gly Tyr Asn Gly Lys Thr
 1           5
```

<210> SEQ ID NO 631

<211> LENGTH: 60

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 631

```
tcgagagatc gtttagtagt accacctgcc ctttattttt cttactacgt tatggacgtc      60
```

<210> SEQ ID NO 632

<211> LENGTH: 20

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 632

```
Ser Arg Asp Arg Leu Val Val Pro Pro Ala Leu Tyr Tyr Ser Tyr Tyr
 1           5           10          15
```

```
Val Met Asp Val
 20
```

<210> SEQ ID NO 633

<211> LENGTH: 336

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 633

```
gatgttgtga tgactcagtc tccactctcc ctgcccgtca cccttggaca gccggccctcc      60
atctcctgca ggtctagtca aagcctcgta tacagtgtatc gaaacacacta cttgaattgg      120
tttcagcaga ggccaggta atctccaagg cgccctaattt ataaggtttc taaccggac      180
tctgggtcc cagacagatt cagcggcagt gggtcaggca ctgatttcac actgaaaatc      240
agcagggtgg aggctgagga tgggggtt tattactgca tgcaaggta acactggccg      300
tacacttttgc cccaggac caagctggag atcaaa                                336
```

<210> SEQ ID NO 634

<211> LENGTH: 112

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 634

```
Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
 1           5           10          15
```

```
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser
 20          25          30
```

```
Asp Gly Asn Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
 35          40          45
```

```
Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Arg Asp 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
```


-continued

1 5

```

<210> SEQ ID NO 641
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 641

caggttcagtc tggtgccatgc tggacctgag gtgaagaacc ctggggcctc agtgaaggtc   60
tcctgcaagg cttctggtta caccttacc acctatggta tcagttgggt acgcacaggcc   120
cctggacaag ggcttgagtg gatggggatgg atcagcggtt acaatggtaa aacaaacgat   180
gcacagaagt tccaggacag agtcgcccattg accacagaca catccacgag cacagcctac   240
atggagctga ggagcctgag atctgacgac acggccattt attactgttc gagagatcgt   300
tttagtagtac cacctgcctt ttattattcc tactacgtta tggacgtctg gggccaaggg   360
accacggtca ccgtctcctc a                                         381

```

```

<210> SEQ ID NO 642
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 642

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

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

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

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

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

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

Ser Arg Asp Arg Leu Val Val Pro Pro Ala Leu Tyr Tyr Ser Tyr Tyr
100          105          110

Val Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115          120          125

```

```

<210> SEQ ID NO 643
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 643

gatgttgta tgactcagtc tccactctcc ctggccgtca cccttggaca gccggcctcc   60
atctcctgca ggtcttagtca aagcctcgta tacagtgtatc gaaacaccta cttgaatttg   120
tttcagcaga ggccagggtca atctccaagg cgcctaattt ataagggttc taaccggac   180
tctggggtcc cagacagatt cagcggcagt gggtcaggca ctgatttcac actgaaaatc   240
agcagggtgg aggctgagga tgggggtt tattactgca tgcaaggtaa acactggccg   300

```


-continued

65	70	75	80
Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys			
85	90	95	
Ser Arg Asp Arg Leu Val Val Pro Pro Ala Leu Tyr Tyr Ser Tyr Tyr			
100	105	110	
Val Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser			
115	120	125	

<210> SEQ ID NO 647
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 647

gatgttgtga tgactcagtc tccactctcc ctgccccgtca cccttggaca gccggccctcc	60
atctccttgca ggtcttagtca aagcctcgta tacagtgtatc gaaacaccta cttgaattgg	120
tttcagcaga ggccaggcca atctccaagg cgccataattt ataaggtttc taaccggac	180
tctggggtcc cagacagatt cagccggcgtt gggtcaggca ctgatccac actgaaaatc	240
agcaggggtgg aggctgagga tgggggtt tattactgca tgcaaggatc acactggccg	300
tacacttttg gccaggggac caagctggag atcaaa	336

<210> SEQ ID NO 648
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 648

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

<210> SEQ ID NO 649
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 649

caggttcagtc tgggtgcagtc tggacctgag gtgaagaacc ctggggcctc agtgaaggtc	60
tcctgcaagg cttctggta cacctttacc acctatggta tcagttgggt acgcacaggcc	120
cctggacaag gggttgatgc gatggatgg atcagcggtt acaaatggtaa aacaaacgt	180

-continued

gcacagaagt	tccaggacag	agtgcctatg	accacagaca	catccacgag	cacagcctac	240
atggagctga	ggagcctgag	atctgacgac	acggccattt	attactgttc	gagagatcg	300
ttagtagtac	cacctgcctt	taattattac	tactacgtta	tggacgtctg	gggccaagg	360
accacggta	ccgtctcctc	a				381

<210> SEQ ID NO 650
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 650

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu	Val	Lys	Asn	Pro	Gly	Ala
1				5				10							15
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Thr	Tyr
	20				25										30
Gly	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
	35				40										45
Gly	Trp	Ile	Ser	Gly	Tyr	Asn	Gly	Lys	Thr	Asn	Asp	Ala	Gln	Lys	Phe
	50				55										60
Gln	Asp	Arg	Val	Ala	Met	Thr	Thr	Asp	Thr	Ser	Thr	Ser	Thr	Ala	Tyr
	65				70										80
Met	Glu	Leu	Arg	Ser	Leu	Arg	Ser	Asp	Asp	Thr	Ala	Ile	Tyr	Tyr	Cys
	85					90									95
Ser	Arg	Asp	Arg	Leu	Val	Val	Pro	Pro	Ala	Leu	Asn	Tyr	Tyr	Tyr	
	100					105									110
Val	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	
	115					120									125

<210> SEQ ID NO 651
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 651

ggttacacctt accatccata ttggt 24

<210> SEQ ID NO 652
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 652

Gly	Tyr	Thr	Phe	Thr	Thr	Tyr	Gly
1				5			

<210> SEQ ID NO 653
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 653

atcagcggtt acaatggtaa aaca 24

-continued

<210> SEQ ID NO 654
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 654

Ile	Ser	Gly	Tyr	Asn	Gly	Lys	Thr
1							5

<210> SEQ ID NO 655
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 655

tcgagagatc gtttagtagt accacctgcc cttattttt actactacgt tatggacgtc	60
--	----

<210> SEQ ID NO 656
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 656

Ser	Arg	Asp	Arg	Leu	Val	Val	Pro	Pro	Ala	Leu	Asn	Tyr	Tyr	Tyr
1				5			10			15				

Val	Met	Asp	Val
20			

<210> SEQ ID NO 657
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 657

gatgttgtga tgactcagtc tccactctcc ctgccccgtca cccttggaca gccggcctcc	60
atctcctgca ggtctagtca aagcctcgta tacagtgtatc gaaacaccta cttgaatttg	120
tttcagcaga ggccagggtca atctccaagg cgccataattt ataaggtttc taaccgggac	180
tctggggtcc cagacagatt cagcggcagt gggtcaggca ctgatccac actgaaaatc	240
agcagggtgg aggctgagga tgggggtt tattactgca tgcaaggtac acactggccg	300
tacacttttg gccaggggac caagctggag atcaaa	336

<210> SEQ ID NO 658
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 658

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

Gln	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	Tyr	Ser
20				25						30					

Asp	Gly	Asn	Thr	Tyr	Leu	Asn	Trp	Phe	Gln	Gln	Arg	Pro	Gly	Gln	Ser
35				40						45					

-continued

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

Asp Arg Phe 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 Gly
 85 90 95

Thr His Trp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> SEQ ID NO 659
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 659

caaaggctcg tatacagtga tggaaacacc tac

33

<210> SEQ ID NO 660
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 660

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

<210> SEQ ID NO 661
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 661

aaggtttct

9

<210> SEQ ID NO 662
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 662

Lys Val Ser
 1

<210> SEQ ID NO 663
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 663

atgcaaggta cacactggcc gtacact

27

<210> SEQ ID NO 664
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 664

Met Gln Gly Thr His Trp Pro Tyr Thr
 1 5

<210> SEQ ID NO 665
 <211> LENGTH: 381
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 665

caggttcagc tggtgcaagg	tggacctgag ctggggcctc	agtgaaggtc	60
tcctgcagg cttctggta	caccattacc acctatggta	tcaagttgggt acgacaggcc	120
cctggacaag ggctttagtg	gatgggatgg atcagcggtt	acaatggtaa acaaaacat	180
gcacagaagt tccaggacag	agtcgccatg accacagaca	catccacgag cacagcctac	240
atggagctga ggagcctgag	atctgacgac acggccattt	attactgttc gagagatcg	300
tttagtagtac cacctgcct	taattattac tactacgtta	tggacgtctg gggccaagg	360
accacggtaa ccgtctcc	ta a		381

<210> SEQ ID NO 666
 <211> LENGTH: 127
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 666

Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Asn Pro Gly Ala			
1 5 10 15			
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr			
20 25 30			
Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met			
35 40 45			
Gly Trp Ile Ser Gly Tyr Asn Gly Lys Thr Asn Asp Ala Gln Lys Phe			
50 55 60			
Gln Asp Arg Val Ala Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr			
65 70 75 80			
Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Ile Tyr Tyr Cys			
85 90 95			
Ser Arg Asp Arg Leu Val Val Pro Pro Ala Leu Asn Tyr Tyr Tyr Tyr			
100 105 110			
Val Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser			
115 120 125			

<210> SEQ ID NO 667
 <211> LENGTH: 336
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 667

gatgttgtaa tgactcagtc tccactctcc ctggccgtca cccttggaca gccggccctcc	60
atctcctgca ggtctagtca aagectcgta tacagtgtatc gaaacacaccta cttgaattgg	120

-continued

tttcagcaga ggccagggtca atctccaagg cgccctaattt ataagggttc taaccgggac	180
tctgggttcc cagacagatt cagcggcagt gggtcagagca ctgatttcac actgaaaatc	240
agcagggtgg aggctgagga tgttgggtt tattactgca tgcaagggtac acactggccg	300
tacacttttq qccqqqqqac caaqctqqaq atcaaa	336

```
<210> SEQ ID NO 668
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

<400> SEQUENCE: 668

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser
20 25 30

Asp Gly Asn Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
 35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Arg Asp 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 Gly
85 90 95

Thr His Trp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110

```
<210> SEQ ID NO 669
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

<400> SEQUENCE: 669

cagggttcagc tgggtgcagtc tggagatcgag gtgaagaagc ctggggcctc agtgaaggtc	60
tcctgtcaagg cttctggtta cacctttacc acctatggta tcagctgggt ggcacaggcc	120
cctggacaag ggcttgagtg gatggatgg atcagcgtt acaatggtaa aacaaactat	180
gcacagaagc tccaggcgac agtcaccatg accacagaca catccacgag cacagccctac	240
atggagactga ggagcctgag atctgacgac acggccgtgtt attactgttc gagagatcgt	300
ttagtagtac cacctgcctt taattattac tactacgtta tggacgtctg ggggcaagg	360
accacgggtca ccgtctcctc a	381

```
<210> SEQ ID NO 670
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

<400> SEQUENCE: 670

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

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

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

-continued

35	40	45
----	----	----

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

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

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

Ser Arg Asp Arg Leu Val Val Pro Pro Ala Leu Asn Tyr Tyr Tyr Tyr		
100	105	110

Val Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser		
115	120	125

<210> SEQ ID NO 671

<211> LENGTH: 336

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 671

gatgttgtga tgactcagtc tccactctcc ctggccgtca cccttggaca gccggcctcc	60
atctcctgca ggtctagtca aagcctcgta tacagtgtatc gaaacaccta cttgaattgg	120
tttcagcaga ggcaggcca atctccaagg cgccataattt ataagggttc taaccggac	180
tctggggtcc cagacagatt cagcggcagt gggtcaggca ctgatttac actgaaaatc	240
agcagggtgg aggctgagga tgttggggtt tattactgca tgcaaggtac acactggccg	300
tacacttttg gccaggggac caagctggag atcaaa	336

<210> SEQ ID NO 672

<211> LENGTH: 112

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 672

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser		
20	25	30

Asp Gly Asn Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser		
35	40	45

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

Asp Arg Phe 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 Gly		
85	90	95

Thr His Trp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys		
100	105	110

<210> SEQ ID NO 673

<211> LENGTH: 381

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 673

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caggttcagc tgggtgcagtc tggaccttagt gtgaagaacc ctggggctc agtgaaggtc	60
tcctcgaaagg cttctgggta cacctttacc acctatggta tcagttgggt acgcacaggcc	120
cctggacaag ggcttgagtg gatggggatgg atcagcggtt acaatggtaa aacaaacgat	180
gcacagaagt tccaggacag agtgcgcatt accacagaca catccacgag cacagcctac	240
atggagctga ggagcctgag atctgacgac acggccattt attactgttc gagagatcg	300
ttagtagtac cacctgcctt ttattattac tactacgtta tggacgtctg gggccaagg	360
accacggta ccgtctcctc a	381

<210> SEQ ID NO 674

<211> LENGTH: 127

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 674

Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Asn Pro Gly Ala			
1	5	10	15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr			
20	25	30	
Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met			
35	40	45	
Gly Trp Ile Ser Gly Tyr Asn Gly Lys Thr Asn Asp Ala Gln Lys Phe			
50	55	60	
Gln Asp Arg Val Ala Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr			
65	70	75	80
Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Ile Tyr Tyr Cys			
85	90	95	
Ser Arg Asp Arg Leu Val Val Pro Pro Ala Leu Tyr Tyr Tyr Tyr			
100	105	110	
Val Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser			
115	120	125	

<210> SEQ ID NO 675

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 675

ggttacacctt ttaccaccta tgg

24

<210> SEQ ID NO 676

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 676

Gly Tyr Thr Phe Thr Thr Tyr Gly

1 5

<210> SEQ ID NO 677

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 677

atcagcggtt acaatggtaa aaca

24

<210> SEQ ID NO 678

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 678

Ile Ser Gly Tyr Asn Gly Lys Thr
1 5

<210> SEQ ID NO 679

<211> LENGTH: 60

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 679

tcgagagatc gtttagtagt accacctgcc ctttattatt actactacgt tatggacgtc 60

<210> SEQ ID NO 680

<211> LENGTH: 20

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 680

Ser Arg Asp Arg Leu Val Val Pro Pro Ala Leu Tyr Tyr Tyr Tyr Tyr
1 5 10 15Val Met Asp Val
20

<210> SEQ ID NO 681

<211> LENGTH: 336

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 681

gatgttgtga tgactcagtc tccactctcc ctgcccgtca cccttggaca gccggcctcc 60

atctcctgca ggtctagtca aagectcgta tacagtgtatc gaaacaccta cttgaattgg 120

tttcagcaga ggccagggtca atctccaagg cgccctaattt ataagggttc taaccggac 180

tctggggtcc cagacagatt cagcggcagt gggtcaggca ctgatttcac actgaaaatc 240

agcagggtgg aggctgagga tggtgggtt tattactgca tgcaaggta acactggccg 300

tacacttttgc cccaggggac caagctggag atcaaa 336

<210> SEQ ID NO 682

<211> LENGTH: 112

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 682

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

-continued

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser
 20 25 30

Asp Gly Asn Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
 35 40 45

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

Asp Arg Phe 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 Gly
 85 90 95

Thr His Trp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> SEQ ID NO 683
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 683

caaaggctcg tatacagtga tggaaacacc tac 33

<210> SEQ ID NO 684
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 684

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

<210> SEQ ID NO 685
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 685

aaggttct 9

<210> SEQ ID NO 686
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 686

Lys Val Ser
 1

<210> SEQ ID NO 687
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 687

atgcaaggta cacactggcc gtacact 27

-continued

<210> SEQ ID NO 688
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 688

Met Gln Gly Thr His Trp Pro Tyr Thr
1 5

<210> SEQ ID NO 689
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 689

caggttcagc tgggtgcagtc tggaccttagt gtgaagaacc ctggggcetc agtgaaggtc	60
tccctgcaagg cttctggta caccttacc acctatggta tcagttgggt acgacaggcc	120
cctggacaag ggctttagtg gatgggatgg atcagcggtt acaatggtaa aacaaacgat	180
gcacagaagt tccaggacag agtcgcccatt accacagaca catccacgag cacagcctac	240
atggagactga ggagcctgag atctgacgac acggccattt attactgttc gagagatcg	300
ttagtagtac cacctgcctt ttattattac tactacgtta tggacgtctg gggccaagg	360
accacggta ccgtctccat a	381

<210> SEQ ID NO 690
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 690

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

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

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

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

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

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

Ser Arg Asp Arg Leu Val Val Pro Pro Ala Leu Tyr Tyr Tyr Tyr
100 105 110

Val Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> SEQ ID NO 691
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

-continued

<400> SEQUENCE: 691

gatgttgta tgactcagtc tccactctcc ctgcccgtca cccttggaca gccggcctcc	60
atctcttgca ggtctagtca aagcctcgta tacagtgtat gaaacaccta cttgaattgg	120
tttcaggcaga ggcagggtca atctccaagg cgccataattt ataaggtttc taaccggac	180
tctggggtcc cagacagatt cageggcagt gggtcaggca ctgatccac actgaaaatc	240
agcagggtgg aggctgagga tgggggtt tattactgca tgcaaggtac acactggccg	300
tacacttttgc gcaggggac caagctggag atcaaaa	336

<210> SEQ ID NO 692

<211> LENGTH: 112

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 692

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

<210> SEQ ID NO 693

<211> LENGTH: 381

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 693

caggttcagtc tgggtcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc	60
tcctgtcaagg cttctgggta caccttacc accttatggta tcagctgggt ggcacaggcc	120
cctggacaag ggcttgagtg gatggatgg atcagcggtt acaatggtaa aacaaactat	180
gcacagaagc tccaggcagc agtcaccatg accacagaca catccacgag cacagcctac	240
atggagctga ggagcctgag atctgacgac acggccgtgt attactgttc gagagatcg	300
ttagtagtac cacctgcct ttattattac tactacgtta tggacgtctg gggcaagg	360
accacggta ccgtctcc a	381

<210> SEQ ID NO 694

<211> LENGTH: 127

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 694

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

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1	5	10	15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr			
20	25	30	
Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met			
35	40	45	
Gly Trp Ile Ser Gly Tyr Asn Gly Lys Thr Asn Tyr Ala Gln Lys Leu			
50	55	60	
Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr			
65	70	75	80
Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys			
85	90	95	
Ser Arg Asp Arg Leu Val Val Pro Pro Ala Leu Tyr Tyr Tyr Tyr Tyr			
100	105	110	
Val Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser			
115	120	125	

<210> SEQ ID NO 695

<211> LENGTH: 336

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 695

gatgttgtga tgactcagtc tccactctcc ctggccgtca cccttggaca gccggcctcc	60
atctcctgca ggtctagtca aagcctcgta tacagtgtatg gaaacaccta cttgaattgg	120
tttcagcaga gcccaggcca atctccaagg cgccataattt ataagggttc taaccggac	180
tctggggtcc cagacagatt cageggcagt gggtcaggca ctgatttcac actgaaaatc	240
agcaggggtgg aggctgagga tgggggttt tattactgca tgcaaggtac acactggccg	300
tacacttttg gccaggggac caagctggag atcaaa	336

<210> SEQ ID NO 696

<211> LENGTH: 112

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 696

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

<210> SEQ ID NO 697

<211> LENGTH: 384

<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 697

```
caggtgcacc tggtgaggc tggggaggc ttggtaaagc ctggagggtc cctgagactc      60
tcctgtgcag cctctggatt caccttcaat gaccactaca tgagctggat ccgcaggct      120
ccagggaaagg ggctggagtg gatttcatac attagtaatg atgggtgtac caaatactat      180
gtggactctg tggaggcccg attcatcatt tccaggaca acgccaagaa ctcatgtat      240
ctacatatga acagcctcag agccgacgac acggccgtgt attactgtgc gagagatcag      300
ggatataattg gctacgactc gtattattac tattcctacg gtatggacgt ctggggcaa      360
gggaccacgg tcaccgtcgc ctca                                         384
```

<210> SEQ ID NO 698

<211> LENGTH: 128

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 698

Gln	Val	His	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Lys	Pro	Gly	Gly
1															
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Asp	His
Tyr	Met	Ser	Trp	Ile	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile
Ser	Tyr	Ile	Ser	Asn	Asp	Gly	Gly	Thr	Lys	Tyr	Tyr	Val	Asp	Ser	Val
Glu	Gly	Arg	Phe	Ile	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr
Leu	His	Met	Asn	Ser	Leu	Arg	Ala	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
Ala	Arg	Asp	Gln	Gly	Tyr	Ile	Gly	Tyr	Asp	Ser	Tyr	Tyr	Tyr	Ser	
Tyr	Gly	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ala	Ser
115															125

<210> SEQ ID NO 699

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 699

```
ggattcacct tcagtgacca ctac                                         24
```

<210> SEQ ID NO 700

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 700

```
Gly Phe Thr Phe Ser Asp His Tyr
1           5
```

-continued

```

<210> SEQ ID NO 701
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 701
attagtaatg atgggtggta caaa 24

<210> SEQ ID NO 702
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 702
Ile Ser Asn Asp Gly Gly Thr Lys
1 5

<210> SEQ ID NO 703
<211> LENGTH: 63
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 703
gcgagagatc agggatata tggctacgac tcgtattatt actattccta cggtatggac 60
gtc 63

<210> SEQ ID NO 704
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 704
Ala Arg Asp Gln Gly Tyr Ile Gly Tyr Asp Ser Tyr Tyr Tyr Ser
1 5 10 15

Tyr Gly Met Asp Val
20

<210> SEQ ID NO 705
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 705
aaaattgtgt tgacgcagtc tccaggcacc ctgccttgtt ttccagggga aagagccacc 60
ctctcctgtta gggccagtca gagtgttaac aacaaattct tagcctggta ccagcagaaa 120
tctggccagg ctcccaggct cctcatctat ggtgcattcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggacc gacttcactc tcaccatcag cggactggag 240
cctgaagatt ttgaagtgtta ttattgtcaa gtatatggta actcactcac tttcgccgga 300
gggaccaagg tggagatcaa g 321

<210> SEQ ID NO 706
<211> LENGTH: 107
<212> TYPE: PRT

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 711

caagtatatg gtaactcact cact

24

<210> SEQ ID NO 712
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 712

Gln Val Tyr Gly Asn Ser Leu Thr
1 5

<210> SEQ ID NO 713
<211> LENGTH: 384
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 713

caggtgcagc	tggtgaggc	tgggggaggc	ttggtcaago	ctggagggtc	cctgagactc	60
tcctgtgcag	cctctggatt	cacccctcgt	gaccactaca	tgagctggat	ccgcaggct	120
ccagggaaagg	ggctggaggc	gatttcatac	atttagtaatg	atgggtggat	caaatactat	180
gtggactctg	tggagggccg	attcatcatt	tccagggaca	acgccaagaa	ctcattgtat	240
ctacatatga	acagcctcag	agccgacgac	acggccgtgt	attactgtgc	gagagatcag	300
ggatatattt	gctacgactc	gtatttattac	tattcctacg	gtatggacgt	ctggggccaa	360
gggaccacacgg	tcaccgtctc	ctca				384

<210> SEQ ID NO 714
<211> LENGTH: 128
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 714

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp His
20 25 30Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45Ser Tyr Ile Ser Asn Asp Gly Gly Thr Lys Tyr Tyr Val Asp Ser Val
50 55 60Glu Gly Arg Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80Leu His Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95Ala Arg Asp Gln Gly Tyr Ile Gly Tyr Asp Ser Tyr Tyr Tyr Ser
100 105 110Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

-continued

<210> SEQ ID NO 715
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 715

gaaatttgtt	tgacgcagtc	tccaggcacc	ctgccttgtt	ttccagggga	aagagccacc	60
ctctcctgtta	ggccagtc	gagtgttaac	aacaaattct	tagcctggta	ccagcagaaa	120
tctggccagg	c当地	cctcatctat	ggtgcatacca	gcagggccac	tggcatccca	180
gacaggttca	gtggcagttgg	gtctgggacc	gacttcactc	tcaccatca	cggactggag	240
cctgaagatt	ttttagtgtt	ttattgtcaa	gtatatggta	actcaactcac	tttcggcgga	300
gggaccaagg	tggagatcaa	a				321

<210> SEQ ID NO 716
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 716

Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Pro	Leu	Phe	Pro	Gly
1															15
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Asn	Asn	Lys
	20														30
Phe	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Ser	Gly	Gln	Ala	Pro	Arg	Leu	Leu
	35														45
Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser
	50														60
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Gly	Leu	Glu
	65														80
Pro	Glu	Asp	Phe	Glu	Val	Tyr	Tyr	Cys	Gln	Val	Tyr	Gly	Asn	Ser	Leu
	85														95
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys					
	100														105

<210> SEQ ID NO 717
<211> LENGTH: 384
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 717

caggtgcago	tgggtggagtc	tgggggaggc	ttgggtcaago	ctggagggtc	cctgagactc	60
tcctgtgcag	cctctggatt	cacttcagt	gaccactaca	tgagctggat	ccgcaggct	120
ccagggagg	ggctggagtg	ggtttcatac	attagtaatg	atgggtgtac	caaatactac	180
gcagactctg	tgaagggccg	attcaccatc	tccagggaca	acgccaagaa	ctcactgtat	240
ctgcaaatga	acagcctgag	agccgaggac	acggccgtgt	attactgtgc	gagagatca	300
ggatatattg	gctacgactc	gtattattac	tattcctacg	gtatggacgt	ctggggcaa	360
gggaccacgg	tcaccgtctc	ctca				384

<210> SEQ ID NO 718
<211> LENGTH: 128

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 718

```

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

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

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

Ser Tyr Ile Ser Asn Asp Gly Gly Thr Lys Tyr 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 Val Tyr Tyr Cys
 85          90          95

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

Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115          120         125

```

<210> SEQ ID NO 719
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 719

```

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc      60
ctctcctgca gggccagtca gagtgtaac aacaaattct tagcctggta ccagcagaaa      120
cctggccagg ctcccaggct cctcatctat ggtgcatacca gcagggccac tggcatccca      180
gacaggttca gtggcagtgg gtctggaca gacttcactc tcaccatcag cagactggag      240
cctgaagatt ttgcagtgtta ttactgtcaa gtatatggta actcaactcac tttcggcgga      300
gggaccaagg tggagatcaa a                                         321

```

<210> SEQ ID NO 720
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 720

```

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 Asn Asn Lys
 20          25          30

Phe 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 Val Tyr Gly Asn Ser Leu
 85          90          95

```

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Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> SEQ ID NO 721
 <211> LENGTH: 378
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 721

caaattctgc tggtgcaatc tggaccttagt gtgaaggagc ctggggcctc agtgaaggtc	60
tccctgcaagg cttctggta caccttacc aactacgcta tcagctgggt gcgacaggtc	120
cctggacaag ggctttagt gatgggatgg gtcagcgctt acaatggtca cacaactat	180
gcacatgaag tccagggcag agtcaccatg accacagaca catccacgac cacagcctac	240
atggagctga ggagccttagt atctgacgac acggccatgt attactgtgc gagaggggg	300
gtagtcgtgc cagttgtcc ccacttctac aacggtatgg acgtctgggg ccaagggacc	360
acggtcaccc ttcctctca	378

<210> SEQ ID NO 722
 <211> LENGTH: 126
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 722

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

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

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

Gly Trp Val Ser Ala Tyr Asn Gly His Thr Asn Tyr Ala His Glu Val
 50 55 60

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

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

Ala Arg Gly Val Val Val Pro Val Ala Pro His Phe Tyr Asn Gly
 100 105 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> SEQ ID NO 723
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 723

ggttacacct ttaccaacta cgct

24

<210> SEQ ID NO 724
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:

-continued

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 724

Gly	Tyr	Thr	Phe	Thr	Asn	Tyr	Ala
1					5		

<210> SEQ ID NO 725

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 725

gtcagcgctt acaatggtca caca

24

<210> SEQ ID NO 726

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 726

Val	Ser	Ala	Tyr	Asn	Gly	His	Thr
1					5		

<210> SEQ ID NO 727

<211> LENGTH: 57

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 727

gcgagagggg gtgttagtcgt gccagttgt ccccaacttct acaacggtat ggacgtc

57

<210> SEQ ID NO 728

<211> LENGTH: 19

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 728

Ala	Arg	Gly	Gly	Val	Val	Val	Pro	Val	Ala	Pro	His	Phe	Tyr	Asn	Gly
1				5				10			15				

Met Asp Val

<210> SEQ ID NO 729

<211> LENGTH: 336

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 729

gatatttgta tgactcagtt tccactctcc ctgccccgtca cccctggaga gccggccctcc 60

atctcctgca ggtctagtca gagcctcctg catattaatg aataacaacta tttggattgg 120

tacctaaaga agccaggggca gtctccacag ctcctgatct atttgggttt taatcgggcc 180

tccggggtcc ctgacaggtt cagtggcagt ggatcaggca cagatttac actgaaaatc 240

agcagagtggtt aggctgagga ttttttttttattactgca tgcaagctct tc当地actccg 300

tggacgttcg gccaaggggac caagggtggaa atcaaa 336

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<210> SEQ ID NO 730
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 730

Asp	Ile	Val	Met	Thr	Gln	Phe	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 His Ile
20 25 30

Asn Glu Tyr Asn Tyr Leu Asp Trp Tyr Leu Lys Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Phe 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

<210> SEQ ID NO 731
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 731

cagagcctcc tgcataattaa tgaataacaac tat 33

<210> SEQ ID NO 732
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 732

Gln	Ser	Leu	Leu	His	Ile	Asn	Glu	Tyr	Asn	Tyr
1				5				10		

<210> SEQ ID NO 733
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 733

ttgggtttt 9

<210> SEQ ID NO 734
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 734

Leu Gly Phe

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1

<210> SEQ ID NO 735
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 735

atgcaagctc ttcaaactcc gtggacg

27

<210> SEQ ID NO 736
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 736

Met Gln Ala Leu Gln Thr Pro Trp Thr
1 5

<210> SEQ ID NO 737
<211> LENGTH: 378
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 737

caggttcagc tgggtcagtc tggaccttagt gtgaaggagc ctggggcttc agtgaaggtc	60
tccctgcaagg cttctggta caccttacc aactacgcta tcagctgggt ggcacaggc	120
cctggacaag ggcttgatgt gatggatgg gtcagcgctt acaatggtca cacaactat	180
gcacatgaag tccaggcag agtcaccatg accacagaca catccacgac cacagcctac	240
atggagctga ggagcctgag atctgacgac acggccatgt attactgtgc gagaggggt	300
gtatgcgtgc cagttgtcc ccacttctac aacggtatgg acgtctgggg ccaaggacc	360
acggtcaccc ttcctca	378

<210> SEQ ID NO 738
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 738

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

Ala Arg Gly Gly Val Val Val Pro Val Ala Pro His Phe Tyr Asn Gly

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100

105

110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> SEQ ID NO 739
 <211> LENGTH: 336
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 739

gatattgtga tgactcagtc tccactctcc ctgcccgtca cccctggaga gccggcctcc	60
atctcttgca ggtctagtca gagectccctg catattaatg aataacaacta tttggattgg	120
tacctaaaga agccaggggca gtctccacag ctcctgatct atttgggttt taatcgggcc	180
tccggggtcc ctgacagggtt cagtggcagt ggatcaggca cagatttac actgaaaatc	240
agcagagtgg aggctgagga tgggggttc tattactgca tgcaagctct tcaaactccg	300
tggacgttcg gccaaggggac caaggtggaa atcaaa	336

<210> SEQ ID NO 740
 <211> LENGTH: 112
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 740

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 His Ile	
20 25 30	

Asn Glu Tyr Asn Tyr Leu Asp Trp Tyr Leu Lys Lys Pro Gly Gln Ser	
35 40 45	

Pro Gln Leu Leu Ile Tyr Leu Gly Phe 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	

<210> SEQ ID NO 741
 <211> LENGTH: 378
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 741

caggttcago tgggtcagtc tggagctgag gtgaagaago ctggggcctc agtgaaggta	60
tcctgcagg cttctggta caccttacc aactacgcta tcagctgggt gcgcacaggcc	120
cctggacaag ggctttagtg gatggatgg gtcagcgctt acaatggtca cacaaactat	180
gcacagaagc tccaggccag agtcaccatg accacagaca catccacgag cacagcctac	240
atggagctga ggagcctgag atctgacgac acggccgtgt attactgtgc gagaggggt	300
gtagtcgtgc cagttgtcc ccacttctac aacggtatgg acgtctgggg gcaaggggacc	360

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acqqtacccq tctcctca

378

<210> SEQ ID NO 742
 <211> LENGTH: 126
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 742

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala
1					5					10					15
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr
20							25							30	
Ala	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
35						40								45	
Gly	Trp	Val	Ser	Ala	Tyr	Asn	Gly	His	Thr	Asn	Tyr	Ala	Gln	Lys	Leu
50						55							60		
Gln	Gly	Arg	Val	Thr	Met	Thr	Thr	Asp	Thr	Ser	Thr	Ser	Thr	Ala	Tyr
65					70				75					80	
Met	Glu	Leu	Arg	Ser	Leu	Arg	Ser	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
								85			90			95	
Ala	Arg	Gly	Gly	Val	Val	Val	Pro	Val	Ala	Pro	His	Phe	Tyr	Asn	Gly
								100		105			110		
Met	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser		
								115		120			125		

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<210> SEQ ID NO 743
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
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<400> SEQUENCE: 743

gtatgttgc	tgactcagtc	tccactctcc	ctggccgtca	ccccctggaga	gccccctcc	60
atctctgc	ggtctagtca	gagcctccctg	catattaatg	aatacaacta	tttggattgg	120
tacctgcaga	agccaggggca	gtctccacag	ctccctgatct	attttgggttc	taatcgggcc	180
tccggggtcc	ctgacagagtt	cagtggcagt	ggatcaggca	cagattttac	actgaaaatc	240
agcagagttgg	aggctgagga	tgttgggtt	tattactgca	tgcaagctct	tcaaactccg	300
tggacgttcg	gccaaggggac	caagggtggaa	atcaaa			336

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<210> SEQ ID NO 744
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
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<400> SEQUENCE: 744

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	His	Ile
				20				25					30		
Asn	Glu	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				

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Asp Arg Phe 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

<210> SEQ ID NO 745
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(8)
<223> OTHER INFORMATION: Xaa = Any amino acid

<400> SEQUENCE: 745

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> SEQ ID NO 746
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(8)
<223> OTHER INFORMATION: Xaa - Any amino acid

<400> SEQUENCE: 746

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> SEQ ID NO 747
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(20)
<223> OTHER INFORMATION: Xaa = Any amino acid

<400> SEQUENCE: 747

Xaa
1 5 10 15

Xaa Xaa Xaa Xaa
20

<210> SEQ ID NO 748
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(12)
<223> OTHER INFORMATION: Xaa = Any amino acid

<400> SEQUENCE: 748

Xaa
1 5 10

-continued

<210> SEQ ID NO 749
 <211> LENGTH: 3
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <220> FEATURE:
 <211> NAME/KEY: VARIANT
 <222> LOCATION: (1)...(3)
 <223> OTHER INFORMATION: Xaa = Any amino acid

<400> SEQUENCE: 749

Xaa Xaa Xaa
1

<210> SEQ ID NO 750
 <211> LENGTH: 9
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <220> FEATURE:
 <211> NAME/KEY: VARIANT
 <222> LOCATION: (1)...(9)
 <223> OTHER INFORMATION: Xaa = Any amino acid

<400> SEQUENCE: 750

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> SEQ ID NO 751
 <211> LENGTH: 330
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 751

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

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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> SEQ ID NO 752
 <211> LENGTH: 327
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 752

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	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

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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			

<210> SEQ ID NO: 753
<211> LENGTH: 327
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<400> SEQUENCE: 753

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	

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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

<210> SEQ ID NO 754

<211> LENGTH: 2076

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 754

atgggcaccc	tcagctccag	gccccctgg	tggccgctgc	cactgctgct	gctgctgctg	60
ctgctcctgg	gtcccgccgg	cggccgtgcg	caggaggacg	aggacggcga	ctacgaggag	120
ctgggtctag	ctttgcgttc	cgaggaggac	ggcctggccg	aagcacccga	gcacggaaacc	180
acagccacct	tccaccgcgt	cggcaaggat	cggtgaggt	tgcctggcac	ctacgtggtg	240
gtgctgaagg	aggagaccca	cctctcgca	tcagagcga	ctgcccgcgc	cctgcaggcc	300
cagggctgccc	gccggggata	cctcaccaag	atcctgcatg	tcttccatgg	ccttcttct	360
ggcttcctgg	tgaagatgag	tggcgacctg	ctggagctgg	ccttgaagtt	gccccatgtc	420
gactacatcg	aggaggactc	ctctgtcttt	gcccagagca	tcccgtggaa	cctggagcgg	480
attaccctc	cacggtaccg	ggcgatgaa	taccagcccc	ccgacggagg	cagectggtg	540
gaggtgtatac	tcctagacac	cagcatacag	agtgaccaco	gggaaatcga	gggcagggtc	600
atggtcaccc	acttcgagaa	tgtgcccag	gaggacggga	cccgcttcca	cagacaggcc	660
agcaagtgtg	acagtcatgg	cacccacctg	gcaggggtgg	tcagcggccg	ggatgccggc	720
gtggccaagg	gtgccagcat	gcccgcctg	cgcgtgccta	actgccaagg	gaagggcacg	780
gttagcgcca	ccctcatagg	cctggagttt	attcgaaaa	gccagctgg	ccagcctgtg	840
gggccactgg	tggtgtctgt	gccccctggcg	ggtgggtaca	gccgcgtct	caacgccccc	900
tgccagcgcc	tggcgaggcc	tggggtcgtg	ctggtcaccc	ctggccggcaa	cttccgggac	960
gatgcctgcc	tctactcccc	agcctcagct	cccgaggta	tcacagttgg	ggccaccaat	1020
gcccaggacc	agccggtgac	cctggggact	ttggggacca	actttggccg	ctgtgtggac	1080
ctcttgcctc	caggggagga	catcattgg	gcctccagcg	actgcagcac	ctgtttgtg	1140
tcacagagtgc	ggacatcaca	ggctgctgcc	cacgtggctg	gcattgcagc	catgtgctg	1200
tctgcggagc	cggagtcac	cctggccgag	ttgaggcaga	gactgatcca	cttctctgcc	1260
aaagatgtca	tcaatgaggc	ctggttccct	gaggaccago	gggtactgac	ccccaacctg	1320
gtggccgccc	tgccccccag	cacccatggg	gcaggttggc	agctgttttgc	caggactgtg	1380
tggtcagcac	actcggggcc	tacacggatg	gccacagcca	tgcggccgt	cgccccagat	1440
gaggagctgc	tgagctgctc	cagttctcc	aggagtggga	agcggcgccgg	cgagcgcac	1500
gaggcccaag	ggggcaagct	ggtctgcccgg	gcccacaacg	ctttggggg	tgagggtgtc	1560
tacgcattg	ccaggtgctg	cctgctaccc	caggccaact	gcagcgtcca	cacagctcca	1620
ccagctgagg	ccagcatggg	gaccgcgtgc	cactgcaccc	aacagggcca	cgtctcaca	1680
ggctgcagct	cccactggga	ggtggaggac	cttggcaccc	acaagccgc	tgtgctgagg	1740
ccacgagggtc	agcccaacca	gtgcgtgggc	cacagggagg	ccagcatcca	cgcttcctgc	1800

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tgccatgcc	caggtctgga	atgaaagtc	aaggagcatg	gaatccggc	ccctcaggag	1860
caggtgaccg	tggcctgcga	ggagggctgg	accctgactg	gctgcagtgc	cctccctggg	1920
acctccccacg	tcctggggc	ctacgcccgt	gacaacacgt	gtgtagtcag	gagccgggac	1980
gtcagcacta	caggcagcac	cagegaagag	gcccgtgacag	ccgttgcct	ctgtgcggg	2040
agccggcacc	tggcgcgagc	ctccaggag	ctccag			2076

<210> SEQ ID NO 755
<211> LENGTH: 692
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 755

Met	Gly	Thr	Val	Ser	Ser	Arg	Arg	Ser	Trp	Trp	Pro	Leu	Pro	Leu	Leu
1				5				10			15				
Leu	Leu	Leu	Leu	Leu	Leu	Gly	Pro	Ala	Gly	Ala	Arg	Ala	Gln	Glu	
						20		25			30				
Asp	Glu	Asp	Gly	Asp	Tyr	Glu	Glu	Leu	Val	Leu	Ala	Leu	Arg	Ser	Glu
	35				40						45				
Glu	Asp	Gly	Leu	Ala	Glu	Ala	Pro	Glu	His	Gly	Thr	Thr	Ala	Thr	Phe
	50				55				60						
His	Arg	Cys	Ala	Lys	Asp	Pro	Trp	Arg	Leu	Pro	Gly	Thr	Tyr	Val	Val
	65				70				75			80			
Val	Leu	Lys	Glu	Glu	Thr	His	Leu	Ser	Gln	Ser	Glu	Arg	Thr	Ala	Arg
		85				90					95				
Arg	Leu	Gln	Ala	Gln	Ala	Ala	Arg	Arg	Gly	Tyr	Leu	Thr	Lys	Ile	Leu
		100				105					110				
His	Val	Phe	His	Gly	Leu	Leu	Pro	Gly	Phe	Leu	Val	Lys	Met	Ser	Gly
	115				120				125						
Asp	Leu	Leu	Glu	Leu	Ala	Leu	Lys	Leu	Pro	His	Val	Asp	Tyr	Ile	Glu
	130				135				140						
Glu	Asp	Ser	Ser	Val	Phe	Ala	Gln	Ser	Ile	Pro	Trp	Asn	Leu	Glu	Arg
	145				150				155			160			
Ile	Thr	Pro	Pro	Arg	Tyr	Arg	Ala	Asp	Glu	Tyr	Gln	Pro	Pro	Asp	Gly
		165				170				175					
Gly	Ser	Leu	Val	Glu	Val	Tyr	Leu	Leu	Asp	Thr	Ser	Ile	Gln	Ser	Asp
		180				185				190					
His	Arg	Glu	Ile	Glu	Gly	Arg	Val	Met	Val	Thr	Asp	Phe	Glu	Asn	Val
	195				200				205						
Pro	Glu	Glu	Asp	Gly	Thr	Arg	Phe	His	Arg	Gln	Ala	Ser	Lys	Cys	Asp
	210				215				220						
Ser	His	Gly	Thr	His	Leu	Ala	Gly	Val	Val	Ser	Gly	Arg	Asp	Ala	Gly
	225				230				235			240			
Val	Ala	Lys	Gly	Ala	Ser	Met	Arg	Ser	Leu	Arg	Val	Leu	Asn	Cys	Gln
		245				250				255					
Gly	Lys	Gly	Thr	Val	Ser	Gly	Thr	Leu	Ile	Gly	Leu	Glu	Phe	Ile	Arg
		260				265				270					
Lys	Ser	Gln	Leu	Val	Gln	Pro	Val	Gly	Pro	Leu	Val	Val	Leu	Leu	Pro
		275				280				285					
Leu	Ala	Gly	Gly	Tyr	Ser	Arg	Val	Leu	Asn	Ala	Ala	Cys	Gln	Arg	Leu
		290				295				300					
Ala	Arg	Ala	Gly	Val	Val	Leu	Val	Thr	Ala	Ala	Gly	Asn	Phe	Arg	Asp
	305				310				315			320			
Asp	Ala	Cys	Leu	Tyr	Ser	Pro	Ala	Ser	Ala	Pro	Glu	Val	Ile	Thr	Val

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325	330	335	
Gly Ala Thr Asn Ala Gln Asp Gln Pro Val Thr Leu Gly			
340	345	350	
Thr Asn Phe Gly Arg Cys Val Asp Leu Phe Ala Pro Gly	Glu Asp Ile		
355	360	365	
Ile Gly Ala Ser Ser Asp Cys Ser Thr Cys Phe Val Ser Gln	Ser Gly		
370	375	380	
Thr Ser Gln Ala Ala Ala His Val Ala Gly Ile Ala Ala Met	Met Leu		
385	390	395	400
Ser Ala Glu Pro Glu Leu Thr Leu Ala Glu Leu Arg Gln Arg	Leu Ile		
405	410	415	
His Phe Ser Ala Lys Asp Val Ile Asn Glu Ala Trp Phe Pro	Glu Asp		
420	425	430	
Gln Arg Val Leu Thr Pro Asn Leu Val Ala Ala Leu Pro Pro	Ser Thr		
435	440	445	
His Gly Ala Gly Trp Gln Leu Phe Cys Arg Thr Val Trp Ser	Ala His		
450	455	460	
Ser Gly Pro Thr Arg Met Ala Thr Ala Ile Ala Arg Cys Ala	Pro Asp		
465	470	475	480
Glu Glu Leu Leu Ser Cys Ser Ser Phe Ser Arg Ser Gly	Lys Arg Arg		
485	490	495	
Gly Glu Arg Met Glu Ala Gln Gly Lys Leu Val Cys Arg Ala	His		
500	505	510	
Asn Ala Phe Gly Gly Glu Val Tyr Ala Ile Ala Arg Cys Cys	Leu		
515	520	525	
Leu Pro Gln Ala Asn Cys Ser Val His Thr Ala Pro Pro Ala	Glu Ala		
530	535	540	
Ser Met Gly Thr Arg Val His Cys His Gln Gln Gly His Val	Leu Thr		
545	550	555	560
Gly Cys Ser Ser His Trp Glu Val Glu Asp Leu Gly Thr His	Lys Pro		
565	570	575	
Pro Val Leu Arg Pro Arg Gly Gln Pro Asn Gln Cys Val Gly	His Arg		
580	585	590	
Glu Ala Ser Ile His Ala Ser Cys Cys His Ala Pro Gly	Leu Glu Cys		
595	600	605	
Lys Val Lys Glu His Gly Ile Pro Ala Pro Gln Glu Gln Val	Thr Val		
610	615	620	
Ala Cys Glu Glu Gly Trp Thr Leu Thr Gly Cys Ser Ala Leu	Pro Gly		
625	630	635	640
Thr Ser His Val Leu Gly Ala Tyr Ala Val Asp Asn Thr Cys	Val Val		
645	650	655	
Arg Ser Arg Asp Val Ser Thr Thr Gly Ser Thr Ser Glu Glu	Ala Val		
660	665	670	
Thr Ala Val Ala Ile Cys Cys Arg Ser Arg His Leu Ala Gln	Ala Ser		
675	680	685	
Gln Glu Leu Gln			
690			

<210> SEQ ID NO 756

<211> LENGTH: 692

<212> TYPE: PRT

<213> ORGANISM: Macaca mulata

<400> SEQUENCE: 756

Met Gly Thr Val Ser Ser Arg Arg Ser Trp Trp Pro Leu Pro Leu Pro

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1	5	10	15
Leu Leu Leu Leu Leu Leu Gly Pro Ala Gly Ala Arg Ala Gln Glu			
20	25	30	
Asp Glu Asp Gly Asp Tyr Glu Glu Leu Val Leu Ala Leu Arg Ser Glu			
35	40	45	
Glu Asp Gly Leu Ala Asp Ala Pro Glu His Gly Ala Thr Ala Thr Phe			
50	55	60	
His Arg Cys Ala Lys Asp Pro Trp Arg Leu Pro Gly Thr Tyr Val Val			
65	70	75	80
Val Leu Lys Glu Glu Thr His Arg Ser Gln Ser Glu Arg Thr Ala Arg			
85	90	95	
Arg Leu Gln Ala Gln Ala Ala Arg Arg Gly Tyr Leu Thr Lys Ile Leu			
100	105	110	
His Val Phe His His Leu Leu Pro Gly Phe Leu Val Lys Met Ser Gly			
115	120	125	
Asp Leu Leu Glu Leu Ala Leu Lys Leu Pro His Val Asp Tyr Ile Glu			
130	135	140	
Glu Asp Ser Ser Val Phe Ala Gln Ser Ile Pro Trp Asn Leu Glu Arg			
145	150	155	160
Ile Thr Pro Ala Arg Tyr Arg Ala Asp Glu Tyr Gln Pro Pro Lys Gly			
165	170	175	
Gly Ser Leu Val Glu Val Tyr Leu Leu Asp Thr Ser Ile Gln Ser Asp			
180	185	190	
His Arg Glu Ile Glu Gly Arg Val Met Val Thr Asp Phe Glu Ser Val			
195	200	205	
Pro Glu Glu Asp Gly Thr Arg Phe His Arg Gln Ala Ser Lys Cys Asp			
210	215	220	
Ser His Gly Thr His Leu Ala Gly Val Val Ser Gly Arg Asp Ala Gly			
225	230	235	240
Val Ala Lys Gly Ala Gly Leu Arg Ser Leu Arg Val Leu Asn Cys Gln			
245	250	255	
Gly Lys Gly Thr Val Ser Gly Thr Leu Ile Gly Leu Glu Phe Ile Arg			
260	265	270	
Lys Ser Gln Leu Val Gln Pro Val Gly Pro Leu Val Val Leu Leu Pro			
275	280	285	
Leu Ala Gly Gly Tyr Ser Arg Val Phe Asn Ala Ala Cys Gln Arg Leu			
290	295	300	
Ala Arg Ala Gly Val Val Leu Val Thr Ala Ala Gly Asn Phe Arg Asp			
305	310	315	320
Asp Ala Cys Leu Tyr Ser Pro Ala Ser Ala Pro Glu Val Ile Thr Val			
325	330	335	
Gly Ala Thr Asn Ala Gln Asp Gln Pro Val Thr Leu Gly Thr Leu Gly			
340	345	350	
Thr Asn Phe Gly Arg Cys Val Asp Leu Phe Ala Pro Gly Glu Asp Ile			
355	360	365	
Ile Gly Ala Ser Ser Asp Cys Ser Thr Cys Phe Val Ser Arg Ser Gly			
370	375	380	
Thr Ser Gln Ala Ala Ala His Val Ala Gly Ile Ala Ala Met Met Leu			
385	390	395	400
Ser Ala Glu Pro Glu Leu Thr Leu Ala Glu Leu Arg Gln Arg Leu Ile			
405	410	415	
His Phe Ser Ala Lys Asp Val Ile Asn Glu Ala Trp Phe Pro Glu Asp			
420	425	430	

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Gln Arg Val Leu Thr Pro Asn Leu Val Ala Ala Leu Pro Pro Ser Thr
435 440 445

His Arg Ala Gly Trp Gln Leu Phe Cys Arg Thr Val Trp Ser Ala His
450 455 460

Ser Gly Pro Thr Arg Met Ala Thr Ala Val Ala Arg Cys Ala Gln Asp
465 470 475 480

Glu Glu Leu Leu Ser Cys Ser Ser Phe Ser Arg Ser Gly Lys Arg Arg
485 490 495

Gly Glu Arg Ile Glu Ala Gln Gly Gly Lys Arg Val Cys Arg Ala His
500 505 510

Asn Ala Phe Gly Gly Glu Val Tyr Ala Ile Ala Arg Cys Cys Leu
515 520 525

Leu Pro Gln Val Asn Cys Ser Val His Thr Ala Pro Pro Ala Gly Ala
530 535 540

Ser Met Gly Thr Arg Val His Cys His Gln Gln Gly His Val Leu Thr
545 550 555 560

Gly Cys Ser Ser His Trp Glu Val Glu Asp Leu Gly Thr His Lys Pro
565 570 575

Pro Val Leu Arg Pro Arg Gly Gln Pro Asn Gln Cys Val Gly His Arg
580 585 590

Glu Ala Ser Ile His Ala Ser Cys Cys His Ala Pro Gly Leu Glu Cys
595 600 605

Lys Val Lys Glu His Gly Ile Pro Ala Pro Gln Glu Gln Val Ile Val
610 615 620

Ala Cys Glu Asp Gly Trp Thr Leu Thr Gly Cys Ser Pro Leu Pro Gly
625 630 635 640

Thr Ser His Val Leu Gly Ala Tyr Ala Val Asp Asn Thr Cys Val Val
645 650 655

Arg Ser Arg Asp Val Ser Thr Thr Gly Ser Thr Ser Lys Glu Ala Val
660 665 670

Ala Ala Val Ala Ile Cys Cys Arg Ser Arg His Leu Val Gln Ala Ser
675 680 685

Gln Glu Leu Gln
690

<210> SEQ ID NO 757
<211> LENGTH: 694
<212> TYPE: PRT
<213> ORGANISM: Mus muscular

<400> SEQUENCE: 757

Met Gly Thr His Cys Ser Ala Trp Leu Arg Trp Pro Leu Leu Pro Leu
1 5 10 15

Leu Pro Pro Leu Leu Leu Leu Leu Leu Leu Cys Pro Thr Gly Ala
20 25 30

Gly Ala Gln Asp Glu Asp Gly Asp Tyr Glu Glu Leu Met Leu Ala Leu
35 40 45

Pro Ser Gln Glu Asp Gly Leu Ala Asp Glu Ala Ala His Val Ala Thr
50 55 60

Ala Thr Phe Arg Arg Cys Ser Lys Glu Ala Trp Arg Leu Pro Gly Thr
65 70 75 80

Tyr Ile Val Val Leu Met Glu Glu Thr Gln Arg Leu Gln Ile Glu Gln
85 90 95

Thr Ala His Arg Leu Gln Thr Arg Ala Ala Arg Arg Gly Tyr Val Ile
100 105 110

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Lys Val Leu His Ile Phe Tyr Asp Leu Phe Pro Gly Phe Leu Val Lys
115 120 125

Met Ser Ser Asp Leu Leu Gly Leu Ala Leu Lys Leu Pro His Val Glu
130 135 140

Tyr Ile Glu Glu Asp Ser Phe Val Phe Ala Gln Ser Ile Pro Trp Asn
145 150 155 160

Leu Glu Arg Ile Ile Pro Ala Trp His Gln Thr Glu Glu Asp Arg Ser
165 170 175

Pro Asp Gly Ser Ser Gln Val Glu Val Tyr Leu Leu Asp Thr Ser Ile
180 185 190

Gln Gly Ala His Arg Glu Ile Glu Gly Arg Val Thr Ile Thr Asp Phe
195 200 205

Asn Ser Val Pro Glu Glu Asp Gly Thr Arg Phe His Arg Gln Ala Ser
210 215 220

Lys Cys Asp Ser His Gly Thr His Leu Ala Gly Val Val Ser Gly Arg
225 230 235 240

Asp Ala Gly Val Ala Lys Gly Thr Ser Leu His Ser Leu Arg Val Leu
245 250 255

Asn Cys Gln Gly Lys Gly Thr Val Ser Gly Thr Leu Ile Gly Leu Glu
260 265 270

Phe Ile Arg Lys Ser Gln Leu Ile Gln Pro Ser Gly Pro Leu Val Val
275 280 285

Leu Leu Pro Leu Ala Gly Gly Tyr Ser Arg Ile Leu Asn Ala Ala Cys
290 295 300

Arg His Leu Ala Arg Thr Gly Val Val Leu Val Ala Ala Ala Gly Asn
305 310 315 320

Phe Arg Asp Asp Ala Cys Leu Tyr Ser Pro Ala Ser Ala Pro Glu Val
325 330 335

Ile Thr Val Gly Ala Thr Asn Ala Gln Asp Gln Pro Val Thr Leu Gly
340 345 350

Thr Leu Gly Thr Asn Phe Gly Arg Cys Val Asp Leu Phe Ala Pro Gly
355 360 365

Lys Asp Ile Ile Gly Ala Ser Ser Asp Cys Ser Thr Cys Phe Met Ser
370 375 380

Gln Ser Gly Thr Ser Gln Ala Ala Ala His Val Ala Gly Ile Val Ala
385 390 395 400

Arg Met Leu Ser Arg Glu Pro Thr Leu Thr Leu Ala Glu Leu Arg Gln
405 410 415

Arg Leu Ile His Phe Ser Thr Lys Asp Val Ile Asn Met Ala Trp Phe
420 425 430

Pro Glu Asp Gln Gln Val Leu Thr Pro Asn Leu Val Ala Thr Leu Pro
435 440 445

Pro Ser Thr His Glu Thr Gly Gly Gln Leu Leu Cys Arg Thr Val Trp
450 455 460

Ser Ala His Ser Gly Pro Thr Arg Thr Ala Thr Ala Thr Ala Arg Cys
465 470 475 480

Ala Pro Glu Glu Leu Leu Ser Cys Ser Ser Phe Ser Arg Ser Gly
485 490 495

Arg Arg Arg Gly Asp Trp Ile Glu Ala Ile Gly Gly Gln Gln Val Cys
500 505 510

Lys Ala Leu Asn Ala Phe Gly Gly Glu Gly Val Tyr Ala Val Ala Arg
515 520 525

Cys Cys Leu Val Pro Arg Ala Asn Cys Ser Ile His Asn Thr Pro Ala
530 535 540

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Ala Arg Ala Gly Leu Glu Thr His Val His Cys His Gln Lys Asp His
 545 550 555 560
 Val Leu Thr Gly Cys Ser Phe His Trp Glu Val Glu Asp Leu Ser Val
 565 570 575
 Arg Arg Gln Pro Ala Leu Arg Ser Arg Arg Gln Pro Gly Gln Cys Val
 580 585 590
 Gly His Gln Ala Ala Ser Val Tyr Ala Ser Cys Cys His Ala Pro Gly
 595 600 605
 Leu Glu Cys Lys Ile Lys Glu His Gly Ile Ser Gly Pro Ser Glu Gln
 610 615 620
 Val Thr Val Ala Cys Glu Ala Gly Trp Thr Leu Thr Gly Cys Asn Val
 625 630 635 640
 Leu Pro Gly Ala Ser Leu Thr Leu Gly Ala Tyr Ser Val Asp Asn Leu
 645 650 655
 Cys Val Ala Arg Val His Asp Thr Ala Arg Ala Asp Arg Thr Ser Gly
 660 665 670
 Glu Ala Thr Val Ala Ala Ile Cys Cys Arg Ser Arg Pro Ser Ala
 675 680 685
 Lys Ala Ser Trp Val Gln
 690

<210> SEQ ID NO 758
 <211> LENGTH: 653
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 758

Glu Phe Arg Cys His Asp Gly Lys Cys Ile Ser Arg Gln Phe Val Cys
 1 5 10 15
 Asp Ser Asp Arg Asp Cys Leu Asp Gly Ser Asp Glu Ala Ser Cys Pro
 20 25 30
 Val Leu Thr Cys Gly Pro Ala Ser Phe Gln Cys Asn Ser Ser Thr Cys
 35 40 45
 Ile Pro Gln Leu Trp Ala Cys Asp Asn Asp Pro Asp Cys Glu Asp Gly
 50 55 60
 Ser Asp Glu Trp Pro Gln Arg Cys Arg Gly Leu Tyr Val Phe Gln Gly
 65 70 75 80
 Asp Ser Ser Pro Cys Ser Ala Phe Glu Phe His Cys Leu Ser Gly Glu
 85 90 95
 Cys Ile His Ser Ser Trp Arg Cys Asp Gly Gly Pro Asp Cys Lys Asp
 100 105 110
 Lys Ser Asp Glu Glu Asn Cys Ala Val Ala Thr Cys Arg Pro Asp Glu
 115 120 125
 Phe Gln Cys Ser Asp Gly Asn Cys Ile His Gly Ser Arg Gln Cys Asp
 130 135 140
 Arg Glu Tyr Asp Cys Lys Asp Met Ser Asp Glu Val Gly Cys Val Asn
 145 150 155 160
 Val Thr Leu Cys Glu Gly Pro Asn Lys Phe Lys Cys His Ser Gly Glu
 165 170 175
 Cys Ile Thr Leu Asp Lys Val Cys Asn Met Ala Arg Asp Cys Arg Asp
 180 185 190
 Trp Ser Asp Glu Pro Ile Lys Glu Cys Gly Thr Asn Glu Cys Leu Asp
 195 200 205
 Asn Asn Gly Gly Cys Ser His Val Cys Asn Asp Leu Lys Ile Gly Tyr
 210 215 220

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Glu Cys Leu Cys Pro Asp Gly Phe Gln Leu Val Ala Gln Arg Arg Cys
 225 230 235 240
 Glu Asp Ile Asp Glu Cys Gln Asp Pro Asp Thr Cys Ser Gln Leu Cys
 245 250 255
 Val Asn Leu Glu Gly Gly Tyr Lys Cys Gln Cys Glu Glu Gly Phe Gln
 260 265 270
 Leu Asp Pro His Thr Lys Ala Cys Lys Ala Val Gly Ser Ile Ala Tyr
 275 280 285
 Leu Phe Phe Thr Asn Arg His Glu Val Arg Lys Met Thr Leu Asp Arg
 290 295 300
 Ser Glu Tyr Thr Ser Leu Ile Pro Asn Leu Arg Asn Val Val Ala Leu
 305 310 315 320
 Asp Thr Glu Val Ala Ser Asn Arg Ile Tyr Trp Ser Asp Leu Ser Gln
 325 330 335
 Arg Met Ile Cys Ser Thr Gln Leu Asp Arg Ala His Gly Val Ser Ser
 340 345 350
 Tyr Asp Thr Val Ile Ser Arg Asp Ile Gln Ala Pro Asp Gly Leu Ala
 355 360 365
 Val Asp Trp Ile His Ser Asn Ile Tyr Trp Thr Asp Ser Val Leu Gly
 370 375 380
 Thr Val Ser Val Ala Asp Thr Lys Gly Val Lys Arg Lys Thr Leu Phe
 385 390 395 400
 Arg Glu Asn Gly Ser Lys Pro Arg Ala Ile Val Val Asp Pro Val His
 405 410 415
 Gly Phe Met Tyr Trp Thr Asp Trp Gly Thr Pro Ala Lys Ile Lys Lys
 420 425 430
 Gly Gly Leu Asn Gly Val Asp Ile Tyr Ser Leu Val Thr Glu Asn Ile
 435 440 445
 Gln Trp Pro Asn Gly Ile Thr Leu Asp Leu Leu Ser Gly Arg Leu Tyr
 450 455 460
 Trp Val Asp Ser Lys Leu His Ser Ile Ser Ser Ile Asp Val Asn Gly
 465 470 475 480
 Gly Asn Arg Lys Thr Ile Leu Glu Asp Glu Lys Arg Leu Ala His Pro
 485 490 495
 Phe Ser Leu Ala Val Phe Glu Asp Lys Val Phe Trp Thr Asp Ile Ile
 500 505 510
 Asn Glu Ala Ile Phe Ser Ala Asn Arg Leu Thr Gly Ser Asp Val Asn
 515 520 525
 Leu Leu Ala Glu Asn Leu Leu Ser Pro Glu Asp Met Val Leu Phe His
 530 535 540
 Asn Leu Thr Gln Pro Arg Gly Val Asn Trp Cys Glu Arg Thr Thr Leu
 545 550 555 560
 Ser Asn Gly Gly Cys Gln Tyr Leu Cys Leu Pro Ala Pro Gln Ile Asn
 565 570 575
 Pro His Ser Pro Lys Phe Thr Cys Ala Cys Pro Asp Gly Met Leu Leu
 580 585 590
 Ala Arg Asp Met Arg Ser Cys Leu Thr Glu Ala Glu Ala Ala Val Ala
 595 600 605
 Thr Gln Glu Thr Ser Thr Val Arg Leu Lys Val Ser Ser Thr Ala Val
 610 615 620
 Arg Thr Gln His Thr Thr Arg Pro Val Pro Asp Thr Ser Arg Leu
 625 630 635 640
 Pro Gly Ala Thr Pro Gly Leu Thr Thr Val Glu Ile Val

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645

650

<210> SEQ ID NO 759

<211> LENGTH: 753

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 759

Met	Glu	Arg	Arg	Ala	Trp	Ser	Leu	Gln	Cys	Thr	Ala	Phe	Val	Leu	Phe
1				5			10					15			

Cys	Ala	Trp	Cys	Ala	Leu	Asn	Ser	Ala	Lys	Ala	Lys	Arg	Gln	Phe	Val
					20		25					30			

Asn	Glu	Trp	Ala	Ala	Glu	Ile	Pro	Gly	Gly	Pro	Glu	Ala	Ala	Ser	Ala
					35		40				45				

Ile	Ala	Glu	Glu	Leu	Gly	Tyr	Asp	Leu	Leu	Gly	Gln	Ile	Gly	Ser	Leu
					50		55				60				

Glu	Asn	His	Tyr	Leu	Phe	Lys	His	Lys	Asn	His	Pro	Arg	Arg	Ser	Arg
65					70		75				80				

Arg	Ser	Ala	Phe	His	Ile	Thr	Lys	Arg	Leu	Ser	Asp	Asp	Asp	Arg	Val
					85		90				95				

Ile	Trp	Ala	Glu	Gln	Gln	Tyr	Glu	Lys	Glu	Arg	Ser	Lys	Arg	Ser	Ala
					100		105				110				

Leu	Arg	Asp	Ser	Ala	Leu	Asn	Leu	Phe	Asn	Asp	Pro	Met	Trp	Asn	Gln
					115		120				125				

Gln	Trp	Tyr	Leu	Gln	Asp	Thr	Arg	Met	Thr	Ala	Ala	Leu	Pro	Lys	Leu
					130		135				140				

Asp	Leu	His	Val	Ile	Pro	Val	Trp	Gln	Lys	Gly	Ile	Thr	Gly	Lys	Gly
145					150			155			160				

Val	Val	Ile	Thr	Val	Leu	Asp	Asp	Gly	Leu	Glu	Trp	Asn	His	Thr	Asp
					165		170			175					

Ile	Tyr	Ala	Asn	Tyr	Asp	Pro	Glu	Ala	Ser	Tyr	Asp	Phe	Asn	Asp	Asn
					180		185				190				

Asp	His	Asp	Pro	Phe	Pro	Arg	Tyr	Asp	Pro	Thr	Asn	Glu	Asn	Lys	His
195					200			205							

Gly	Thr	Arg	Cys	Ala	Gly	Glu	Ile	Ala	Met	Gln	Ala	Asn	Asn	His	Lys
210					215			220							

Cys	Gly	Val	Gly	Val	Ala	Tyr	Asn	Ser	Lys	Val	Gly	Gly	Ile	Arg	Met
225					230			235			240				

Leu	Asp	Gly	Ile	Val	Thr	Asp	Ala	Ile	Glu	Ala	Ser	Ser	Ile	Gly	Phe
					245		250			255					

Asn	Pro	Gly	His	Val	Asp	Ile	Tyr	Ser	Ala	Ser	Trp	Gly	Pro	Asn	Asp
					260		265			270					

Asp	Gly	Lys	Thr	Val	Glu	Gly	Pro	Gly	Arg	Leu	Ala	Gln	Lys	Ala	Phe
275					280			285							

Glu	Tyr	Gly	Val	Lys	Gln	Gly	Arg	Gln	Gly	Lys	Gly	Ser	Ile	Phe	Val
290					295			300							

Trp	Ala	Ser	Gly	Asn	Gly	Gly	Arg	Gln	Gly	Asp	Asn	Cys	Asp	Cys	Asp
305					310			315			320				

Gly	Tyr	Thr	Asp	Ser	Ile	Tyr	Thr	Ile	Ser	Ile	Ser	Ser	Ala	Ser	Gln
325					330			335			335				

Gln	Gly	Leu	Ser	Pro	Trp	Tyr	Ala	Glu	Lys	Cys	Ser	Ser	Thr	Leu	Ala
340					345			350			350				

Thr	Ser	Tyr	Ser	Ser	Gly	Asp	Tyr	Thr	Asp	Gln	Arg	Ile	Thr	Ser	Ala
355					360			365			365				

Asp	Leu	His	Asn	Asp	Cys	Thr	Glu	Thr	His	Thr	Gly	Thr	Ser	Ala	Ser
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441**442**

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370	375	380
Ala Pro Leu Ala Ala Gly Ile Phe Ala Leu Ala Leu Glu Ala Asn Pro		
385	390	395
Asn Leu Thr Trp Arg Asp Met Gln His Leu Val Val Trp Thr Ser Glu		
405	410	415
Tyr Asp Pro Leu Ala Asn Asn Pro Gly Trp Lys Lys Asn Gly Ala Gly		
420	425	430
Leu Met Val Asn Ser Arg Phe Gly Phe Gly Leu Leu Asn Ala Lys Ala		
435	440	445
Leu Val Asp Leu Ala Asp Pro Arg Thr Trp Arg Ser Val Pro Glu Lys		
450	455	460
Lys Glu Cys Val Val Lys Asp Asn Asp Phe Glu Pro Arg Ala Leu Lys		
465	470	475
Ala Asn Gly Glu Val Ile Ile Glu Ile Pro Thr Arg Ala Cys Glu Gly		
485	490	495
Gln Glu Asn Ala Ile Lys Ser Leu Glu His Val Gln Phe Glu Ala Thr		
500	505	510
Ile Glu Tyr Ser Arg Arg Gly Asp Leu His Val Thr Leu Thr Ser Ala		
515	520	525
Ala Gly Thr Ser Thr Val Leu Leu Ala Glu Arg Glu Arg Asp Thr Ser		
530	535	540
Pro Asn Gly Phe Lys Asn Trp Asp Phe Met Ser Val His Thr Trp Gly		
545	550	555
560		
Glu Asn Pro Ile Gly Thr Trp Thr Leu Arg Ile Thr Asp Met Ser Gly		
565	570	575
Arg Ile Gln Asn Glu Gly Arg Ile Val Asn Trp Lys Leu Ile Leu His		
580	585	590
Gly Thr Ser Ser Gln Pro Glu His Met Lys Gln Pro Arg Val Tyr Thr		
595	600	605
Ser Tyr Asn Thr Val Gln Asn Asp Arg Arg Gly Val Glu Lys Met Val		
610	615	620
Asp Pro Gly Glu Glu Gln Pro Thr Gln Glu Asn Pro Lys Glu Asn Thr		
625	630	635
640		
Leu Val Ser Lys Ser Pro Ser Ser Ser Val Gly Gly Arg Arg Asp		
645	650	655
Glu Leu Glu Glu Gly Ala Pro Ser Gln Ala Met Leu Arg Leu Leu Gln		
660	665	670
Ser Ala Phe Ser Lys Asn Ser Pro Pro Lys Gln Ser Pro Lys Lys Ser		
675	680	685
Pro Ser Ala Lys Leu Asn Ile Pro Tyr Glu Asn Phe Tyr Glu Ala Leu		
690	695	700
Glu Lys Leu Asn Lys Pro Ser Gln Leu Lys Asp Ser Glu Asp Ser Leu		
705	710	715
720		
Tyr Asn Asp Tyr Val Asp Val Phe Tyr Asn Thr Lys Pro Tyr Lys His		
725	730	735
Arg Asp Asp Arg Leu Leu Gln Ala Leu Val Asp Ile Leu Asn Glu Glu		
740	745	750

Asn

<210> SEQ ID NO 760
<211> LENGTH: 785
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 760

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Met Pro Lys Gly Arg Gln Lys Val Pro His Leu Asp Ala Pro Leu Gly
 1 5 10 15
 Leu Pro Thr Cys Leu Trp Leu Glu Leu Ala Gly Leu Phe Leu Leu Val
 20 25 30
 Pro Trp Val Met Gly Leu Ala Gly Thr Gly Gly Pro Asp Gly Gln Gly
 35 40 45
 Thr Gly Gly Pro Ser Trp Ala Val His Leu Glu Ser Leu Glu Gly Asp
 50 55 60
 Gly Glu Glu Glu Thr Leu Glu Gln Ala Asp Ala Leu Ala Gln Ala
 65 70 75 80
 Ala Gly Leu Val Asn Ala Gly Arg Ile Gly Glu Leu Gln Gly His Tyr
 85 90 95
 Leu Phe Val Gln Pro Ala Gly His Arg Pro Ala Leu Glu Val Glu Ala
 100 105 110
 Ile Arg Gln Gln Val Glu Ala Val Leu Ala Gly His Glu Ala Val Arg
 115 120 125
 Trp His Ser Glu Gln Arg Leu Leu Arg Arg Ala Lys Arg Ser Val His
 130 135 140
 Phe Asn Asp Pro Lys Tyr Pro Gln Gln Trp His Leu Asn Asn Arg Arg
 145 150 155 160
 Ser Pro Gly Arg Asp Ile Asn Val Thr Gly Val Trp Glu Arg Asn Val
 165 170 175
 Thr Gly Arg Gly Val Thr Val Val Val Asp Asp Gly Val Glu His
 180 185 190
 Thr Ile Gln Asp Ile Ala Pro Asn Tyr Ser Pro Glu Gly Ser Tyr Asp
 195 200 205
 Leu Asn Ser Asn Asp Pro Asp Pro Met Pro His Pro Asp Val Glu Asn
 210 215 220
 Gly Asn His His Gly Thr Arg Cys Ala Gly Glu Ile Ala Ala Val Pro
 225 230 235 240
 Asn Asn Ser Phe Cys Ala Val Gly Val Ala Tyr Gly Ser Arg Ile Ala
 245 250 255
 Gly Ile Arg Val Leu Asp Gly Pro Leu Thr Asp Ser Met Glu Ala Val
 260 265 270
 Ala Phe Asn Lys His Tyr Gln Ile Asn Asp Ile Tyr Ser Cys Ser Trp
 275 280 285
 Gly Pro Asp Asp Asp Gly Lys Thr Val Asp Gly Pro His Gln Leu Gly
 290 295 300
 Lys Ala Ala Leu Gln His Gly Val Ile Ala Gly Arg Gln Gly Phe Gly
 305 310 315 320
 Ser Ile Phe Val Val Ala Ser Gly Asn Gly Gln His Asn Asp Asn
 325 330 335
 Cys Asn Tyr Asp Gly Tyr Ala Asn Ser Ile Tyr Thr Val Thr Ile Gly
 340 345 350
 Ala Val Asp Glu Glu Gly Arg Met Pro Phe Tyr Ala Glu Glu Cys Ala
 355 360 365
 Ser Met Leu Ala Val Thr Phe Ser Gly Gly Asp Lys Met Leu Arg Ser
 370 375 380
 Ile Val Thr Thr Asp Trp Asp Leu Gln Lys Gly Thr Gly Cys Thr Glu
 385 390 395 400
 Gly His Thr Gly Thr Ser Ala Ala Ala Pro Leu Ala Ala Gly Met Ile
 405 410 415
 Ala Leu Met Leu Gln Val Arg Pro Cys Leu Thr Trp Arg Asp Val Gln

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445**446**

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420	425	430
His Ile Ile Val Phe Thr Ala Thr Arg Tyr Glu Asp Arg Arg Ala Glu		
435	440	445
Trp Val Thr Asn Glu Ala Gly Phe Ser His Ser His Gln His Gly Phe		
450	455	460
Gly Leu Leu Asn Ala Trp Arg Leu Val Asn Ala Ala Lys Ile Trp Thr		
465	470	475
Ser Val Pro Tyr Leu Ala Ser Tyr Val Ser Pro Val Leu Lys Glu Asn		
485	490	495
Lys Ala Ile Pro Gln Ser Pro Arg Ser Leu Glu Val Leu Trp Asn Val		
500	505	510
Ser Arg Met Asp Leu Glu Met Ser Gly Leu Lys Thr Leu Glu His Val		
515	520	525
Ala Val Thr Val Ser Ile Thr His Pro Arg Arg Gly Ser Leu Glu Leu		
530	535	540
Lys Leu Phe Cys Pro Ser Gly Met Met Ser Leu Ile Gly Ala Pro Arg		
545	550	555
Ser Met Asp Ser Asp Pro Asn Gly Phe Asn Asp Trp Thr Phe Ser Thr		
565	570	575
Val Arg Cys Trp Gly Glu Arg Ala Arg Gly Thr Tyr Arg Leu Val Ile		
580	585	590
Arg Asp Val Gly Asp Glu Ser Phe Gln Val Gly Ile Leu Arg Gln Trp		
595	600	605
Gln Leu Thr Leu Tyr Gly Ser Val Trp Ser Ala Val Asp Ile Arg Asp		
610	615	620
Arg Gln Arg Leu Leu Glu Ser Ala Met Ser Gly Lys Tyr Leu His Asp		
625	630	635
Asp Phe Ala Leu Pro Cys Pro Pro Gly Leu Lys Ile Pro Glu Glu Asp		
645	650	655
Gly Tyr Thr Ile Thr Pro Asn Thr Leu Lys Thr Leu Val Leu Val Gly		
660	665	670
Cys Phe Thr Val Phe Trp Thr Val Tyr Tyr Met Leu Glu Val Tyr Leu		
675	680	685
Ser Gln Arg Asn Val Ala Ser Asn Gln Val Cys Arg Ser Gly Pro Cys		
690	695	700
His Trp Pro His Arg Ser Arg Lys Ala Lys Glu Glu Gly Thr Glu Leu		
705	710	715
Glu Ser Val Pro Leu Cys Ser Ser Lys Asp Pro Asp Glu Val Glu Thr		
725	730	735
Glu Ser Arg Gly Pro Pro Thr Thr Ser Asp Leu Leu Ala Pro Asp Leu		
740	745	750
Leu Glu Gln Gly Asp Trp Ser Leu Ser Gln Asn Lys Ser Ala Leu Asp		
755	760	765
Cys Pro His Gln His Leu Asp Val Pro His Gly Lys Glu Glu Gln Ile		
770	775	780
Cys		
785		

<210> SEQ ID NO 761
<211> LENGTH: 692
<212> TYPE: PRT
<213> ORGANISM: Macaca fascicularis

<400> SEQUENCE: 761

Met Gly Thr Val Ser Ser Arg Arg Ser Trp Trp Pro Leu Pro Leu Pro

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1	5	10	15
Leu Leu Leu Leu Leu Leu Gly Pro Ala Gly Ala Arg Ala Gln Glu			
20	25	30	
Asp Glu Asp Gly Asp Tyr Glu Glu Leu Val Leu Ala Leu Arg Ser Glu			
35	40	45	
Glu Asp Gly Leu Ala Asp Ala Pro Glu His Gly Ala Thr Ala Thr Phe			
50	55	60	
His Arg Cys Ala Lys Asp Pro Trp Arg Leu Pro Gly Thr Tyr Val Val			
65	70	75	80
Val Leu Lys Glu Glu Thr His Arg Ser Gln Ser Glu Arg Thr Ala Arg			
85	90	95	
Arg Leu Gln Ala Gln Ala Ala Arg Arg Gly Tyr Leu Thr Lys Ile Leu			
100	105	110	
His Val Phe His His Leu Leu Pro Gly Phe Leu Val Lys Met Ser Gly			
115	120	125	
Asp Leu Leu Glu Leu Ala Leu Lys Leu Pro His Val Asp Tyr Ile Glu			
130	135	140	
Glu Asp Ser Ser Val Phe Ala Gln Ser Ile Pro Trp Asn Leu Glu Arg			
145	150	155	160
Ile Thr Pro Ala Arg Tyr Arg Ala Asp Glu Tyr Gln Pro Pro Lys Gly			
165	170	175	
Gly Ser Leu Val Glu Val Tyr Leu Leu Asp Thr Ser Ile Gln Ser Asp			
180	185	190	
His Arg Glu Ile Glu Gly Arg Val Met Val Thr Asp Phe Glu Ser Val			
195	200	205	
Pro Glu Glu Asp Gly Thr Arg Phe His Arg Gln Ala Ser Lys Cys Asp			
210	215	220	
Ser His Gly Thr His Leu Ala Gly Val Val Ser Gly Arg Asp Ala Gly			
225	230	235	240
Val Ala Lys Gly Ala Gly Leu Arg Ser Leu Arg Val Leu Asn Cys Gln			
245	250	255	
Gly Lys Gly Thr Val Ser Gly Thr Leu Ile Gly Leu Glu Phe Ile Arg			
260	265	270	
Lys Ser Gln Leu Val Gln Pro Val Gly Pro Leu Val Val Leu Leu Pro			
275	280	285	
Leu Ala Gly Gly Tyr Ser Arg Val Phe Asn Ala Ala Cys Gln Arg Leu			
290	295	300	
Ala Arg Ala Gly Val Val Leu Val Thr Ala Ala Gly Asn Phe Arg Asp			
305	310	315	320
Asp Ala Cys Leu Tyr Ser Pro Ala Ser Ala Pro Glu Val Ile Thr Val			
325	330	335	
Gly Ala Thr Asn Ala Gln Asp Gln Pro Val Thr Leu Gly Thr Leu Gly			
340	345	350	
Thr Asn Phe Gly Arg Cys Val Asp Leu Phe Ala Pro Gly Glu Asp Ile			
355	360	365	
Ile Gly Ala Ser Ser Asp Cys Ser Thr Cys Phe Val Ser Arg Ser Gly			
370	375	380	
Thr Ser Gln Ala Ala Ala His Val Ala Gly Ile Ala Ala Met Met Leu			
385	390	395	400
Ser Ala Glu Pro Glu Leu Thr Leu Ala Glu Leu Arg Gln Arg Leu Ile			
405	410	415	
His Phe Ser Ala Lys Asp Val Ile Asn Glu Ala Trp Phe Pro Glu Asp			
420	425	430	

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Gln Arg Val Leu Thr Pro Asn Leu Val Ala Ala Leu Pro Pro Ser Thr
435 440 445

His Arg Ala Gly Trp Gln Leu Phe Cys Arg Thr Val Trp Ser Ala His
450 455 460

Ser Gly Pro Thr Arg Met Ala Thr Ala Val Ala Arg Cys Ala Gln Asp
465 470 475 480

Glu Glu Leu Leu Ser Cys Ser Ser Phe Ser Arg Ser Gly Lys Arg Arg
485 490 495

Gly Glu Arg Ile Glu Ala Gln Gly Gly Lys Arg Val Cys Arg Ala His
500 505 510

Asn Ala Phe Gly Gly Glu Val Tyr Ala Ile Ala Arg Cys Cys Leu
515 520 525

Leu Pro Gln Val Asn Cys Ser Val His Thr Ala Pro Pro Ala Gly Ala
530 535 540

Ser Met Gly Thr Arg Val His Cys His Gln Gln Gly His Val Leu Thr
545 550 555 560

Gly Cys Ser Ser His Trp Glu Val Glu Asp Leu Gly Thr His Lys Pro
565 570 575

Pro Val Leu Arg Pro Arg Gly Gln Pro Asn Gln Cys Val Gly His Arg
580 585 590

Glu Ala Ser Ile His Ala Ser Cys Cys His Ala Pro Gly Leu Glu Cys
595 600 605

Lys Val Lys Glu His Gly Ile Pro Ala Pro Gln Glu Gln Val Ile Val
610 615 620

Ala Cys Glu Asp Gly Trp Thr Leu Thr Gly Cys Ser Ala Leu Pro Gly
625 630 635 640

Thr Ser His Val Leu Gly Ala Tyr Ala Val Asp Asn Thr Cys Val Val
645 650 655

Arg Ser Arg Asp Val Ser Thr Thr Gly Ser Thr Ser Glu Glu Ala Val
660 665 670

Ala Ala Val Ala Ile Cys Cys Arg Ser Arg His Leu Val Gln Ala Ser
675 680 685

Gln Glu Leu Gln
690

<210> SEQ ID NO 762
<211> LENGTH: 698
<212> TYPE: PRT
<213> ORGANISM: Mesocricetus auratus

<400> SEQUENCE: 762

Met Gly Thr Ser Cys Ser Ala Arg Pro Arg Trp Leu Leu Ser Pro Leu
1 5 10 15

Leu Leu Leu Leu Leu Arg Tyr Met Gly Ala Ser Ala Gln Asp
20 25 30

Glu Asp Ala Glu Tyr Glu Glu Leu Met Leu Thr Leu Gln Ser Gln Asp
35 40 45

Asp Gly Leu Ala Asp Glu Thr Asp Glu Ala Pro Gln Gly Ala Thr Ala
50 55 60

Ala Phe His Arg Cys Pro Glu Glu Ala Trp Arg Val Pro Gly Thr Tyr
65 70 75 80

Ile Val Met Leu Ala Glu Glu Ala Gln Trp Val His Ile Glu Gln Thr
85 90 95

Met His Arg Leu Gln Thr Gln Ala Ala Arg Arg Gly Tyr Val Ile Lys
100 105 110

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Ile Gln His Ile Phe Tyr Asp Phe Leu Pro Ala Phe Val Val Lys Met
115 120 125

Ser Ser Asp Leu Leu Asp Leu Ala Leu Lys Leu Pro His Val Lys Tyr
130 135 140

Ile Glu Glu Asp Ser Leu Val Phe Ala Gln Ser Ile Pro Trp Asn Leu
145 150 155 160

Asp Arg Ile Ile Pro Ala Gly Arg Gln Ala Gln Glu Tyr Ser Ser Ser
165 170 175

Arg Lys Val Pro Ser Gly Ser Gly Gln Val Glu Val Tyr Leu Leu Asp
180 185 190

Thr Ser Ile Gln Ser Asp His Arg Glu Ile Glu Gly Arg Val Thr Val
195 200 205

Thr Asp Phe Asn Ser Val Pro Glu Glu Asp Gly Thr Arg Phe His Arg
210 215 220

Gln Ala Ser Lys Cys Asp Ser His Gly Thr His Leu Ala Gly Val Val
225 230 235 240

Ser Gly Arg Asp Ala Gly Val Ala Lys Gly Thr Ile Leu His Gly Leu
245 250 255

Arg Val Leu Asn Cys Gln Gly Lys Gly Ile Val Ser Gly Ile Leu Thr
260 265 270

Gly Leu Glu Phe Ile Trp Lys Ser Gln Leu Met Gln Pro Ser Gly Pro
275 280 285

Gln Val Val Leu Leu Pro Leu Ala Gly Arg Tyr Ser Arg Val Leu Asn
290 295 300

Thr Ala Cys Gln His Leu Ala Arg Thr Gly Val Val Leu Val Ala Ala
305 310 315 320

Ala Gly Asn Phe Arg Asp Asp Ala Cys Leu Tyr Ser Pro Ala Ser Ala
325 330 335

Pro Glu Val Ile Thr Val Gly Ala Thr Asp Val Gln Asp Gln Pro Val
340 345 350

Thr Leu Gly Thr Leu Gly Thr Asn Phe Gly Arg Cys Val Asp Leu Phe
355 360 365

Ala Pro Gly Lys Asp Ile Ile Gly Ala Ser Ser Asp Cys Ser Ala Cys
370 375 380

Phe Met Ser Gln Ser Gly Thr Ser Gln Ala Ala Ala His Val Ala Gly
385 390 395 400

Ile Val Ala Met Met Leu Thr Leu Glu Pro Glu Leu Thr Leu Thr Glu
405 410 415

Leu Arg Gln Arg Leu Ile His Phe Ser Thr Lys Asp Ala Ile Asn Met
420 425 430

Ala Trp Phe Pro Glu Asp Gln Arg Val Leu Thr Pro Asn Leu Val Ala
435 440 445

Thr Leu Pro Pro Ser Thr His Gly Thr Gly Gln Leu Leu Cys Arg
450 455 460

Thr Val Trp Ser Ala His Ser Gly Pro Thr Arg Ala Ala Thr Ala Thr
465 470 475 480

Ala Arg Cys Ala Pro Gly Glu Leu Leu Ser Cys Ser Ser Phe Ser
485 490 495

Arg Ser Gly Arg Arg Arg Gly Asp Arg Ile Glu Ala Ala Gly Thr Gln
500 505 510

Gln Val Cys Lys Ala Leu Asn Ala Phe Gly Gly Glu Gly Val Tyr Ala
515 520 525

Val Ala Arg Cys Cys Leu Leu Pro Arg Ala Asn Cys Ser Ile His Thr
530 535 540

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Thr Pro Ala Ala Arg Thr Ser Leu Glu Thr His Ala His Cys His Gln
 545 550 555 560
 Lys Asp His Val Leu Thr Gly Cys Ser Leu His Trp Glu Val Glu Gly
 565 570 575
 Ile Gly Val Gln Pro Leu Ala Val Leu Arg Ser Arg His Gln Pro Gly
 580 585 590
 Gln Cys Thr Gly His Arg Glu Ala Ser Val His Ala Ser Cys Cys His
 595 600 605
 Ala Pro Gly Leu Glu Cys Lys Ile Lys Glu His Gly Ile Ser Gly Pro
 610 615 620
 Ala Glu Gln Val Thr Val Ala Cys Glu Ala Gly Trp Thr Leu Thr Gly
 625 630 635 640
 Cys Asn Val Leu Pro Gly Ala Phe Ile Thr Leu Gly Ala Tyr Ala Val
 645 650 655
 Asp Asn Thr Cys Val Ala Arg Ser Arg Val Thr Asp Thr Ala Gly Arg
 660 665 670
 Thr Gly Glu Glu Ala Thr Val Ala Ala Ala Ile Cys Cys Arg Asn Arg
 675 680 685
 Pro Ser Ala Lys Ala Ser Trp Val His Gln
 690 695

<210> SEQ ID NO 763
 <211> LENGTH: 691
 <212> TYPE: PRT
 <213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 763

Met	Gly	Ile	Arg	Cys	Ser	Thr	Trp	Leu	Arg	Trp	Pro	Leu	Ser	Pro	Gln
1				5				10				15			

Leu	Leu	Leu	Leu	Leu	Leu	Cys	Pro	Thr	Gly	Ser	Arg	Ala	Gln	Asp
						20		25				30		

Glu	Asp	Gly	Asp	Tyr	Glu	Glu	Leu	Met	Leu	Ala	Leu	Pro	Ser	Gln	Glu
35					40				45						

Asp	Ser	Leu	Val	Asp	Glu	Ala	Ser	His	Val	Ala	Thr	Ala	Thr	Phe	Arg
50					55				60						

Arg	Cys	Ser	Lys	Glu	Ala	Trp	Arg	Leu	Pro	Gly	Thr	Tyr	Val	Val	Val
65					70			75					80		

Leu	Met	Glu	Glu	Thr	Gln	Arg	Leu	Gln	Val	Glu	Gln	Thr	Ala	His	Arg
					85			90			95				

Leu	Gln	Thr	Trp	Ala	Ala	Arg	Arg	Gly	Tyr	Val	Ile	Lys	Val	Leu	His
						100		105			110				

Val	Phe	Tyr	Asp	Leu	Phe	Pro	Gly	Phe	Leu	Val	Lys	Met	Ser	Ser	Asp
115					120				125						

Leu	Leu	Gly	Leu	Ala	Leu	Lys	Leu	Pro	His	Val	Glu	Tyr	Ile	Glu	Glu
130					135				140						

Asp	Ser	Leu	Val	Phe	Ala	Gln	Ser	Ile	Pro	Trp	Asn	Leu	Glu	Arg	Ile
145					150				155			160			

Ile	Pro	Ala	Trp	Gln	Gln	Thr	Glu	Asp	Ser	Ser	Pro	Asp	Gly	Ser
					165			170			175			

Ser	Gln	Val	Glu	Val	Tyr	Leu	Leu	Asp	Thr	Ser	Ile	Gln	Ser	Gly	His
						180		185			190				

Arg	Glu	Ile	Glu	Gly	Arg	Val	Thr	Ile	Thr	Asp	Phe	Asn	Ser	Val	Pro
					195			200			205				

Glu	Glu	Asp	Gly	Thr	Arg	Phe	His	Arg	Gln	Ala	Ser	Lys	Cys	Asp	Ser
210					215				220						

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His Gly Thr His Leu Ala Gly Val Val Ser Gly Arg Asp Ala Gly Val
 225 230 235 240
 Ala Lys Gly Thr Ser Leu His Ser Leu Arg Val Leu Asn Cys Gln Gly
 245 250 255
 Lys Gly Thr Val Ser Gly Thr Leu Ile Gly Leu Glu Phe Ile Arg Lys
 260 265 270
 Ser Gln Leu Ile Gln Pro Ser Gly Pro Leu Val Val Leu Leu Pro Leu
 275 280 285
 Ala Gly Gly Tyr Ser Arg Ile Leu Asn Thr Ala Cys Gln Arg Leu Ala
 290 295 300
 Arg Thr Gly Val Val Leu Val Ala Ala Ala Gly Asn Phe Arg Asp Asp
 305 310 315 320
 Ala Cys Leu Tyr Ser Pro Ala Ser Ala Pro Glu Val Ile Thr Val Gly
 325 330 335
 Ala Thr Asn Ala Gln Asp Gln Pro Val Thr Leu Gly Thr Leu Gly Thr
 340 345 350
 Asn Phe Gly Arg Cys Val Asp Leu Phe Ala Pro Gly Lys Asp Ile Ile
 355 360 365
 Gly Ala Ser Ser Asp Cys Ser Thr Cys Tyr Met Ser Gln Ser Gly Thr
 370 375 380
 Ser Gln Ala Ala Ala His Val Ala Gly Ile Val Ala Met Met Leu Asn
 385 390 395 400
 Arg Asp Pro Ala Leu Thr Leu Ala Glu Leu Arg Gln Arg Leu Ile Leu
 405 410 415
 Phe Ser Thr Lys Asp Val Ile Asn Met Ala Trp Phe Pro Glu Asp Gln
 420 425 430
 Arg Val Leu Thr Pro Asn Arg Val Ala Thr Leu Pro Pro Ser Thr Gln
 435 440 445
 Glu Thr Gly Gly Gln Leu Leu Cys Arg Thr Val Trp Ser Ala His Ser
 450 455 460
 Gly Pro Thr Arg Thr Ala Thr Ala Arg Cys Ala Pro Glu Glu
 465 470 475 480
 Glu Leu Leu Ser Cys Ser Ser Phe Ser Arg Ser Gly Arg Arg Gly
 485 490 495
 Asp Arg Ile Glu Ala Ile Gly Gly Gln Gln Val Cys Lys Ala Leu Asn
 500 505 510
 Ala Phe Gly Gly Glu Gly Val Tyr Ala Val Ala Arg Cys Cys Leu Leu
 515 520 525
 Pro Arg Val Asn Cys Ser Ile His Asn Thr Pro Ala Ala Arg Ala Gly
 530 535 540
 Pro Gln Thr Pro Val His Cys His Gln Lys Asp His Val Leu Thr Gly
 545 550 555 560
 Cys Ser Phe His Trp Glu Val Glu Asn Leu Arg Ala Gln Gln Pro
 565 570 575
 Leu Leu Arg Ser Arg His Gln Pro Gly Gln Cys Val Gly His Gln Glu
 580 585 590
 Ala Ser Val His Ala Ser Cys Cys His Ala Pro Gly Leu Glu Cys Lys
 595 600 605
 Ile Lys Glu His Gly Ile Ala Gly Pro Ala Glu Gln Val Thr Val Ala
 610 615 620
 Cys Glu Ala Gly Trp Thr Leu Thr Gly Cys Asn Val Leu Pro Gly Ala
 625 630 635 640
 Ser Leu Pro Leu Gly Ala Tyr Ser Val Asp Asn Val Cys Val Ala Arg

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645

650

655

Ile Arg Asp Ala Gly Arg Ala Asp Arg Thr Ser Glu Glu Ala Thr Val
660 665 670

Ala Ala Ala Ile Cys Cys Arg Ser Arg Pro Ser Ala Lys Ala Ser Trp
675 680 685

Val His Gln
690

We claim:

1. An antibody or antigen binding fragment of an antibody that specifically binds hPCSK9, comprising heavy and light chain CDR sequences from the HCVR and LCVR sequence pair having SEQ ID NOs: 90/92.

2. The antibody or antigen-binding fragment of claim 1 comprising heavy and light chain CDR sequences having SEQ ID NOs; 76, 78, 80, 84, 86, and 88.

3. The antibody or antigen-binding fragment of claim 2 comprising an HCVR having the amino acid sequence, of SEQ ID NO:90 and an LCVR having the amino acid sequence of SEQ ID NO:92.

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