



US010023654B2

(12) **United States Patent**
Sleeman et al.

(10) **Patent No.:** US 10,023,654 B2
(45) **Date of Patent:** *Jul. 17, 2018

(54) ANTI-PCSK9 ANTIBODIES

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(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 0 days.

This patent is subject to a terminal disclaimer.

(21) Appl. No.: 15/377,364

(22) Filed: Dec. 13, 2016

(65) Prior Publication Data

US 2017/0096496 A1 Apr. 6, 2017

Related U.S. Application Data

(60) Continuation of application No. 14/737,488, filed on Jun. 12, 2015, now Pat. No. 9,550,837, which is a (Continued)

(51) Int. Cl.

A61K 39/395	(2006.01)
C07K 16/40	(2006.01)
A61K 39/00	(2006.01)

(52) U.S. Cl.

CPC C07K 16/40 (2013.01); C12Y 304/21061 (2013.01); A61K 2039/505 (2013.01); (Continued)

(58) Field of Classification Search

CPC C07K 16/40; C12Y 304/21061 See application file for complete search history.

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Primary Examiner — Cherie M Stanfield

(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.

18 Claims, 14 Drawing Sheets

H1H316P VH (SEQ ID NO:90)	EV Q L V E S G G G L V Q P G G S L R L S C A A S G F T F N N Y A M N W V R Q A P G K G
H1M300N VH (SEQ ID NO:218)	E M Q L V E S G G G L V Q P G G S L R L S C A A S G F T F S S H W M K W V R Q A P G K G

CDR1

H1H316P VH (SEQ ID NO:90)	L D W V S T I S G S G G T T I N Y A D S V K G R F I I S R D S S K H T L Y L Q M N S L R A
H1M300N VH (SEQ ID NO:218)	L E W V A N I N Q D G S E K Y Y Y D S V K G R F T I S R D N A K N S L F L Q M N S L R A

CDR2

H1H316P VH (SEQ ID NO:90)	E D T A V Y Y C A K D S N W G N F D L - - - - - W G R G T L V T V S S
H1M300N VH (SEQ ID NO:218)	E D T A V Y Y C A R D I V L M V Y D M D Y Y Y Y G M D V W G Q G T T V T V S S

CDR3

H1H316P VK (SEQ ID NO:92)	D I V M T Q S P D S L A V S L G E R A T I N C K S S Q S V L Y R S N N R N F L G W Y Q Q
H1M300N VK (SEQ ID NO:226)	D I V M T Q S P L S L P V T P G E P A S I S C R S S Q S L L H S N G N N Y - L D W Y L Q

CDR1

H1H316P VK (SEQ ID NO:92)	K P G Q P P N L L I Y W A S T R E S G V P D R F S G S G S G T D F T L T I S S L Q A E D
H1M300N VK (SEQ ID NO:226)	K P G Q S P Q L L I Y L G S N R A S G V P D R F S G S G S G T D F T L K I S R V E A E D

CDR2

H1H316P VK (SEQ ID NO:92)	V A V Y Y C Q Q Y Y T T P Y T F G Q G T K L E I K
H1M300N VK (SEQ ID NO:226)	V G V Y Y C M Q T L Q T P L T F G G G T K V E I K

CDR3

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Related U.S. Application Data

continuation of application No. 13/690,585, filed on Nov. 30, 2012, now abandoned, which is a continuation of application No. 12/949,846, filed on Nov. 19, 2010, now Pat. No. 8,501,184, which is a division of application No. 12/637,942, filed on Dec. 15, 2009, now Pat. No. 8,062,640.

- (60) Provisional application No. 61/122,482, filed on Dec. 15, 2008, provisional application No. 61/210,566, filed on Mar. 18, 2009, provisional application No. 61/168,753, filed on Apr. 13, 2009, provisional application No. 61/218,136, filed on Jun. 18, 2009, provisional application No. 61/249,135, filed on Oct. 6, 2009, provisional application No. 61/261,776, filed on Nov. 17, 2009.

(52) **U.S. Cl.**

CPC C07K 2317/21 (2013.01); C07K 2317/33 (2013.01); C07K 2317/34 (2013.01); C07K 2317/56 (2013.01); C07K 2317/565 (2013.01); C07K 2317/76 (2013.01); C07K 2317/92 (2013.01)

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<p>H1H316P VH (SEQ ID NO:90) H1M300N VH (SEQ ID NO:218)</p> <p>H1H316P VH (SEQ ID NO:90) H1M300N VH (SEQ ID NO:218)</p> <p>H1H316P VH (SEQ ID NO:90) H1M300N VH (SEQ ID NO:218)</p> <p>H1H316P VK (SEQ ID NO:92) H1M300N VK (SEQ ID NO:226)</p> <p>H1H316P VK (SEQ ID NO:92) H1M300N VK (SEQ ID NO:226)</p> <p>H1H316P VK (SEQ ID NO:92) H1M300N VK (SEQ ID NO:226)</p>	<p>EVQLVESGGGLVQPGGSLRLSCAASGFTFNNYAMNWVRQAPGKG EMQLVESGGGLVQPGGSLRLSCAASGFTFSSHWMKWVRQAPGKG</p> <p>LDWVSTISGSGGTTNYADSVKGRFIISRDSSKHTLYLQMNSLRA LEWWANINQDGSEKYYVDSSVKGRFTISRDNAKNSLFLQMNSLRA</p> <p>EDTAVYYCAKDSNWGNFDL... EDTAVYYCARDIVLMVYDMDYYGMDVWGQQGTTVTVS</p> <p>DIVMTQSPDSSLAVSLGERATINCKSSQSVLYRSNNRNFLGWYQQ DIVMTQSPPLSLPVTPGEPAISCRRSSQSLLHSNGNNYLDWYLQ</p> <p>KPGQPPNLLIWASTRESSGVPDFSGSGSGTDFTLTSSLQAED KPGQSPQLLILGSINRASGVPDFSGSGSGTDFTLKSRLVEAED</p> <p>VAVYYCQQYTTPYTFGQGTKLEIK VGVYYCMQTLQTPLTFGGTKVEIK</p>	<p>10 20 30 40 50 60 70 80 90 100 110 120</p> <p>10 20 30 40 50 60 70 80 90 100 110 120</p> <p>10 20 30 40 50 60 70 80 90 100 110 120</p> <p>10 20 30 40 50 60 70 80 90 100 110 120</p>
		<p>CDR1</p> <p>CDR2</p> <p>CDR3</p> <p>CDR1</p> <p>CDR2</p> <p>CDR3</p>

Fig. 1

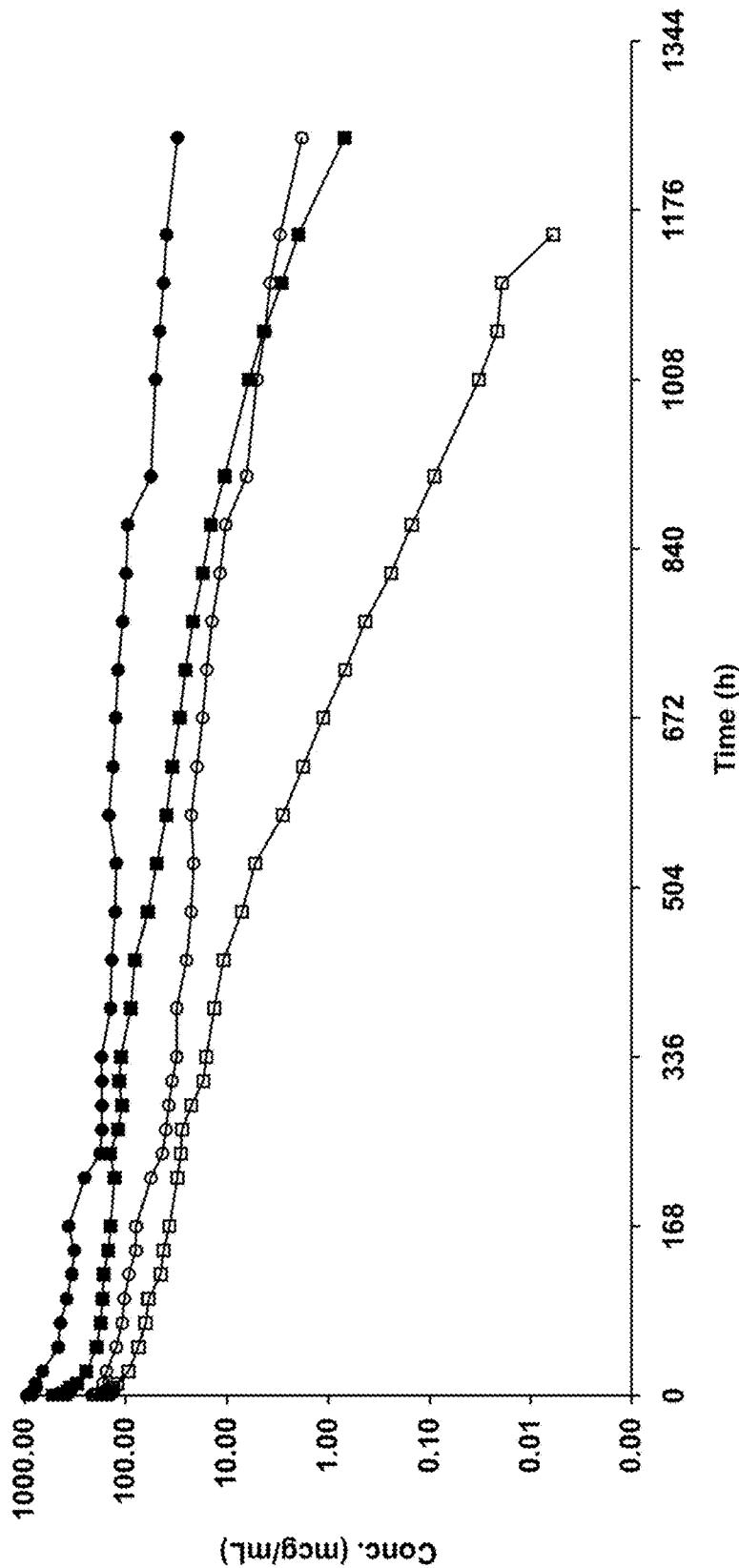


Fig. 2

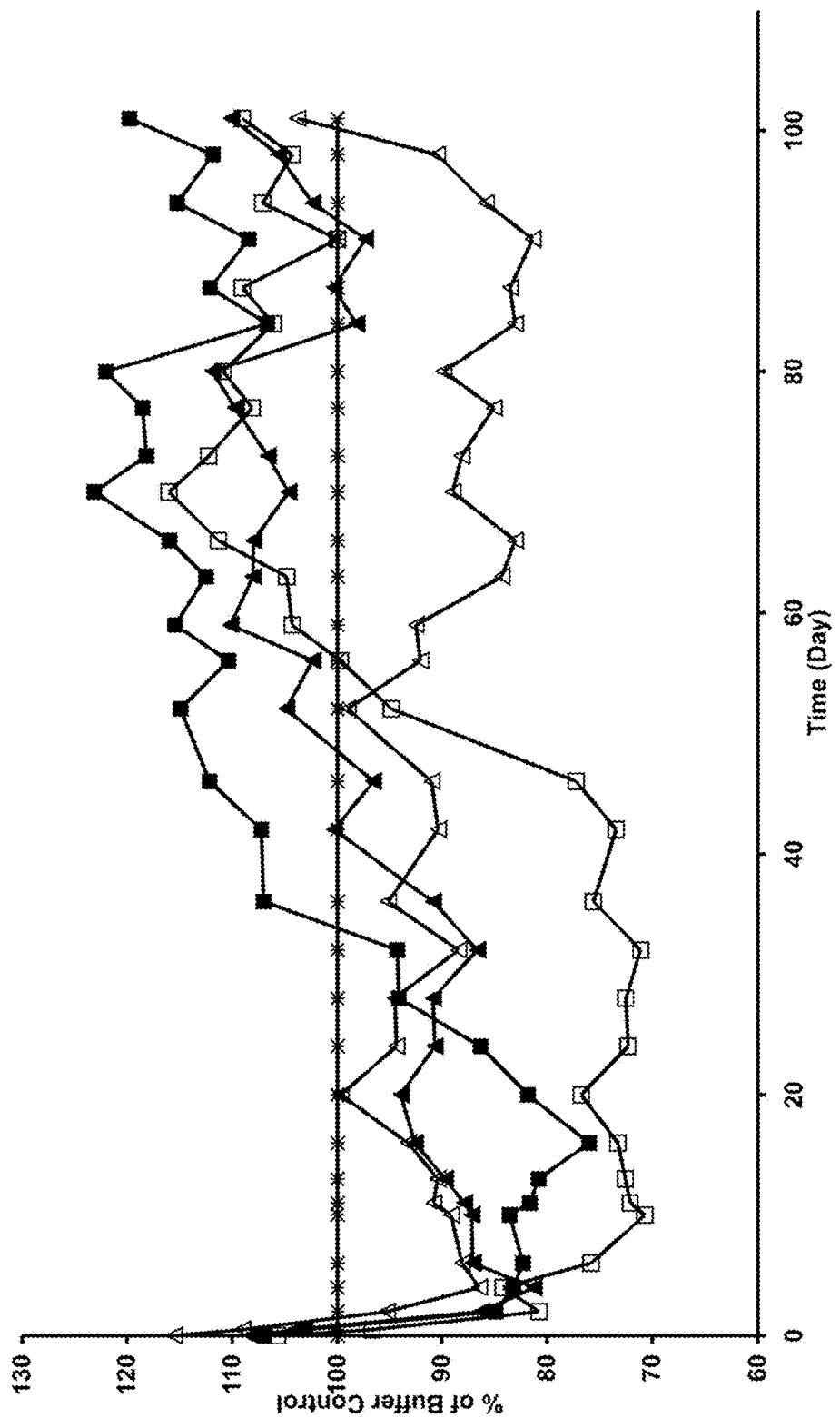


Fig. 3

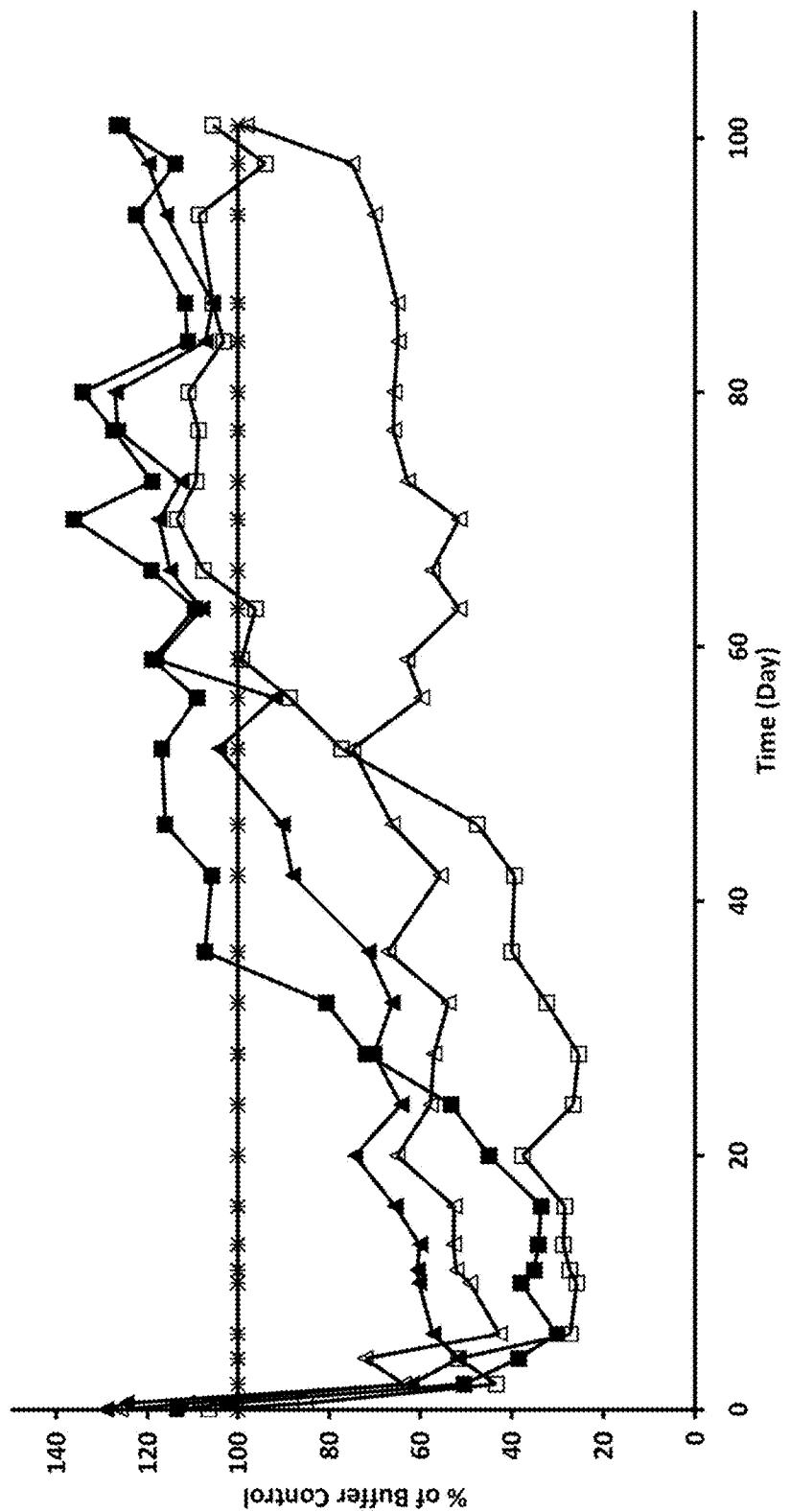


Fig. 4

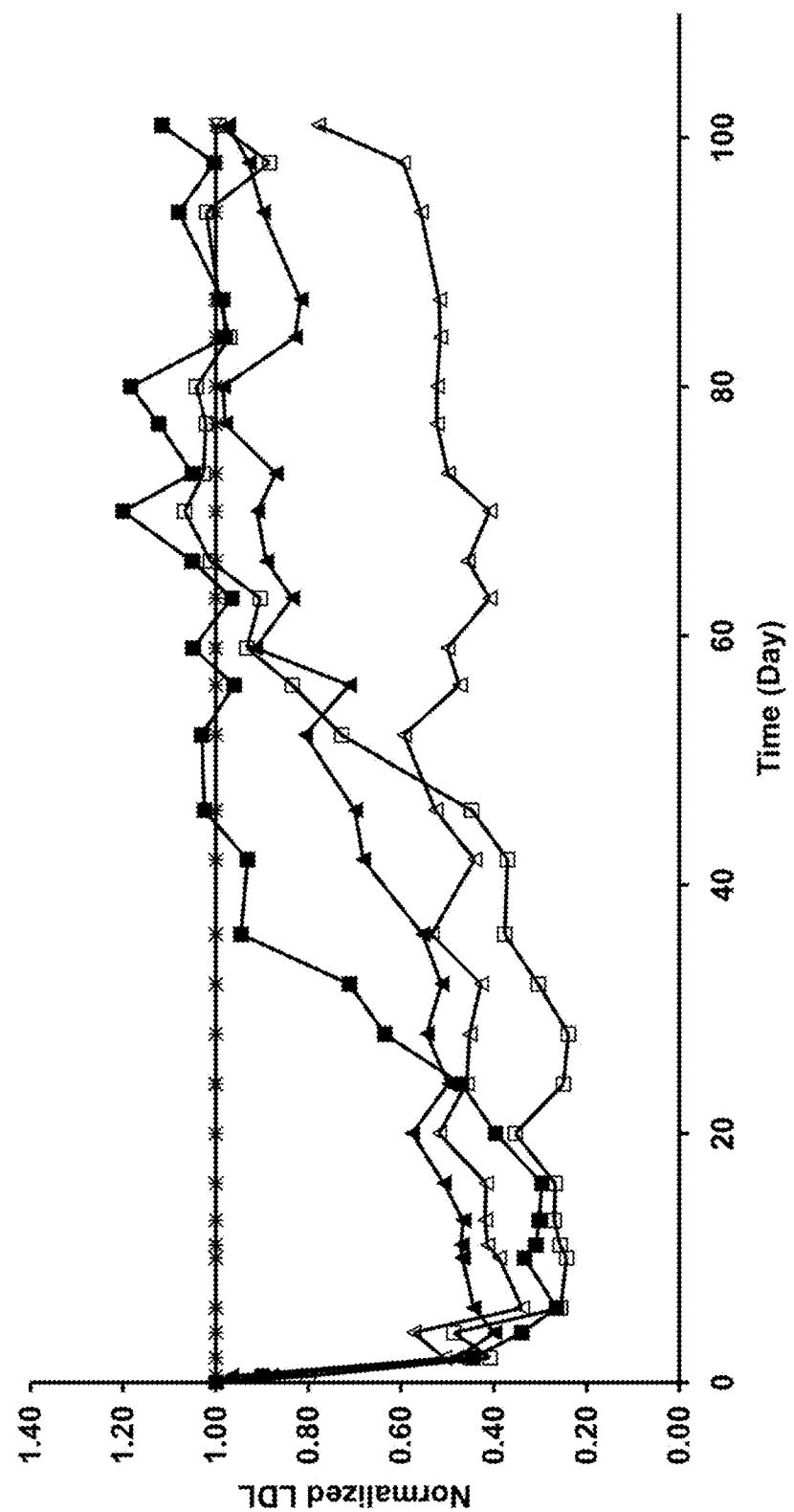


Fig. 5

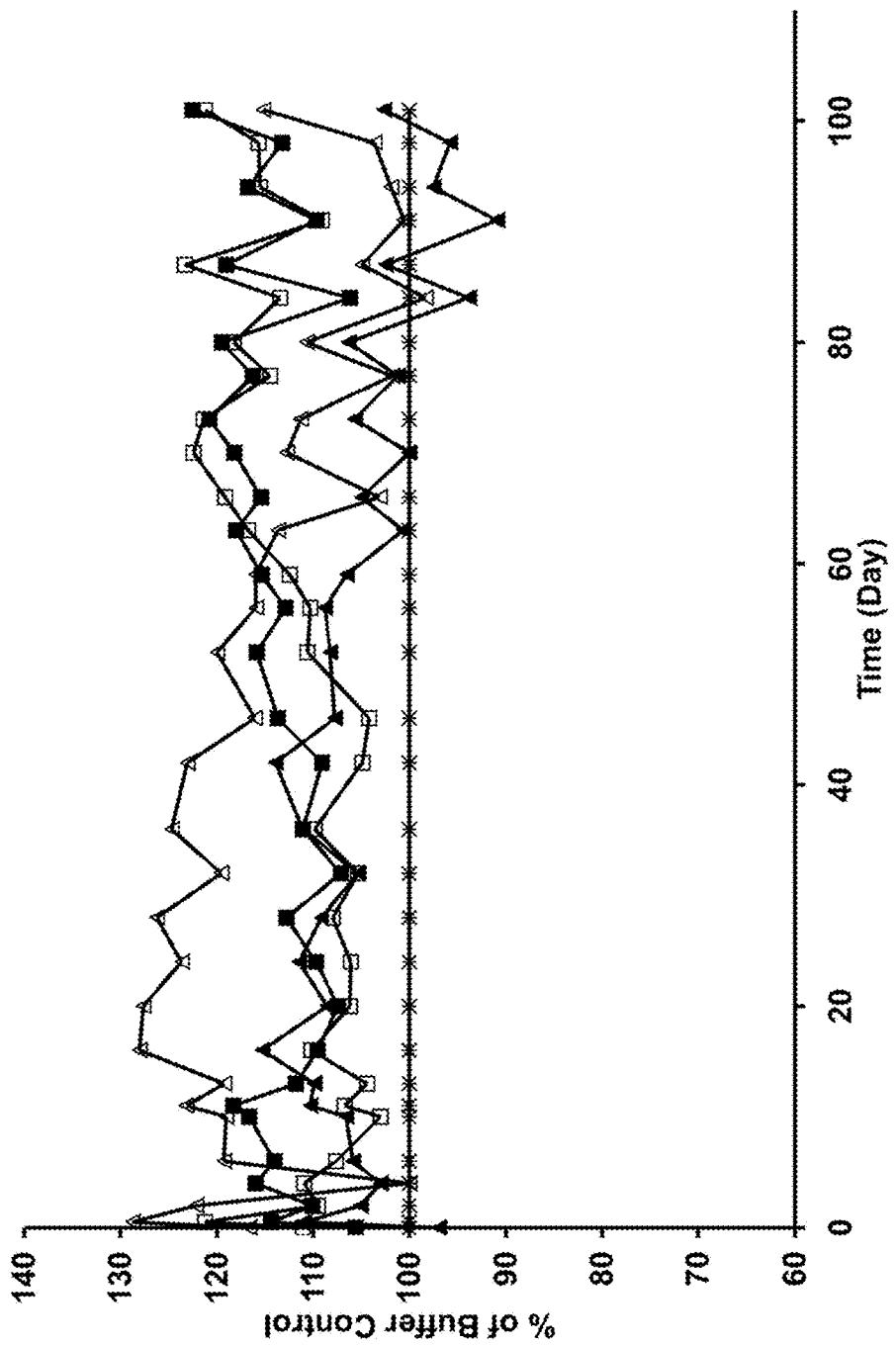


Fig. 6

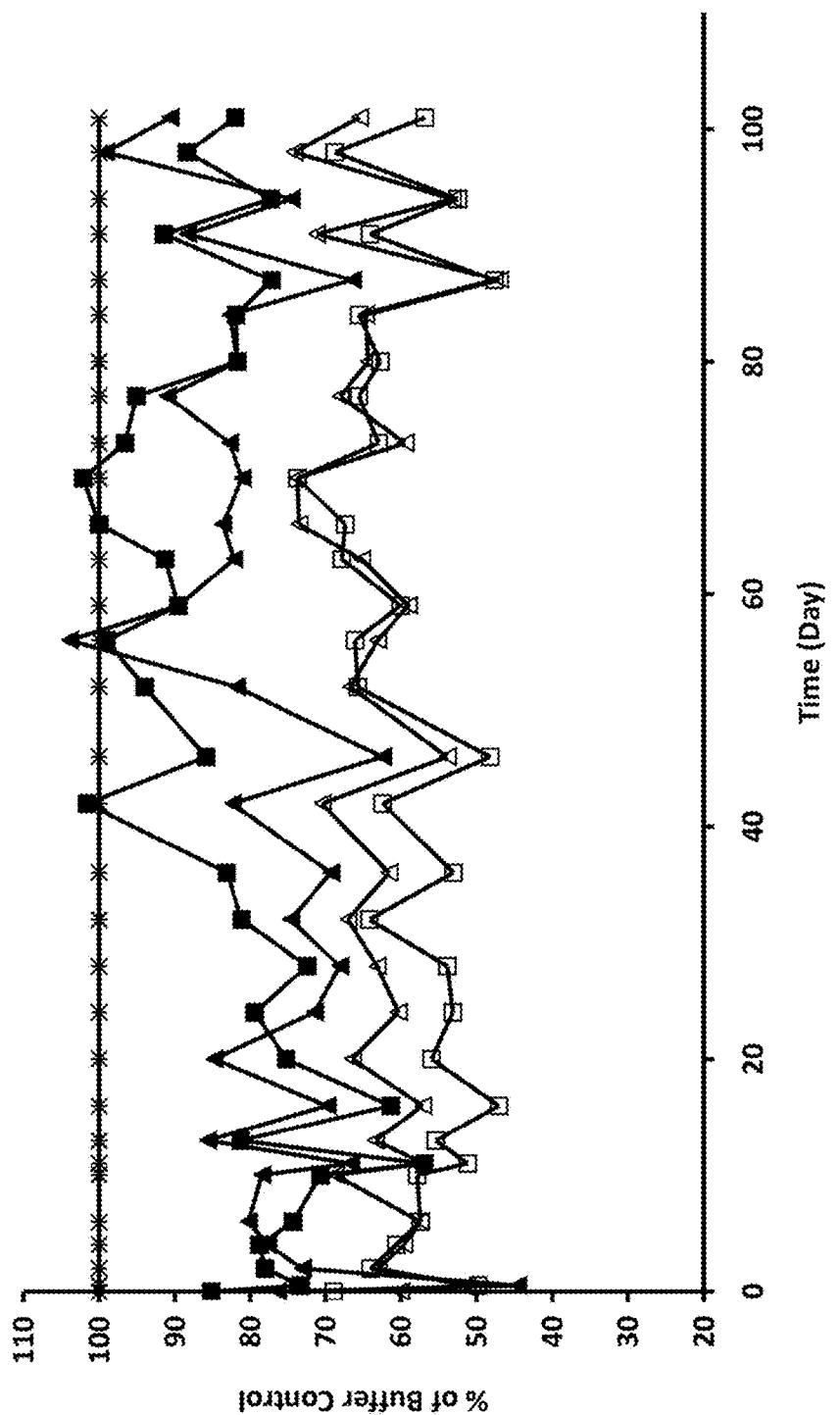


Fig. 7

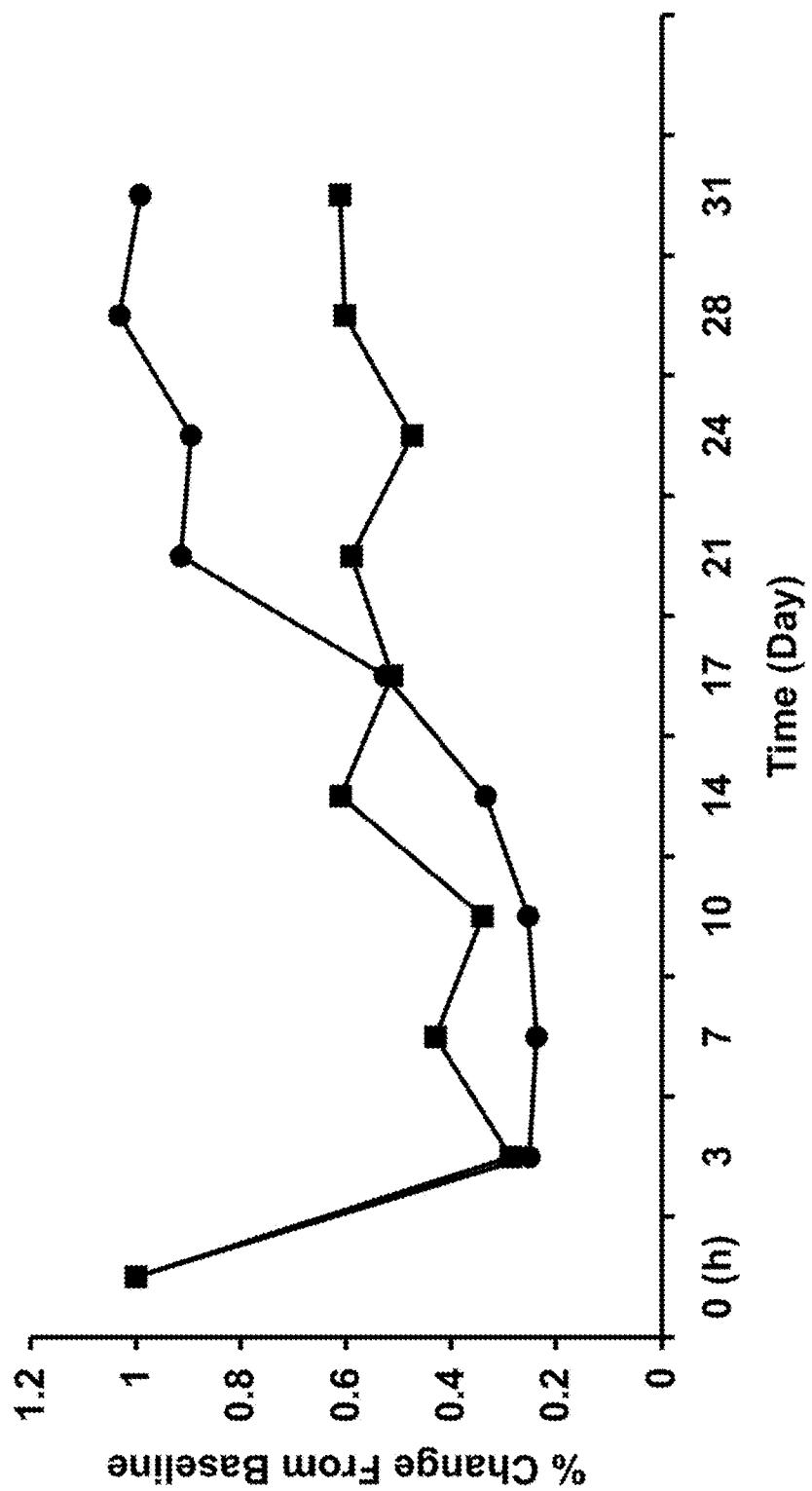


Fig. 8

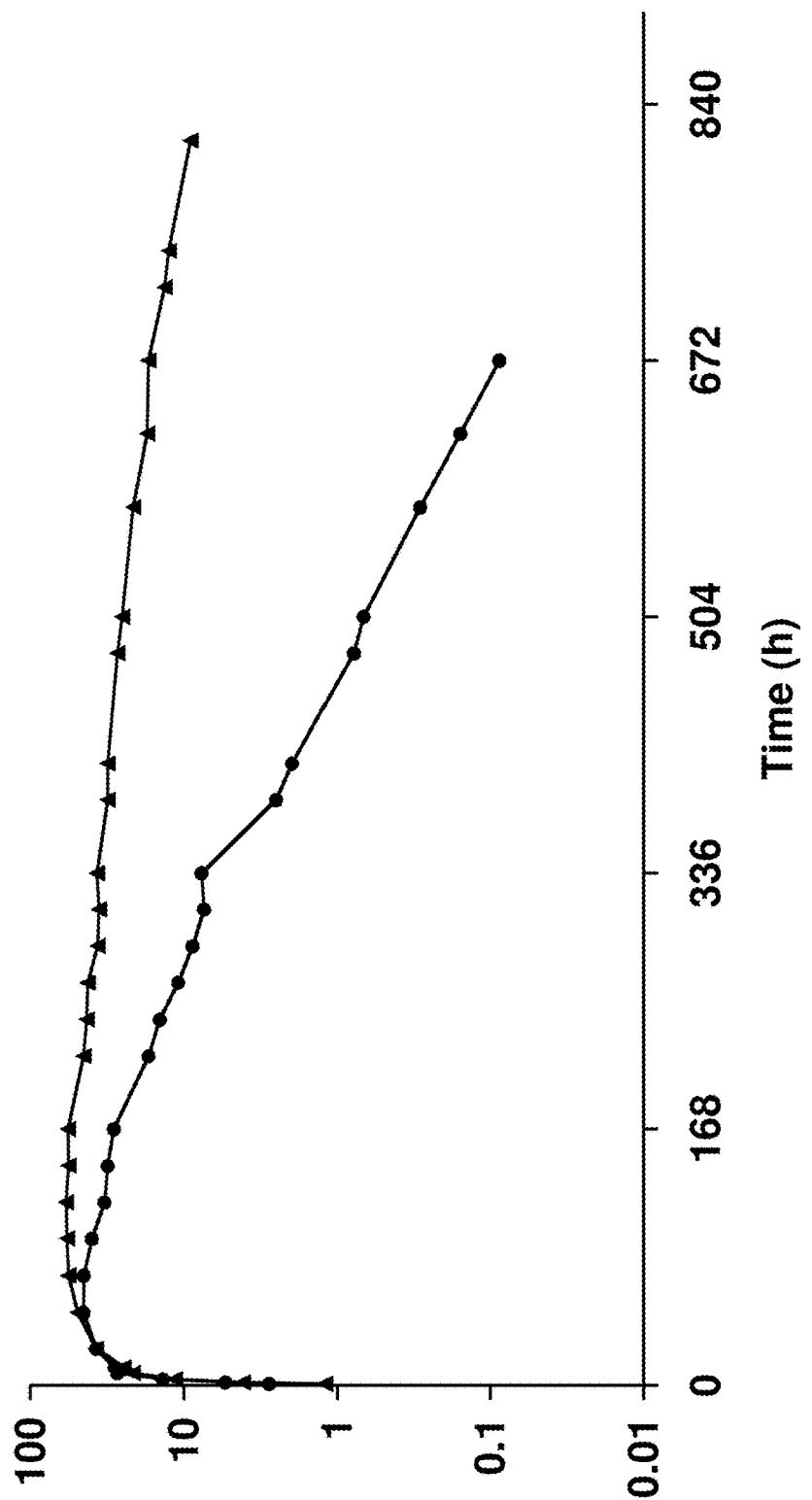


Fig. 9

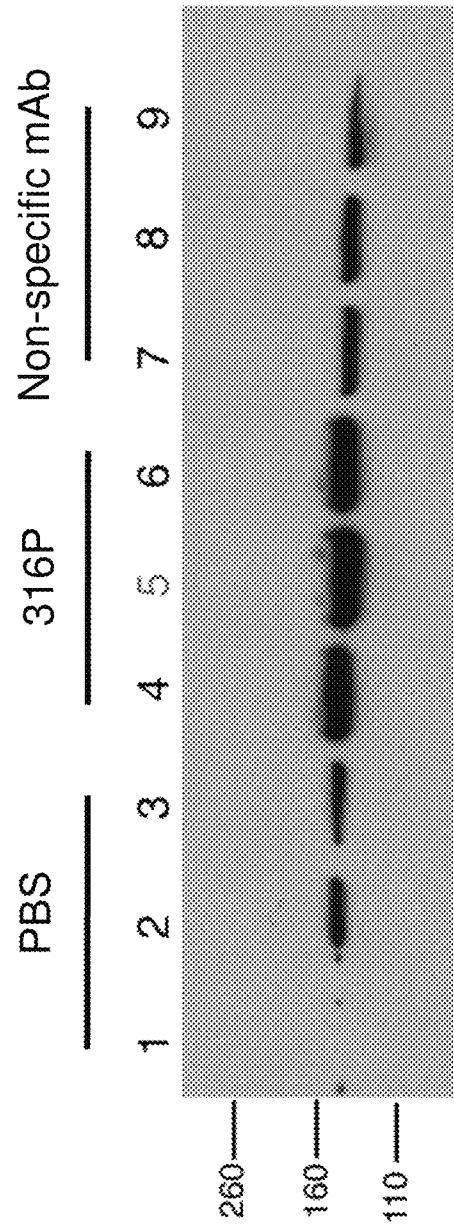


Fig. 10

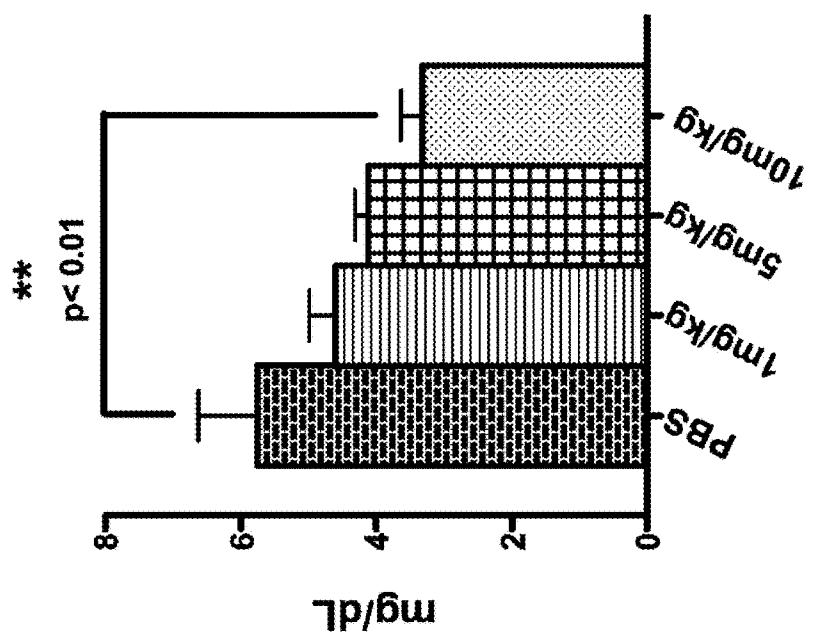


Fig. 11

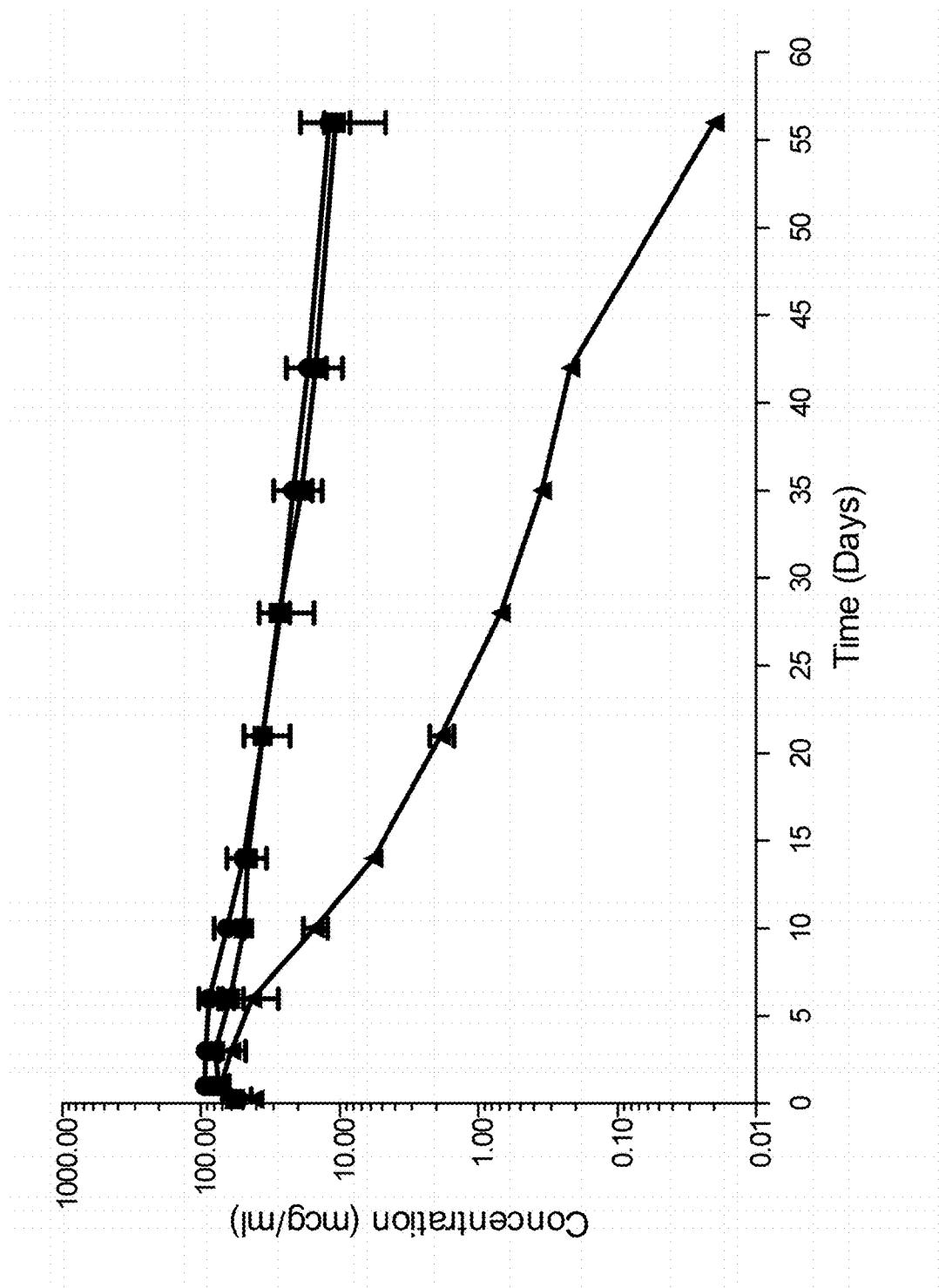


Fig. 12

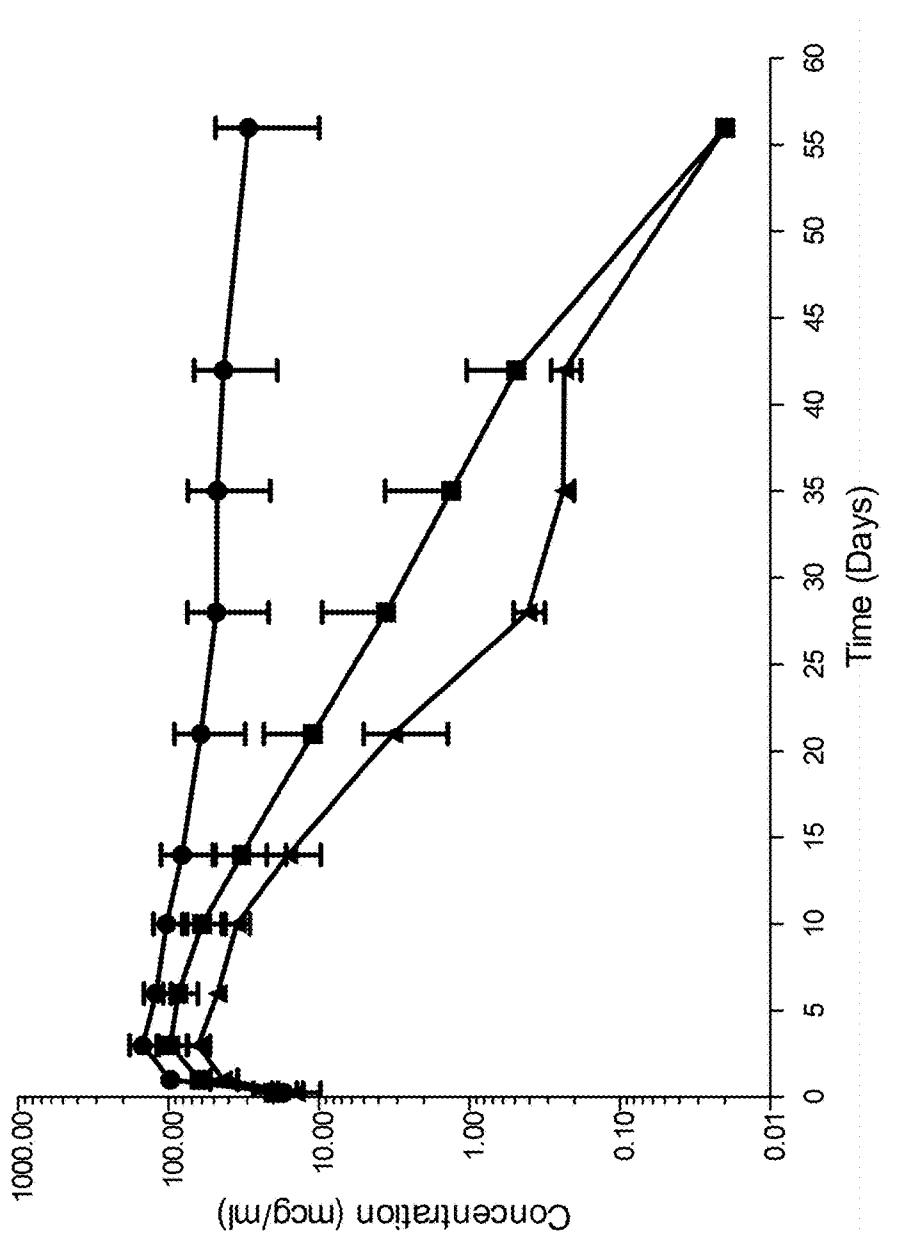


Fig. 13

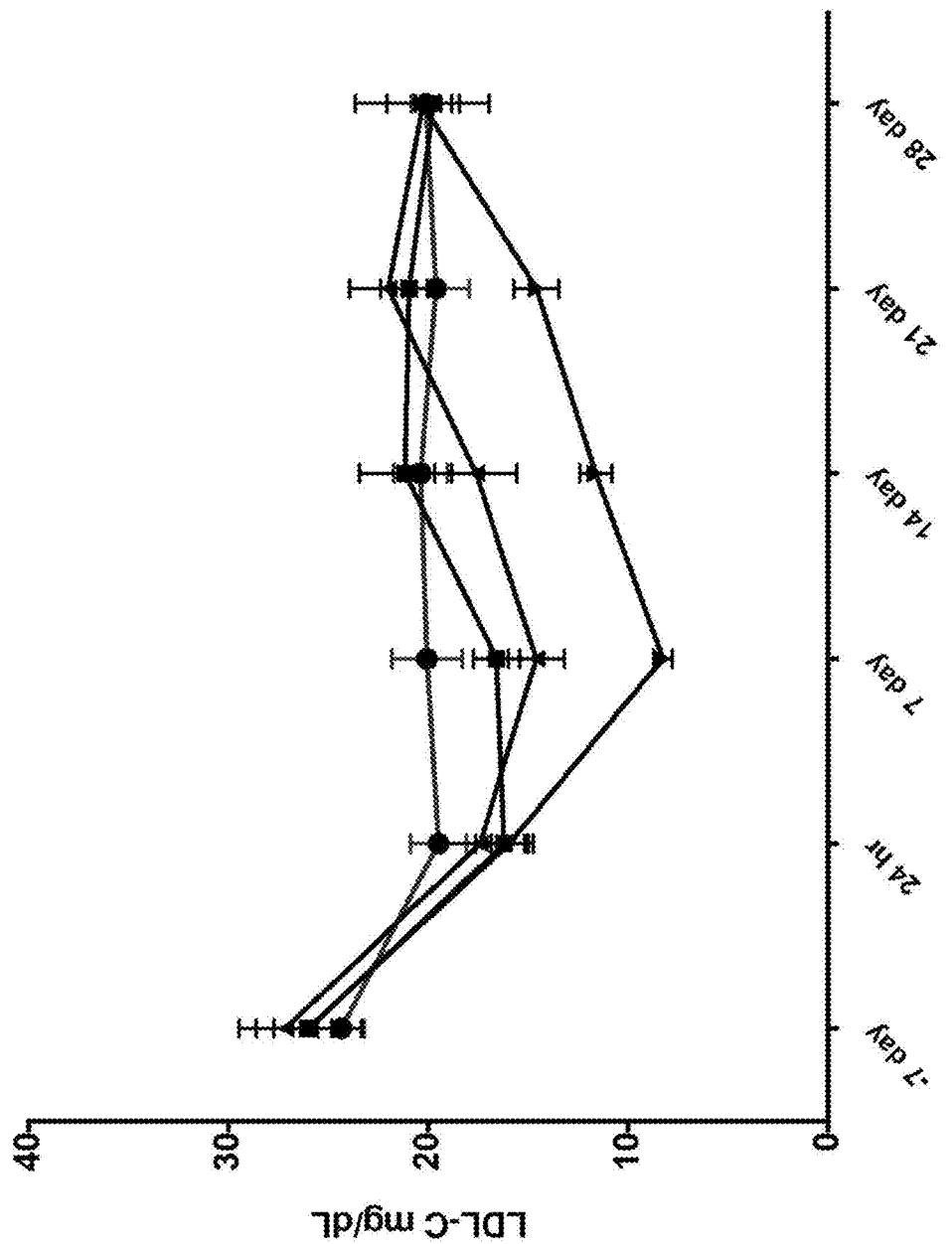


Fig. 14

1**ANTI-PCSK9 ANTIBODIES****CROSS-REFERENCE TO RELATED APPLICATIONS**

This application is a continuation of U.S. application Ser. No. 14/737,488, filed on 12 Jun. 2015, which is a continuation of U.S. application Ser. No. 13/690,585, filed on 30 Nov. 2012, which is a continuation of U.S. application Ser. No. 12/949,846 filed on 19 Nov. 2010, now U.S. Pat. No. 8,501,184, Issued 6 Aug. 2013, which is a divisional of U.S. application Ser. No. 12/637,942, filed 15 Dec. 2009, now U.S. Pat. No. 8,062,640, Issued 22 Nov. 2011, which 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 61/122,482 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.

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, 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 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,

ment, 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 embodiments, 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 $X^1-X^2-X^3-X^4-X^5-X^6-X^7-X^8$ (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-methylglutaryl (HMG)-coenzyme A (CoA) reductase, such as, for example, cerovastatin, 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-hydroxycholesterol.

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 FIGURES

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 inter-connected 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

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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

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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.

10 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.

15 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 more of several standard in vitro or in vivo assays known in the art (see examples below).

20 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 in protein concentrations within a biosensor matrix, for example using the BIACORE™ system (Pharmacia Biosensor AB, Uppsala, Sweden and Piscataway, N.J.).

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

30 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 35 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 sulfonyl groups, and, in certain embodiments, may have specific three-dimensional structural characteristics, and/or specific charge characteristics.

35 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 by any well-known algorithm of sequence identity, such as FASTA, BLAST or GAP, as discussed below.

40 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 45 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).

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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 amino acids that have side chains with similar chemical properties include 1) aliphatic side chains: glycine, alanine, valine, leucine and isoleucine; 2) aliphatic-hydroxyl side chains: serine and threonine; 3) amide-containing side chains: asparagine and glutamine; 4) aromatic side chains: phenylalanine, tyrosine, and tryptophan; 5) basic side chains: lysine, arginine, and histidine; 6) acidic side chains: aspartate and glutamate, and 7) sulfur-containing side chains: 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

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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 V821 (by IMGT; D356E, L358M, N384S, K392N, V397M, and V422I by EU) in the case of IgG1 mAbs; N44S, K52N, and V821 (IMGT; N384S, K392N, and V422I by EU) in the case of IgG2 mAbs; and Q15R, N44S, K52N, V57M, R69K, E79Q, and V821 (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

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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 and light chain may be isolated and linked to desirable isotypic 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

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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, 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

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($\sim 0.7 \times 10^{-9}$ 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.

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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, 366K and V380M.

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.

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

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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 fragment 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

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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 LIPOFECTIN™), DNA conjugates, anhydrous absorption pastes, oil-in-water and water-in-oil emulsions, emulsions carbowax (polyethylene glycols of various molecular weights), semi-solid gels, and semi-solid mixtures containing carbowax. See also Powell et al. "Compendium of excipients for parenteral formulations" PDA (1998) J Pharm Sci Technol 52:238-311.

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

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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, intra-nasal, 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, N.Y., 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

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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 AUTOPEN™ (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, Denmark), 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 FLEXPEN™ (Novo Nordisk), and the KWIKPEN™ (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, colestevam), 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, omacor).

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

VELOCIMMUNETTM 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		
	VH	D	JH	VK	JK
H1H313	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

TABLE 1-continued

5	Antibody	Heavy Chain Variable Region		Light Chain Variable Region	
		VH	D	JH	VK
	H1M494	3-11	5-12	6	3-20
	H1M309	3-21	6-13	4	1-5
	H1M312	3-21	6-13	4	1-5
	H1M499	3-21	6-13	4	1-5
10	H1M493	3-21	6-13	4	1-5
	H1M496	3-13	6-19	4	3-15
	H1M503	1-18	2-2	6	2-28
	H1M502	3-13	6-13	4	3-15
	H1M508	3-13	6-13	4	3-15
15	H1M495	3-9	4-17	6	1-9
	H1M492	3-23	3-3	2	3-20

Example 3. Antigen Binding Affinity Determination

20 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 (BIACORETM 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 BIACORETM 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

35	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

55 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 (BIACORETM 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 BIACORETM 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.

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 H1M300 ("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 (mfPCSK9, 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).

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

TABLE 7-continued

Antigen	pH Effect at 37° C.			
	pH 7.4		pH 5.5	
	K _D	T _{1/2}	K _D	T _{1/2}
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
maPCSK9-h	8830	0.5	ND	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 µl/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 µl/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 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.	
	K _D	T _{1/2}	K _D	T _{1/2}
hPCSK9-mmh	1800	9	580	36
hPCSK9(D374Y)-mmh	4200	4	1690	15
mmPCSK9-mmh	1800	21	550	92
mfPCSK9-mmh	1800	11	520	60
mPCSK9-mmh	4700	3	2300	11
maPCSK9-h	19000	1	6810	5
rPCSK9-mmh	37500	1	14500	2

TABLE 10

Antigen	300N mAb			
	37° C.		25° C.	
	K _D	T _{1/2}	K _D	T _{1/2}
hPCSK9-mmh	2400	22	740	110
hPCSK9(D374Y)-mmh	2200	14	900	65
mmPCSK9-mmh	1600	26	610	79
mfPCSK9-mmh	3800	11	1500	45
mPCSK9-mmh	NB	NB	NB	NB
maPCSK9-h	NB	NB	NB	NB
rPCSK9-mmh	NB	NB	NB	NB

TABLE 11

Antigen	Control I mAb			
	37° C.		25° C.	
	K _D	T _{1/2}	K _D	T _{1/2}
hPCSK9-mmh	226000	2	27500	16
hPCSK9(D374Y)-mmh	ND	ND	23600	25
mmPCSK9-mmh	420000	3	291000	2

TABLE 11-continued

Control I mAb				
	37° C.		25° C.	
Antigen	K _D	T _{1/2}	K _D	T _{1/2}
mfPCSK9-mmh	14300	10	24900	14
mPCK9-mmh	NB	NB	NB	NB
maPCSK9-h	NB	NB	NB	NB
rPCSK9-mmh	NB	NB	NB	NB

TABLE 12

Control II mAb				
	37° C.		25° C.	
Antigen	K _D	T _{1/2}	K _D	T _{1/2}
hPCSK9-mmh	91	162	61	372
hPCSK9(D374Y)-mmh	93	90	66	216
mfPCSK9-mmh	33	252	26	546
mPCK9-mmh	4700	3	2300	11
maPCSK9-h	60800	0.4	25000	2
rPCSK9-mmh	14100	1	6900	3

TABLE 13

Control III mAb				
	37° C.		25° C.	
Antigen	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
mPCK9-mmh	33500	1	10900	4
maPCSK9-h	780	107	2100	67
rPCSK9-mmh	NB	NB	33200	2

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

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 H1H321 P 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 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	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

domain (amino acids 313-355 of SED 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.

The ability of the mAbs to block hPCSK9 GOF mutant 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.

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TABLE 15

	pH 7.2		pH 5.5	
	Plate Coating Surface		EGF-A	EGF-AB
	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

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 (IC_{50} 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 mmh-tagged mmPCSK9 or 1 nM of mPCSK9.

TABLE 16

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

The ability of the mAbs to block hPCSK9, mmPCSK9, rPCSK9, maPCSK9, mfPCSK9, or mPCSK9 binding to hLDLR EGF-A domain (IC_{50} 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 BIACORE™ 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 μ l/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

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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 SEQ 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; +OD0.4–1.0; –OD<0.4).

TABLE 19

	Antibody	hPCSK9	mPCSK9	Chimeric Protein			
				#1	#2	#3	hPCSK9 (D374Y)
50	H1M300	++	-	++	+	-	++
	H1M309	++	-	-	-	++	++
	H1M312	++	-	-	-	++	++
	H1M492	++	-	-	-	-	+
	H1M493	++	-	-	-	++	++
	H1M494	++	-	-	+	++	++
	H1M495	++	-	-	-	++	++
	H1M496	++	-	-	-	++	++
	H1M497	++	-	-	++	+	++
	H1M498	++	-	-	-	+	++
55	H1M499	++	-	-	-	++	++
	H1M500	++	-	++	-	-	++
	H1M502	++	-	-	-	++	++
	H1M503	++	-	-	++	-	++
	H1M504	++	-	-	-	-	+
	H1M505	++	-	++	+	-	++
60	H1M508	++	-	-	-	++	++
	H1H318P	++	-	++	-	-	++
65							

TABLE 19-continued

Antibody	hPCSK9	mPCSK9	Chimeric Protein			hPCSK9 (D374Y)
			#1	#2	#3	
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; +=OD0.7-1.5; ++=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 BIACORE™ 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.

TABLE 21

Antibody	hPCSK9	mPCSK9	Chimeric Protein		
			#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-mmh, 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-mmh (2 µg/ml) 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-mmh was not affected by the presence of mAbs specific for either chimeric protein #2 or chimeric protein #3, 316P binding to hPCSK9-mmh 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-mmh 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-mmh, 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 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 H1 M508 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

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-mmh, mfPCSK9-mmh, mPCSK9-mmh, rPCSK9-mmh, 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 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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TABLE 24

	316P	300N	Control I	Control II	Control III
hPCSK9-mmh	14.1	12.6	>500	13.4	12.4
hPCSK9(D374Y)-mmh	2.1	1.1	>50	0.7	0.6
mPfPCSK9-mmh	14.7	13.4	>500	14.2	13.6
mPfPCSK9-mmh	21.2	>500	>500	19	>500
rPfPCSK9-mmh	27.7	>500	>500	21.9	>500
maPfPCSK9-h	14.4	>500	>500	29.5	12.7

Example 12. Neutralization of Biological Effect of hPfPCSK9 In Vivo

To assess the biological effect of neutralizing PCSK9, hPfPCSK9 was over-expressed in C57BL/6 mice by hydrodynamic delivery (HDD) of DNA constructs encoding full-length hPfPCSK9-mmh. 4 mice (C57BL/6) were injected with empty vector/saline (control), and 16 mice were injected with a 50 µg hPfPCSK9-mmh-DNA/saline mixture in the tail vein equal to 10% of their body weight. At day 7 after HDD, delivery of hPfPCSK9 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 hPfPCSK9 levels on day 7 were all greater than 1 µg/ml, as assessed by quantitative ELISA.

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 H1 M300N treated groups, respectively.

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

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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, 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 hPfPCSK9-mmh. Test mAb 316P or 300N was then captured on the hPfPCSK9-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	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). 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 cynomolgous 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 40 hPCSK9; a 25% increase compared to 135% with vehicle). Prior administration of the non-hPCSK9 specific mAb blocked LDL-C increases by 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 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 50 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 24 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 55 (pre-diet) values within 24 hours.

Example 15. Mouse PK Studies

A PK study was conducted in 6-week-old C57BL/6 mice 65 and 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 hlgG

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

Example 16. 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 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-hIgG surface created through direct chemical coupling to a BIACORE™ chip to form a captured antibody surface. 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 μ l/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 ($K_D = M \times 10^{-9}$; $T_{1/2} = \text{min}$; WT=wildtype).

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.

300N binding to hPCSK9 was reduced about 50-fold when the residue at position 366 was mutated, resulting in a decreased K_D of from about 0.7 $\times 10^{-9}$ M to about 36 $\times 10^{-9}$ M and a shorter $T_{1/2}$ from about 120 to 2 min. These results indicate that 300N binds an epitope on hPCSK9 comprising 10 E366 of hPCSK9 (SEQ ID NO:755). Additionally, the BIACORE™ assays show that 300N binding affinity and $T_{1/2}$ were reduced between 2– to >10-fold when a residue at 147 or 380 was mutated. Specifically, K_D was reduced from 15 about 0.69 $\times 10^{-9}$ M to between about 2–9 $\times 10^{-9}$ M when any of S147 or V380 were mutated; while $T_{1/2}$ was shortened from about 120 min to between about 24–66 min. Compared to 316P, 300N binding to hPCSK9 was not reduced by a mutation at residue 238.

20 In contrast, Control I antibody did not exhibit an altered binding affinity or $T_{1/2}$ in response to any of the positional mutations tested; Control II antibody exhibited a 40-fold decreased affinity when residue 215 was mutated (R215E) (from ~0.1 $\times 10^{-9}$ to ~4.5 $\times 10^{-9}$), and $T_{1/2}$ was about 27-fold shorter (from ~333 to 12 min); while Control III antibody exhibited a decreased affinity when residue 237 was mutated (K_D decreased from ~0.6 $\times 10^{-9}$ to ~5.9 $\times 10^{-9}$, and $T_{1/2}$ decreased from ~481 to ~43 min).

Binding specificity of 316P, 300N, and control anti-hPCSK9 mAbs to hPCSK9 variants was tested using an

TABLE 27

	316P		300N		Control I		Control II		Control III	
	K_D	$T_{1/2}$	K_D	$T_{1/2}$	K_D	$T_{1/2}$	K_D	$T_{1/2}$	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 $\times 10^{-9}$ M to 410 $\times 10^{-9}$ 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 $\times 10^{-9}$ M

60 ELISA-based immunoassay. Anti-PCSK9 mAbs were coated on a 96-well plate overnight at 4° C. Each mmh-tagged variant hPCSK9 in CHO-k1 transient transfection lysate supernatants was added to the antibody-coated plate at various concentrations ranging from 0 to 5 nM. After 1 hr binding at RT, the plate was washed and bound variant hPCSK9 was detected using HRP-conjugated anti-myc polyclonal antibody (=OD<0.7; +OD0.7–1.5; ++OD>1.5).

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TABLE 28

hPCSK9 or Variant	316P	300N	Control I	Control II	Control III
hPCSK9(WT)	++	++	++	++	++
hPCSK9(S127R)	++	++	++	++	++
hPCSK9(D129G)	++	++	++	++	++
hPCSK9(S153R)	++	++	++	++	++
hPCSK9(R215H)	++	++	++	++	++
hPCSK9(F216L)	++	++	++	++	++
hPCSK9(R237E)	++	++	++	++	++
hPCSK9(D238R)	-	++	++	++	++
hPCSK9(A341R)	++	++	++	++	++
hPCSK9(D343R)	++	++	++	++	++
hPCSK9(R357H)	++	++	++	++	++
hPCSK9(E159R)	++	++	++	++	++
hPCSK9(T162R)	++	++	++	++	++
hPCSK9(D192R)	++	++	++	++	-
hPCSK9(R194E)	++	++	++	++	-
hPCSK9(E197R)	++	++	++	++	-
hPCSK9(R215E)	++	++	++	++	++
hPCSK9(P70A)	++	++	++	++	++
hPCSK9(S147F)	++	++	++	++	++
hPCSK9(E366K)	++	+	++	++	++
hPCSK9(V380M)	++	++	++	++	++
hPCSK9(P70A, S147F)	++	++	++	++	++
hPCSK9(E366K, V380M)	++	+	++	++	++

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Example 17. Effect of 316P on Normolipemic and Hyperlipemic Hamster

The ability of anti-PCSK9 mAb 316P to reduce serum LDL-C was tested in normolipemic or hyperlipemic Gold Syrian hamsters (*Mesocricetus auratus*). Male Syrian Hamsters, age 6-8 weeks, weighing between 80-100 grams, were 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

<160> NUMBER OF SEQ ID NOS: 763

<210> SEQ ID NO 1
<211> LENGTH: 351
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1

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caggtccagc tggtgacgtc tgggggaggc ttggcacgc ctggggggc cctgagactc      60
tcctgtcgac cctctggatt tactctaagt agttacgaca tgcactgggt ccggcaatct    120
acaggaaaag gtctggagtg ggtctcagct attggttcta ccgttgacac atactatcca    180
ggctccgtga agggccgatt caccatcacc agagaaaaag ccaagaactc cgtgtatctt    240
caaatgaaca gcctgagagc cggggacacg gctgtgtatt actgtgtaag agaggggtgg    300
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<210> SEQ ID NO 2
<211> LENGTH: 117
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 2

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Gly	Gly	Ley	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	Ley	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					

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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
 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 3
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<400> SEQUENCE: 3

ggatttactc taagtagtta cgac 24

<210> SEQ ID NO 4
<211> LENGTH: 8
<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

atgggttcta ccgggtgacac a 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 ggtggggaggt accctttgac tac 33

<210> SEQ ID NO 8
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<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	tgacccagtc	tccagccacc	ctgtctgtgt	ctccaggaga	aagagccgcc	60
ctctcctgca	gggcaggta	gagtgttagc	agcaacttag	cctggtagcca	ccagaaacct	120
ggccaggctc	ccaggctct	catctatggt	gatccacca	ggccactgg	tatcccagcc	180
aggttcagtg	gcattgggtc	tgggacagag	ttcaactctca	ttatcagcag	cctgcagtc	240
gaagattttg	cattttat	ctgtcagcag	tataataact	ggcctccatt	cactttcg	300
cctgggacca	agggtggagat	caaacga				327

<210> SEQ ID NO 10
<211> LENGTH: 109
<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										

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

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<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

ggtgcatcc

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<210> SEQ ID NO 14

<211> LENGTH: 3

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<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 ataactggcc 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

gaggtgcagc tggggaggc ttggtagacgc ctggggggtc cctgagactc 60

tcctgtgcag ccttggatt tactctaagt agttacgaca tgcaactgggt ccgccaatct 120

acaggaaaaag gcttggaggc ggtctcagct attgggtcta ccggtagacac atactatcca 180

ggctccgtga agggccgatt caccatcacc agagaaaaag ccaagaactc cgtgtatctt 240

caaataaca gcctgagacg cggggacacg gctgtgtatt actgtgtaa agaggggtgg 300

gaggtaccct ttgactactg gggccaggga accctggtaa ccgtctccctc a 351

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49**50**

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<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	Ley	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					

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	ctccaggggga	aagagccgcc	60
ctctcctgca	gggcgcagtca	gagtgttagc	agcaacttag	cctggtagcca	ccagaaacct	120
ggccaggctc	ccaggctctt	catctatggt	gcatccacca	gggccactgg	tatcccagcc	180
aggttcagtg	gcattgggtc	tgggacagag	ttcaactctca	ttatcagcag	cctgcagtc	240
gaagattttg	catttttattt	ctgtcagcag	tataataact	ggcctccatt	cactttcgcc	300
cctgggacca	aagtggatat	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
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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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
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<210> SEQ ID NO 21

<211> LENGTH: 351

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 21

gagggtgcagc tgggtggagtc tggggggaggc ttgggtacagc ctgggggggtc cctgagactc	60
tcctgtgcag cctctggatt tactctaagt agttacgaca tgcactgggt ccgccaagct	120
acaggaaaaag gtctggagtg ggtctcagct attgggtcttcc cccgtgacac atactatccca	180
ggctccgtga agggcccgatt caccatctcc agagaaaaatg ccaagaactc cttgttatctt	240
caaataaca gcctgagagc cggggacacg gctgtgttatt actgtgtaa agaggggtgg	300
gagggtaccctt ttgactactg gggccaggga accctggtca 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 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
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<210> SEQ ID NO 23

<211> LENGTH: 324

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 23

gaaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccaggggaaagagccacc	60
ctctcctgca gggccagtca gagtgttagc agcaacttag cctggtagcca gcagaaacct	120
ggccaggctc ccaggctct catctatggt gcatccacca gggccactgg tatcccagcc	180

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aggttcagtg gcagtgggtc tgggacagag ttcaactctca ccatcagcag cctgcagtct	240
gaagattttgc agtttata ctgtcagcag tataataact ggccctccatt cactttcgcc	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 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 25
<211> LENGTH: 342
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 25

caggtgcagtc tggtgcagtc tgggggaggc gtgggtccagc ctggggaggc cctgagactc	60
tcctgtgcag cgtctggatt caccttcagtc agctatggca tgcactgggt ccggcaggct	120
ccaggcaagg ggctggagtg ggtggcgttt ataggatttgc atggaaatggataatacattat	180
ggagactccg tgaggggccc aatcatcata tccagagaca attccgagaa cacgttgtat	240
ctggaaatga acagcctgag agccgaggac acggcaatgt actattgtgc gagagagaag	300
ggtttagact gggggccaggc aaccacggtc accgtctccct ca	342

<210> SEQ ID NO 26
<211> LENGTH: 114
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 26

Gln Val Gln Leu Val Gln 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	

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```

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

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<400> SEQUENCE: 27

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ggattcacct tcagtagcta tggc           24
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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

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<400> SEQUENCE: 28

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

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

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<400> SEQUENCE: 29

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ataggatttg atggaagtaa tata           24
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<210> SEQ ID NO 30
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 30

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Ile Gly Phe Asp Gly Ser Asn Ile
  1          5
```

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

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<400> SEQUENCE: 31

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gcgagagaga agggttttaga c           21
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<210> SEQ ID NO 32
<211> LENGTH: 7

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<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 tgacccagtc tccttccacc ctgtctgcat ctgttaggaga cagagtacc	60
atcacttgcc gggccagtca gagtattagt agctggttgg cctggtatca gcagaaacca	120
gggaaagccc ctaagctct gatctataag gcgtcttagtt tagaaagtgg ggtccccatca	180
aggttcagcg gcagtggatc tgggacagaaa ttcaactctca ccatcagcag cctgcagcct	240
gatgattttg caacttatta ctgccAACAG tataatagtt attacacttt 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

<210> SEQ ID NO 36
<211> LENGTH: 6
<212> TYPE: PRT

-continued

<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

<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 tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tccttgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcgttt ataggatttg atggaagtaa tatacattat 180

ggagactccg tgaggggccc aatcatcata tccagagaca attccgagaa cacgttgtat 240

ctggaaatga acagccttag agccgaggac acggcaatgt actattgtgc gagagagaag 300

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```
ggtttagact ggggccaggg aaccctggtc accgtctccct 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 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 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 ctgttaggaga cagagtccacc      60
```

```
atcaacttgcg gggccagtcgca gagtattatgt agctggttgg cctggtatca gcagaaacca    120
```

```
gggaaagccc ctaagctctt gatctataag gcgtcttagtt tagaaaatgg ggtcccatca    180
```

```
aggttcagecg gcagtggatc tgggacagaa ttcaactctca ccatcagcag cctgcagcct    240
```

```
gatgattttg 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
```

-continued

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

cagggtgcagc tgggtggagtc tgggggaggc gtgggtccagc ctggggaggc cctgagactc	60
tccctgtgcag cctctggatt caccttcagt agctatggca tgcactgggt ccggccaggct	120
ccaggcaagg ggctggagtg ggtggcaggat ataggattt atggaaagtaa tatataactat	180
gcagactccg tgaagggcccg attcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcaaatga acagccttag agtggaggac acggctgtgtt attactgtgc gagagagaag	300
ggtttagact gggggccaggg aaccctggtc accgtctctt ca	342

<210> SEQ ID NO 46

<211> LENGTH: 114

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 46

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 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 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 cagagtccacc	60
atcacttgcc gggccagtca gagtatttagt agctgggtgg cctggtatca gcagaaacca	120
ggaaagcccc ctaagctctt gatctataag gcgtctagtt tagaaaatgg ggtcccatca	180

-continued

aggttcagcg gcagtggatc tgggacagaa ttcaactctca ccatcagcag cctgcagcct	240
gatgattttg caacttatta ctgccaacag tataatagtt attacacttt tggccaggg	300
accaagctgg agatcaaac	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
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 tgcaggagtc tgggggaggc gtgggtccagc ctggggaggtc cctgagactc	60
tcctgtgcag cgtctggatt caccttcaagt agctatggca tgcactgggt ccggcaggct	120
ccaggcaagg ggctggagtg ggtggcgttt ataggattt atggaaagtaa tatataattat	180
ggagactccg tgaggggccc aatcatcata tccagagaca attccgagaa cacgttgtat	240
ctggaaatga acagcctgag agccgaggac acggcagtgt attattgtgc gagagagaag	300
ggttagact ggggccaggg aaccctggtc actgtctccct 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	

-continued

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

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

-continued

<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	ctctggcgaa	gaggggcacc	60
atcaactgca	agtccagcca	gagtgtttt	cacacctcca	acaataagaa	ctacttagtt	120
tggttatcagc	agaaaccagg	acagcctcc	aagttgctcc	tttactgggc	ctctacccgg	180
gaatccgggg	tccctgaccg	attcagtggc	acggggtctg	ggacagattt	cactctcacc	240
atcagcagcc	tgcaggctga	agatgtggca	aattattact	gtcaccaata	ttacagtatt	300
ccgtggacgt	tcggccaagg	gaccaagggtg	gagatcaaac	ga		342

<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 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

-continued

<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											
									10		

<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
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

caccaatatt acagtattcc 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

caggtgcagc	tgggtggagtc	tgggggaggc	gtgggtccagc	ctggggaggc	cctgagactc	60
tcctgtgcag	cgtctggatt	cacttcagt	agctatggca	tgcactgggt	ccgccaggct	120
ccaggcaagg	ggctggagtg	ggtggcggtt	ataggattt	atggaagtaa	tatataattat	180
ggagactccg	tgagggggccg	aatcatcata	tccagagaca	attccgagaa	cacgttgtat	240

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ctggaaatga acagccttag	agccgaggac acggcagtgt	attatttgc gagagagaag	300
ggttttagact ggggccaggg	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

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

gacatcgta tgacccagtc tccagactcc ctggctgtgt	ctctggcga gagggccacc	60
--	----------------------	----

atcaactgca agtccagecca gagtgtttt cacacccca	acaataagaa ctacttagtt	120
--	-----------------------	-----

tggtatcgc agaaaaccagg acagcctcc aagttgtcc	tttactggc ctctaccgg	180
---	---------------------	-----

gaatccgggg tccctgaccg attcagtggc agcgggtctg	ggacagattt cactctacc	240
---	----------------------	-----

atcagcagcc tgcaggctga agatgtggc 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 Leu Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val

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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

<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 tgggtggagtc tgggggaggc gtgggtccagc ctggggaggc cctgagactc        60
tcctgtgcag cctctggatt caccttcagt agctatggca tgcactgggt ccgccaggct        120
ccaggcaagg ggctggagtg ggtggcagtt ataggatttg atggaagtaa tatatactat        180
gcagactccg tgaaggggcgc attcaccatc tccagagaca attccaagaa cacgctgtat        240
ctgcaaatga acagcctgag agctgaggac acggctgtgtt attactgtgc gagagagaag        300
ggttagact ggggcccaggg aaccctggtc accgtctcct ca                            342
```

<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 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 tgacccagtc tccagactcc ctggctgtgtt ctctgggcga gagggccacc        60
```

-continued

atcaactgca agtccagcca gagtgaaaa cacacccca acaataagaa ctacttagct	120
tggtaaccagg agaaaaccagg acagcctcct aagctgctca tttactgggc ctctaccgg	180
gaatccgggg tccttgaccg attcagtggc agcgggtctg ggacagattt cacttcacc	240
atcagcagcc tgcaaggctga agatgtggca gtttattact gtcaccaata ttacagtatt	300
ccgtggacgt tcggccaagg gaccaaggtg 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 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			
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 tggtgcaagtc tgggggaggc ttggtagacgc ctggggggtc cctgagactc	60
tcctgtgcag cctctggatt cacctttaac aactatgcca tgaactgggt ccggccaggct	120
ccagggaaagg gactggactg ggtctcaact attagtggta gcggtggtac tacaaactac	180
gcagactccg tgaaggggccg tttcatttatt tcccgagaca gttccaaaca cacgctgtat	240
ctgcaaataa acagcctgag agccgaggac acggccgtat attactgtgc gaaagattct	300
aactggggaa attcgatct ctggggccgtt 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 Leu Val Gln Pro Gly Gly			
1	5	10	15

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79**80**

-continued

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

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

attatggta gcgggtggta tacata 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

-continued

<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 tgaccaggc tccagactcc ctggctgtgt ctctggcgaa gagggccacc	60
atcaactgca agtccagccaa gagtgtttt tacagggtcca acaataggaa cttcttaggt	120
tggtaccaggc agaaaaccagg gcagccctccct aatctactca ttactgggc atctaccgg	180
gaatccgggg tccctgaccc attcagtggc agcgggtctg ggacagattt cactctcacc	240
atcagcagcc tgcaggctga agatgtggc gtttattact gtcaacaata ttatactact	300
ccgtacactt ttggccaggg gaccaaggta gaaatcaaac ga	342

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

-continued

<400> SEQUENCE: 83

cagagtgtt tatacaggc caacaatagg aacttc

36

<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

tgggcatct

9

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

<400> SEQUENCE: 86

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 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 tggggggaggc ttggcacagc ctggggggtc cctgagactc

60

-continued

tcctgtcag cctctggatt caccttaac aactatgcca tgaactgggt ccgccaggct	120
ccagggaaagg gactggactg ggtctcaact attagtggta gcgggtggtag tacaaactac	180
gcagactccg tgaagggccg tttcatttatt tcccgagaca gttccaaaca cacgctgtat	240
ctgcaaatac acagcctgag agccgaggac acggccgtat attactgtgc gaaagattct	300
aactggggaa 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	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	35	40	45	
Ser Thr Ile Ser Gly Ser 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	
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 ctctggcga gagggccacc	60
atcaactgca agtccagcca gagtgttta tacaggtcca acaataggaa cttcttaggt	120
tggtaccaggc agaaaccagg gcagcctccat aatctactca ttactggc atctaccgg	180
gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc	240
atcagcagcc tgcaggctga agatgtggca gtttattact gtcaacaata ttatactact	300
ccgtacactt ttggccaggg gaccaagctg gagatcaaa	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
---	---	---	----	----

-continued

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 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 tggtgaggc tgggtacagc ctgggggtc cctgagactc      60
tcctgtgcag cctctggatt caccttaac aactatgcca tgagctgggt ccgcaggct    120
ccagggaaagg ggctggagtg ggtctcagct attagtggta gcgggtggtag tacatactac    180
gcagactccg tgaaggcccg gttcaccatc tccagagaca attccaagaa cacgctgtat    240
ctgcaaatga acagccttag agccgaggac acggccgtat attactgtgc gaaagattct    300
aactggggaa atttcgatct ctggggccgt ggcaccctgg tcactgtctc ctca      354

```

<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 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 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

-continued

<211> LENGTH: 339
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 95

```

gacatcgtga tgaccaggc tccagactcc ctggctgtgt ctctggcgaa gaggccacc       60
atcaactgca agtccagcca gagtgttta tacaggcca acaataggaa cttcttagct      120
tggtaccaggc agaaaccagg acagccctcc aagctgctca ttactggc atctaccgg      180
gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctacc      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 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 97
<211> LENGTH: 351
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 97

```

caggtgcagc tgggtcagtc tggggggaggc ttggcacagc ctggggggtc cctgagactc      60
tcctgtgcag tctctggatt caccctcagt agctacgata tgcactgggt ccgcacac          120
acaggaaaag gtctggagt ggtctcagct attggttcta ctggtgacac atactatcca      180
ggctccgtga agggccgatt caccatctcc agagaaaatg ccaagaactc cttgtatctt      240
caaataaca gcctgagacg cggggacacg gctgtgtatt actgtgcaag agagggatgg      300
gacgtaccct ttgacttctg gggccaggaa accctggtca ccgtctccctc a            351

```

<210> SEQ ID NO 98
<211> LENGTH: 117
<212> TYPE: PRT

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-continued

<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           5           10          15
```

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

```
Asp Met His Trp Val Arg Gln Pro 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
```

<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
 <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

```
attggttctta ctgggtacac 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
```

-continued

<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 tgaccaggc tccatccctcc ctgtctgcatt ctgttaggaga cagagtcacc      60
atcaacttgcc gggcaagtca ggacattttaga aatgatttag gctggtatca gcagaaacca      120
ggaaaagccc ctaagctctt gatctatgct gcatccaggatt tacaaagtgg ggtccccatca      180
cggttcagcg gcagttggatc tggcacagat ttcaactctca ccatcagcag cctgcagcct      240
gaagattttg caacttatta ctgtctacaatt gattacaatt acccggtggac gttcgcccaa      300
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           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

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 Arg
 100         105
```

-continued

<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 gaaatgat

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 5

<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

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

-continued

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

<400> SEQUENCE: 113

```

gaggtgcagc tggggaggc ttggtagacgc ctgggggtc cctgagactc      60
tccctgtcgag tctctggatt caccctcagt agctacgata tgcactgggt ccgccaacct    120
acagaaaaag gtctggagtg ggtctcagct attgggtcta ctggtgacac atactatcca    180
ggctccgtga agggccgatt caccatctcc agagaaaatg ccaagaactc cttgtatctt    240
caaatgaaca gcctgagacg cggggacacg gctgtgtatt actgtgcaag agagggatgg    300
gacgtaccct ttgacttctg gggccaggaa accctggtca ccgtctcctc 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	Ley	Val	Gln	Pro	Gly	Gly
1														

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

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

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

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

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

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

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

```

gccatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtccacc      60
atcaacttgcc gggcaagtca ggacattaga aatgatttag gctggtatca gcagaaacca    120
gggaaagccc ctaagctct gatctatgct gcatccaggat tacaaatgg ggtcccatca    180
cggttcagcg gcagttggatc tggcacatg ttcactctca ccatcagcag cctgcagcct    240
gaagattttgc caacttattat ctgtctacaa gattacaatt acccgtggac gttcggccaa    300
gggaccaagg tggaaatcaa a            321

```

<210> SEQ ID NO 116

<211> LENGTH: 107

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

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-continued

<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           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

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 117
<211> LENGTH: 351
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 117

```

gagggtgcagc tgggtggagtc tggggggaggc ttggcacgc ctggggggtc cctgagactc      60
tcctgtgcag cctctggatt caccctcagt agctacgata tgcactgggt ccgc当地agct      120
acaggaaaaag gtctggagtg ggtctcagct attgggtcta ctgggtgacac atactatcca      180
ggctccgtga agggccgatt caccatctcc agagaaaaatg ccaagaactc cttgtatctt      240
caaataaca acgtcgagacg cggggacacg gctgtgtatt actgtgcaag agagggatgg      300
gacgtaccct ttgacttctg gggccagggg accctggtca ccgtctccctc a            351

```

<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

```

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-continued

Val Thr Val Ser Ser
115

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

<400> SEQUENCE: 119

gccatccaga	tgaccaggc	tccatcctcc	ctgtctgat	ctgttaggaga	cagagtccacc	60
atcaacttgc	ggcaaggta	ggacattaga	aatgatttag	gctggtatca	gcagaaacca	120
gggaaagccc	ctaagctct	gatctatgct	gcatccagtt	tacaaagtgg	ggtccccatca	180
aggttcagcg	gcagtggatc	tggcacagat	ttcactctca	ccatcagcag	cctgcagcct	240
gaagattttgc	caacttatta	ctgtctacaa	gattacaatt	accctgtggac	gttcggccaa	300
gggaccaagg	tggaaatcaa	a				321

<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															15
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Asp	Ile	Arg	Asn	Asp
															30
Leu	Gly	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
															45
Tyr	Ala	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
															60
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
															80
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Leu	Gln	Asp	Tyr	Asn	Tyr	Pro	Trp
															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

cagggtgcagc	tgcaggagtc	ggggccagga	ctggtaaagc	cttcggagac	cctgtccctc	60
acctgcactg	tctctgggta	ctccatcaat	acttactact	ggagctgtt	ccggcagccc	120
ccagggaaagg	gactggagtg	gattgggtat	atctattata	gtggaaccac	caactacaac	180
ccctccctca	agagtcgagt	caccaatatca	atagacacgc	ccaggaacca	gttctccctg	240
aagctgatct	ctgtgaccgc	agcgacacg	gcccgtgtt	actgtgcag	agagaggatt	300
actatgattc	ggggagttac	cctctactat	tactcctacg	gtatggacgt	ctggggccaa	360
gggaccacgg	tcaccgtctc	ctca				384

-continued

```
<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 24

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

atctattata atggaaaccac S

31

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

-continued

<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 gattcgggaa gttaccctct actattactc ctacggatg      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 tgaccttgc tccatccttc ctgtctgcat ctgtaggaga cagagtacc      60
atcaacttgc gggccagtca ggacatttgc agttatattag cctggtatca gcaaaaacca    120
gggatagccc ctaagcttgc gatctatgct gcatccactt tgcaaagtgg ggtcccatca    180
aggttcggcg gcagtggatc tgggacagaa ttcaacttca caatcagcag cctgcagcct    240
gaagattttgc caacttatttgc ctgtcaacag cttaatagtt accctcggac 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           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
```

-continued

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 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

caggacatttgcagttat 18

<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
1 5

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

<400> SEQUENCE: 133

gctgcatttc 9

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

-continued

<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

caggtgcagc	tgcaggagtc	ggggccagga	ctggtaagc	cttcggagac	cctgtccctc	60
acctgcactg	tctctgggaa	ctccatcaat	acttactact	ggagctggtt	ccggcagccc	120
ccagggaaagg	gactggagtg	gattgggtat	atctattata	gtggaaccac	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
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	tccatccctc	ctgtctgcat	ctgttaggaga	cagagtccacc	60
atcacttgc	gggcacgtca	ggacattagc	agttattnag	cctggtatca	gcaaaaaacca	120
gggatagccc	ctaagctct	gatctatgct	gatccactt	tgcaaagtgg	ggtccccatca	180

-continued

aggttcggcg gcagtggatc tgggacagaa ttcaactctca caatcagcag cctgcagcct	240
gaagattttg caacttatta ctgtcaacag cttaatagtt accctcgac gttcggccaa	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 gggcccagga ctgggtgaagc cttcggagac cctgtccctc	60
acctgcactg tctctgggaa ctccatcaat acttactact ggagctggat ccggcagccc	120
ccagggaaagg gactggagtg gattgggtat atctattata gtggaaccac caactacaac	180
ccctccctca agagtcgagt caccatatca gtagacacgt ccaagaacca gttctccctg	240
aagctgagct ctgtgaccgc tgccggacacg gccgtgtatt actgtgcgag agagaggatt	300
actatgattc ggggagttac cctctactat tactcctacg gtatggacgt ctggggccaa	360
gggaccacgg tcaccgtctc ctca	384

<210> SEQ ID NO 142
<211> LENGTH: 128
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 142

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 Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile			

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

Lys Leu Ser 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 143

<211> LENGTH: 321

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 143

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgttaggaga cagagtacc 60
 atcaacttgcg gggcaagtca ggacatttgc agttattnag gctggtatca gcagaaacca 120
 gggaaaggccc ctaaggcgct gatctatgcg gcatccagg ttgaaaatgg ggtccccatca 180
 aggttcagecg gcagtggtatc tgggacagaa ttcaactctca caatcagcag cctgcagcct 240
 gaagattttg caaccttata ctgtcaacag cttaatagtt accctcgagc gttcggccaa 300
 gggaccaagg tggaaatcaa a 321

<210> SEQ ID NO 144

<211> LENGTH: 107

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 144

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys 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

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```
caggtgcagc tgggtcgagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggc 60
tcctgcagg cttctggta cacctttacc aactatggta tcagctgggt gcgacaggcc 120
cctggacaag gacttgagtt aatgggatgg attagtggtt acaatggtaa cacaactat 180
gcacaagaac tccaggccag agtcaccatg accacagaca catccacgag cacagctac 240
atggagctga ggaacctgag atctgacgac acggccgtat attactgtgc gagagataga 300
gtcggttag cagctgctaa ttactacttt tattctatgg acgtctgggg ccaagggacc 360
acggtcaccc 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
```

```
<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
```

-continued

<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 gagtcgttgtt agcagctgct aattactact tttattctat ggacgta

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

gccatccaga tgacccagtc tccactctcc ctgtccgtca cccttgaca gcccgcctcc 60

atctcctgca ggtctagtca aagcctcgta tacagtgtatc gagacaccta cttgaattgg 120

tttcagcaga ggcaggcca atctccaagg cgccataattt ataaggtttc taaccgggac 180

tctggggtcc cagacagatt cagcggcagt gggtcaggca ctgctttcac actgaaaatc 240

agcggggtgg aggccgagga ttttttttt tactactgca tgcaagctac acactggcct 300

cggacgttcg gccaaggac caagggtggaa 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

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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
caaaaggctcg tatacagtga tggagacacc tac
```

```
<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
aaggtttct 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 1

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

-continued

<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 tggtgcaagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggc	60
tcctgcaagg cttctggta cacctttacc aactatggta tcagctgggt gcgacaggcc	120
cctggacaag gacttgagtt aatgggatgg attagtggtt acaatggtaa cacaactat	180
gcacaagaac tccaggccag agtcaccatg accacagaca catccacgag cacagctac	240
atggagctga ggaacctgag atctgacgac acggccgtat attactgtgc gagagataga	300
gtcggtgttag cagctgctaa ttactacttt tattctatgg acgtctgggg ccaagggacc	360
acggtcacccg tctcctca	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 15Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Leu Met
35 40 45Gly Trp Ile Ser Gly Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Glu Leu
50 55 60Gln Ala Arg Val Thr Met Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80Met Glu Leu Arg Asn Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95Ala Arg Asp Arg Val Val Ala Ala Asn Tyr Tyr Phe Tyr Ser
100 105 110Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> SEQ ID NO 163

-continued

<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 aaggcctcgta tacagtgtat gagacaccta cttgaattgg     120
tttcagcaga ggccaggcca atctccaagg cgccataattt ataaggtttc taaccgggac     180
tctggggtcc cagacagatt cagcggcagt gggtcaggca ctgcattcac actgaaaatc     240
agcgggggtgg aggccgagga tgttgggtt tactactgca tgcaagctac acactggcct    300
cggacgttgcg gccaaggac caaggtggaa atcaaa                                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	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

```

caggttcagtc tggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggc      60
tcctgcaagg cttctggta cacctttacc aactatggta tcagctgggt gcgcacaggcc    120
cctggacaag ggcttgatgt gatggatgg attagtggtt acaatggtaa cacaactat     180
gcacagaagc tccaggcagc agtcaccatg accacagaca catccacgac cacagctac    240
atggagctga ggagcctgag atctgacgac acggccgtgt attactgtgc gagagataga   300
gtcgtttag cagctgctaa ttactactt tattctatgg acgtctgggg ccaaggacc     360
acggtcaccc tctcctca                                         378

```

<210> SEQ ID NO 166
<211> LENGTH: 126
<212> TYPE: PRT

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-continued

<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	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

gatgttgtga	tgactcagtc	tccactctcc	ctgccccgtca	cccttggaca	gccggcctcc	60
atctcctgca	ggctctagtca	aaggcctcgta	tacagtgtat	gagacaccta	cttgaattgg	120
tttcagcaga	ggccaggcga	atctccaagg	cgcctaattt	ataaggtttc	taaccgggac	180
tctggggtcc	cagacagatt	cagcggcagt	gggtcaggca	ctgatttac	actgaaaatc	240
agcagggtgg	aggctgagga	tgttggggtt	tattactgca	tgcaagctac	acactggcct	300
cggacgttgc	gccaagggac	caaggtggaa	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

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										

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-continued

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

```
caggtccact tgaaggagtc tggcctacg ctggtaaac ccacacagac cctcacgctg      60
acctgcacct tctctggatt ctcactcatc actagtggag tgggtgtggg ctggattcgt     120
cagccccccg gaaaggccct ggagtggctt gcactcattt attggaatgg tgataagcgc    180
tacagcccat ctctgaagag caggctcacc atcaccaagg acacctccaa aaaccaggtg   240
gtccttacaa tgaccaacat ggaccctgtg gacacagcca catattactg tgcacacagg   300
ataactgaaa cttagttacta cttctactac ggtatggacg tctggggcca agggaccacg  360
gtcaccgtct 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

<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 tcatcaactag tggagtggtt 30

<210> SEQ ID NO 172
 <211> LENGTH: 10
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence

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

<400> SEQUENCE: 177

gacatccaga tgacccagtc tccactctcc ctgccccgtca cccctggaga gccggcctcc	60
atctcctgca ggtcttagtca gagcctcctg catagtcatg gatacgacta tttggattgg	120
tacctgcaga agccagggtca gtctccacag ctccctgatct atttgggttc taatcggggcc	180
tccgggggcc ctgacaggtt cagtggcagt ggatcaggca cagattttac actgaaaatc	240
agcagagtggtt aggctgagga tgttgggtt tattactgca tgcaagctct acaaaactccg	300

ctcactttcg gcggaggac caaggtggaa atcaaacga

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
<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:

-continued

<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

atgcaagctc tacaaactcc gctcact

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 ctggtgaaaac ccacacagac cctcacgctg	60
acctgcacct tctctggatt ctcactcatc actagtggag tgggtgtggg ctggattcgt	120
cagccccccg gaaaggccct ggagtggctt gcactcattt attggaatgg tgataagcgc	180
tacagcccat ctctgaagag caggctaccat atcaccaagg acaccccaa aaaccagggt	240
gtccttacaa tgaccaacat ggaccctgtg gacacagcca catattactg tgcacacagg	300
ataactgaaa ctatgttacta cttctactac ggtatggacg 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

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

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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 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 gccggccctcc	60
atctccttgca ggtcttagtca gagcctctcg catagtcatg gatacgcacta tttggattgg	120
tacctgcaga agccaggcca gtctccacag ctccctgatct atttgggttc taatcgggcc	180
tccggggtcc ctgacagggtt cagtggcagt ggatcaggca cagattttac actgaaaatc	240
agcagagtggtgg aggctgagga tttttgggtt tattactgca tgcaagctct acaaaactccg	300
ctcactttcg gcggaggac caagggtggag atcaaa	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

<211> LENGTH: 375

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 189

cagatcacct tgaaggagtc tggtcctacg ctgggtgaaac ccacacagac cctcaacgctg	60
acctgcacct tctctggatt ctcactcatc actagtggag tgggtgtggg ctggatccgt	120
cagccccccag gaaaggccct ggagtggctt gcactcattt attggaatgg tgataagcgc	180

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tacagccat	ctctgaagag	caggctacc	atcaccaagg	acacctccaa	aaaccagg	tg	240
gtccttacaa	tgaccaacat	ggaccctgtg	gacacagcc	cataattactg	tgcacacagg		300
ataactgaaa	ctagttacta	cttctactac	ggtatggacg	tctggggcca	agggaccacg		360
gtcaccgtct	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															15
Thr	Leu	Thr	Leu	Thr	Cys	Thr	Phe	Ser	Gly	Phe	Ser	Leu	Ile	Thr	Ser
															30
Gly	Val	Gly	Val	Gly	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Ala	Leu	Glu
															45
Trp	Leu	Ala	Leu	Ile	Tyr	Trp	Asn	Gly	Asp	Lys	Arg	Tyr	Ser	Pro	Ser
															60
Leu	Lys	Ser	Arg	Leu	Thr	Ile	Thr	Lys	Asp	Thr	Ser	Lys	Asn	Gln	Val
															80
Val	Leu	Thr	Met	Thr	Asn	Met	Asp	Pro	Val	Asp	Thr	Ala	Thr	Tyr	Tyr
															95
Cys	Ala	His	Arg	Ile	Thr	Glu	Thr	Ser	Tyr	Tyr	Phe	Tyr	Tyr	Gly	Met
															110
Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser			
															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	tgactcagtc	tccactctcc	ctgccccgtca	cccctggaga	gccggcctcc		60
atctcctgca	ggtctagtca	gagcctcctg	catagtcatg	gatacgacta	tttggattgg		120
tacctgcaga	agccagggca	gtctccacag	ctcctgatct	atttgggttc	taatcgggccc		180
tccggggtcc	ctgacaggtt	cagtggcagt	ggatcaggca	cagattttac	actgaaaaatc		240
agcagagtg	aggctgagga	tgttgggtt	tattactgca	tgcaagctct	acaaactccg		300
ctcactttcg	gcggagggac	caaggtggag	atcaaa				336

<210> SEQ ID NO 192
<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															15
Glu	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Leu	His	Ser

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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 ctgggtaaac cttcacagac cttcacgctg 60
 acctgcacct tctctgggtt ctcactcagc actagtggag tgggtgtggg ctggatccgt 120
 cagccccca gaaaggcccgt ggagtggctt gcactcattt attggaaattc tgataagcgc 180
 tacagccccat ctctgaagag caggctcacc atcaccaagg acaccccaa aaaccaggt 240
 gtccttacaa tgaccaacat ggaccctgtg gacacagcca catattactg tgcacacaga 300
 catgacagct cgtcctacta cttctactac ggtatggacg tctggggcca agggatcag 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

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

-continued

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

<400> SEQUENCE: 195

gggttctcac tcagcactag tggagtgggt

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 attctgataa 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 atgacagactc 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
 1 5 10 15

Val

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

-continued

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 201

gacatccaga	tgacccagtc	tccgctctcc	ctgcccgtca	cccctggaga	gcgggctcc	60
atctcctgca	ggtctagtca	gagcctcctc	catagtcatg	gataacaacta	tttggattgg	120
tacctgcaga	agccaggcga	gtctccacaa	ctcctgatct	atttgggttc	taatcgggcc	180
tccggggtcc	ctgacaggtt	cagtgggggt	ggatcaggca	cagatttac	actgaaaatc	240
agcagagtg	aggctgagga	tgttgggatt	tattactgca	tgcaagctct	acagactcct	300
ctcactttcg	gcggaggac	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	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	tggatacaac	tat			33
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<210> SEQ ID NO 204

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 204

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

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

<400> SEQUENCE: 205

ttgggttct

9

<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

cagatcacct tgaaggagtc tggcctact ctggtgaaaac cctcacagac cctcacgctg	60
acctgcacct tctctgggtt ctcactcagc actagtggag tgggtgtggg ctggatccgt	120
cagccccca gaaaggccct ggagtggctt gcactcattt attggaattc tgataagcgc	180
tacagcccat ctctgaagag caggctcacc atcaccaagg acaccccaa aaaccaggt	240
gtccttacaa tgaccaacat ggaccctgtg gacacagcca catattactg tgcacacaga	300
catgacagct cgtcctacta cttctactac ggtatggacg tctggggcca agggaccacg	360
gtcaccgtct cctca	375

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

<400> SEQUENCE: 210

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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	ctggccgtca	ccccctggaga	gccggcctcc	60
atctccctgca	ggtctagtca	gagcctcctc	catagtcatg	gataacaacta	tttggattgg	120
tacctgcaga	agccaggcca	gtctccacaa	ctcctgatct	atttgggttc	taatcgggccc	180
tccggggtcc	ctgacaggtt	cagtggcggt	ggatcaggca	cagattttac	actgaaaatc	240
agcagagtg	aggctgagga	tgttggatt	tattactgca	tgcaagctct	acagactcct	300
ctcaacttcg	gccccggggac	caaggtggag	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
				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

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

 <400> SEQUENCE: 213

 cagatcacct tgaaggagtc tggtcctacg ctgggtgaaac ccacacagac cctcagcg 60
 acctgcacct tctctgggtt ctcactcagc actagtggag tgggtgtggg ctggatccgt 120
 cagccccca gaaaggccct ggagtggctt gcactcattt attggaattc tgataagcgc 180
 tacagccccat ctctgaagag caggctcacc atcacaagg acaccccaa aaaccagg 240
 gtccttacaa tgaccaacat ggaccctgtg gacacagcca catattactg tgcacacaga 300
 catgacagct cgtcctacta cttctactac ggtatggacg tctggggca agggaccacg 360
 gtcaccgtct 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 ctgccccgtca cccctggaga gccggcctcc 60
 atctcctgca ggtctagtca gagcctcctc catagtcatg gataacaacta tttggattgg 120
 tacctgcaga agccaggcgtc gtctccacag ctcctgatct atttgggttc taatcgggccc 180
 tccggggtcc ctgacaggtt cagtgccagt ggatcaggca cagattttac actgaaaatc 240
 agcagagtgg aggctgagga tttttttttt tattactgca tgcaagctct acagactcct 300
 ctcactttcg gcggaggagca caaggtggag atcaaa 336

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<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								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 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

gagatgcac	tggtgaggc	tgggtccagc	ctggggggtc	cctgagactc	60	
tcctgtcag	cctctggatt	caccttttagt	agtcaactgga	tgaagtgggt	ccgcccaggct	120
ccagggagg	ggctggagg	ggtgccaaac	ataaaccaag	atggaaagtga	gaaatactat	180
gtggactctg	tgaaggcccg	attcaccatc	tccagagaca	acgccaagaa	ctcaactgttt	240
ctgcaaatga	acagcctgag	agccgaggac	acggctgtgt	attactgtgc	gagagatatt	300
gtactaatgg	tctatgatat	ggactactac	tactacggta	tggacgtctg	gggccaagg	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	Ley	Val	Gln	Pro	Gly	Gly
1									10					15

Ser Leu Arg Ley 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 Ley 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 Ley Phe
65 70 75 80

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

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<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	ctgccccgtca	ccccctggaga	gccgggcctcc	60
atctccctgca	ggtcttagtca	gagcctcctg	catacgtaatg	gaaacaacta	tttggattgg	120
tacctgcaga	agccaggggca	gtctccacag	ctcctgatct	atttgggttc	taatcgggcc	180
tccgggggtcc	ctgacaggtt	cagtggcagt	ggatcaggca	cagattttac	actgaaaatc	240
agcagagtggtt	aggctgagga	tggttgggggtt	tattactgca	tgcaaactct	acaaactccg	300
ctcactttcg	gcggaggggac	caaggtggag	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
								25							30

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

Pro	Gln	Leu	Leu	Ile	Tyr	Leu	Gly	Ser	Asn	Arg	Ala	Ser	Gly	Val	Pro
								35							50

Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile
								65							70

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

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

<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
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<210> SEQ ID NO 228

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

-continued

<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 tacaaactcc 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 tgggtggagtc tggggggaggc ttgggtccagc ctggggggtc cctgagactc 60

tcctgtgcag cctctggatt caccttttagt agtcacttgga tgaagtgggt ccggccaggct 120

ccagggaaagg ggctggagtg ggtggccaac ataaaccaag atggaagtga gaaatactat 180

gtggactctg tgaaggggccg attcaccatc tccagagaca acggccaagaa ctcactgttt 240

ctgcaaatga acagcctgag agccgaggac acggctgtgtt attactgtgc gagagatatt 300

gtactaatgg tctatgatat ggactactac tactacggta tggacgtctg gggccaagg 360

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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	Ley	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	ctgccccgtca	ccccctggaga	gccggcctcc	60
atctccctgca	ggctctagtca	gagcctctcg	catactaatg	gaaacaacta	tttggattgg	120
tacctgcaga	agccaggcga	gtctccacag	ctcctgatct	atttgggttc	taatcgggccc	180
tccgggggtcc	ctgacaggtt	cagtggcagt	ggatcaggca	cagattttac	actgaaaatc	240
agcagagtgg	aggctgagga	tgttgggtt	tattactgca	tgcaaactct	acaaactccg	300
ctcactttcg	gcggaggggac	caaggtggag	atcaaaa			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
	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 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

gagggtgcagc	tgggtggagtc	tgggggaggc	ttgggtccagc	ctggggggtc	cctgagactc	60
tcctgtgcag	cctctggatt	caccttagt	agtcaactgga	tgagctgggt	ccggcaggct	120
ccagggaaagg	ggctggagtg	ggtggccaac	ataaaccaag	atggaaagtga	gaaatactat	180
gtggactctg	tgaaggggccg	attcaccatc	tccagagaca	acgccaagaa	ctcaactgtat	240
ctgcaaatga	acagcctgag	agccgaggac	acggctgtgt	attactgtgc	gagagatatt	300
gtactaatgg	tctatgatat	ggactactac	tactacggta	tggacgtctg	ggggcaaggg	360
accacggta	ccgtctccctc	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 Tyr
100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr 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 gcccggctcc 60

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atctcctgca ggtctagtca gagcctcctg catagtaaatg gaaacaacta tttggattgg	120
tacctgcaga agccaggcca gtctccacag ctccctgatct atttgggttc taatcgggcc	180
tccggggtcc ctgacaggtt cagttggcagt ggatcaggca cagattttac actgaaaatc	240
agcagagtgg aggctgagga tgttgggtt tattactgca tgcaaactct acaaaactccg	300
ctcactttcg gcggagggac 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 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 tggtgaggc tgggggaggc gtgggtccagc ctggggagtc cctgagactc	60
tcctgtcag tctctggatt cacttcagt agctatggca tgcactgggt ccgcaggct	120
ccaggcaagg ggctggagtg ggtggcagct atatcatatg atggaagtaa taaatactat	180
gtagactccg tgaaggcccg attcaccatc tccagagaca attccaagaa aacgctgtat	240
ctgcaaatga acagcctgag agctgaggac acggctgtgt ataattgtgc gaaaaatatt	300
gtactagtga tgtatgatat agactatcac tactatggga tggacgtctg gggccaagg	360
accacggtca ccgtctccca 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

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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 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

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-continued

<400> SEQUENCE: 247

gcgaaaaata ttgtactagt gatgtatcat 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 tgactcagtc tccactctcc ctgccccgtca cccctggaga gccggcctcc 60
atctccctgca ggtcttagtca gagcctcctg catatgtatg gatacaacta tttggattgg 120
tacctgcaga agccaggcgtca gtctccacaa ctcctgatct atttgggttt taatcgccc 180
tccggggtcc ctgacaggtt cagttggcgtt ggatcaggca cagattttac actgaaaatc 240
agcagagtggtt aggctgagga tttttttttt tattactgca tgcaagctct acaaactcct 300
ctcactttcg gcggaggac caaggtggatcaga 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 15Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln 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 Leu Thr Phe Gly Gly Thr Lys Val Glu Ile Arg
100 105 110

<210> SEQ ID NO 251

<211> LENGTH: 33

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 251

cagagcctcc tgcatagtaa tggatacaac 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

ttgggtttt

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

atgcaagctc tacaaactcc tctcact

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

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caggtgcagc tgggtggagtc tgggggaggc gtggccagc ctggggagtc cctgagactc	60
tccctgtcag tctctggatt cacccatcgt agctatggca tgcactgggt ccgccaggct	120
ccaggcaagg ggctggagtg ggtggcagct atatcatatg atggaagtaa taaatactat	180
gttagactccg tgaaggcgcg attcaccatc tccagagaca attccaagaa aacgctgtat	240
ctgc当地atga acagcctgag agctgaggac acggctgtgt ataattgtgc gaaaaatatt	300
gtactagtga tgttatgatat agactatcac tactatggga tggacgtctg gggccaaggg	360
accacggtca ccgtctccctc 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
atctcctgcgtca ggtcttagtca gagcctctcg catagataatg gataacaacta tttggattgg	120
tacctgcaga agccagggca gtctccacaa ctccctgatct atttgggttt taatcgggccc	180
tccgggggtcc ctgacagggtt cagtggcagt ggatcaggca cagattttac actgaaaatc	240
agcagagtggtt aggctgagga tttttttttt tattactgca tgcaagctct acaaactcct	300
ctcactttcg gcggaggac 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

-continued

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 261
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<400> SEQUENCE: 261
caggtgcagc tgggggaggc gtgggtccagc ctggggaggc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactat 180
gcagactccg tgaaggggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agctgaggac acggctgtgtt attactgtgc gaaaaatatt 300
gtactagtga tgtatgatat agactatcac tactatggta tggacgtctg ggggcaaggg 360
accacggta ccgtctccctc 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

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<210> SEQ ID NO 263
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 263

gatattgtga tgactcagtc tccactctcc ctgccccgtca cccctggaga gccggcctcc 60
atctccgtca ggtcttagtca gagecctcctg catagtaatg gataacaacta tttggattgg 120
tacctgcaga agccaggcgtca gtctccacag ctccctgatct atttgggttt taatcgcc 180
tccgggggtcc ctgacaggtt cagtggcagt ggatcaggca cagattttac actgaaaatc 240
agcagagtggtt aggctgaggta tgttgggttt tattactgca tgcaagctct acaaaactcct 300
ctcaactttcg gcggaggggac caaggtggag atcaaa 336
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<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 Gly Thr Lys Val Glu Ile Lys
100 105 110

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<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 tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tccttgtgcag tctctggatt caccttcagt agctatggca tgcactgggt ccgcaggct 120
ccaggcaagg ggctggagtg ggtggcagct atatcatatg atggaagtaaaatactat 180
gttagactccg tgaaggcccg attcaccatc tccagagaca attccaagaa aacgctgtat 240
ctgcaaataatgaa acagcctgag agctgaggac acggctgtgt ataattgtgc gaaaaatatt 300
gtacttagtga tgtatgatat agactatcac tactatggta tggacgtctg gggccaagg 360
accacgggtca ccgtctccctc a 381
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<210> SEQ ID NO 266
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 266

Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	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 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

-continued

Ile Ser Tyr Asp Gly Ser Asn Lys
1 5

<210> SEQ ID NO 271
<211> LENGTH: 60
<212> TYPE: DNA
<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 ctgccccgtca cccctggaga gccggcctcc 60
atctcctgca ggtcttagtca gagcctcttg catagtaatg gataacaacta tttggattgg 120
tacctgcaga agccaggcca gtctccacaa ctcctgatct atttggggtt taatcgggcc 180
tccgggggtcc ctgacaggtt cagtggcagt ggatcaggca cagattttac actgaaaatc 240
agcagagtggtt aggctgagga tgttgggtt tattactgca tgcaaggtct acaaaactcct 300
ctcactttcg gcggaggac caagggtggag 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

-continued

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

<400> SEQUENCE: 275

cagagcctcc tgcatagtaa tggataacaac 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

tggggttt 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 tacaaactcc 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

-continued

1 5

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

<400> SEQUENCE: 281

caggtgcagc tgggggaggc gtggccagc ctggggagtc cctgagactc      60
tcctgtcag tctctggatt cacccatcg agctatggca tgcactgggt ccgccaggct    120
ccaggcaagg ggctggagtg ggtggcagct atatcatatg atggaagtaa taaatactat    180
gttagactccg tgaaggccg attcaccatc tccagagaca attccaagaa aacgctgtat    240
ctgcaaatga acagcctgag agctgaggac acggctgtgt ataattgtgc gaaaaatatt    300
gtactagtga tgtatgatat agactatcac tactatggta tggacgtctg gggccaaggg    360
accacggtca ccgtctccca a                                         381

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<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 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 Ser Ser
115         120          125

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<210> SEQ ID NO 283
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 283

gatattgtga tgactcagtc tccactctcc ctgccccgtca cccctggaga gccggccctcc    60
atctcctgca ggtcttagtca gagcctcctg catagtaatg gataacaacta tttggattgg    120
tacctgcaga ageccaggccaa gtctccacaa ctccctgatct atttgggttt taatcggggcc    180
tccgggggtcc ctgacaggtt cagtgccagtg ggatcaggca cagattttac actgaaaatc    240
agcagagtggtt aggctgagga tttttttttt tattactgca tgcaagctct acaaactcct    300

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ctcactttcg gcgaggagca	caagggtggag atcaaa	336
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<210> SEQ ID NO 284
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<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
	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 285
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 285

caggtgcagc	tgggtggagtc	tgggggaggc	gtgggtccagc	ctggggaggc	cctgagactc	60
tcctgtgcag	cctctggatt	cacccatagt	agctatggca	tgcactgggt	ccggccaggct	120
ccaggcaagg	ggctggagtg	ggtggcagtt	atatcatatg	atggaaagtaa	taaataactat	180
gcagactccg	tgaaggccg	attcaccatc	tccagagaca	attccaagaa	cacgctgtat	240
ctgcaaatga	acagcctgag	agctgaggac	acggctgtgt	attactgtgc	aaaaaatatt	300
gtactagtga	tgtatgatat	agactatcac	tactatggta	tggacgtctg	ggggcaaggg	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
	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						

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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 287

<211> LENGTH: 336

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 287

gatatttgtga tgactcagtc tccactctcc ctggccgtca cccctggaga gcccggctcc 60

atctcctgcga ggtcttagtca gagcctcctg catacataatg gataacaacta tttggattgg 120

tacacctgcaga agccagggtca gtotccacag ctcctgatct atttgggttt taatcggggcc 180

tccgggggtcc ctgacaggtt cagtggcagt ggatcaggca cagattttac actgaaaatc 240

agcagagtggtt aggctgagga tttttttttt tattactgcgtca tgcaagctct acaaactcct 300

ctcactttcg gcggaggggac caaggtggag atcaaa 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 cctcacgtc 60

acctgcacct tctctgggtt ctcactcagc gctagtggag tgggtgtggg ctggttccgt 120

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cagccccccag gaaaggccct ggagtggcgt gcactcattt attggaatga tgataagcgt	180
tacagcccat ctctaaagaa cagcctaccat atcaccaagg acaccccaa aaaccagggtg	240
gtccttacaa tgaccaacat ggaccctgtg gacacagcca catattactg tgcacacaga	300
atacatctat ggtcctactt ctactacggt atggacgtct ggggccaagg gaccacggtc	360
accgtctcct ca	372

<210> SEQ ID NO 290
<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

-continued

atttatttggaa 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
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 ctgccegtca cccctggaga gccggcctcc 60
atctcctgca ggtcttagtca gactctcctg catagtaatg gataacaacta ttccgattgg 120
tacctgcaga agccaggcga gtctccacag ctccctgatct atttgggttc taatggggcc 180
tccggggtcc ctgacagatt cagtggcagt ggatcaggca cagattttac actgaaaatc 240
agcagagtg 297 aggctgagga ttttggaaatt tattactgca tgcaagctct acaaaactcct 300
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 30

-continued

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	Arg	
100						105			110						

<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 tggataacaac 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 tacaaaactcc tctcact

27

<210> SEQ ID NO 304

-continued

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

<400> SEQUENCE: 305

cagatcacct tgaaggagtc tggcctacg ctggtaaaac ccacacagac cctcacgctg	60
acctgcaccc tctctgggtt ctcactcaggc gctagtggag tgggtgtggg ctggttccgt	120
cagccccccag gaaaggccct ggagtggott gcactcattt attggaatga tgataagcgt	180
tacagccccat ctctaaagaa cagcctcacc atcacaagg acaccccaa aaaccagggtg	240
gtccttacaa tgaccaacat ggaccctgtg gacacagcca catattactg tgcacacaga	300
atacatctat ggtctactt ctactacggt atggacgctt ggggccaagg gaccacggtc	360
accgtctcct ca	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

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gatattgtga tgactcagtc tccactctcc ctgccccgtca cccctggaga gccggcctcc	60
atctcctgca ggtcttagtca gactctcctcg catagtaaatg gataacaacta tttcgattgg	120
tacctgcaga agccaggggca gtctccacag ctcctgatct atttgggttc taatcgggcc	180
tccgggggtcc ctgacagatt cagtggcagt ggatcaggca cagattttac actgaaaatc	240
agcgagatgg aggctgagga tggttggaaatt tattactgca tgcaagctct acaaactcct	300
ctcactttcg gcggaggggac caaggtggag atcaaa	336

<210> SEQ ID NO 308

<211> LENGTH: 112

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<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 tggtcctacg ctggtaaac ccacacagac cctcacgtc	60
acctgcacct tctctgggtt ctcactcagc gctagtggag tgggtgtggg ctggatccgt	120
cagccccccag gaaaggccct ggagtggtt gcactcattt attggaatga tgataagcgc	180
tacagcccat ctctgaagag caggctcacc atcaccaagg acaccccaa aaaccaggta	240
gtccttacaa tgaccaacat ggaccctgtg gacacagcca catattactg tgcacacaga	300
atacatctat ggtctactt ctactacggt atggacgtct gggggcaagg gaccacggtc	360
accgtctccat 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

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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

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 ctgccccgtca cccctggaga gccggcctcc 60
 atctccctgca ggtcttagtca gactctcctcg catagtaatg gataacaacta tttggattgg 120
 tacctgcaga agccaggcca gtctccacag ctcctgatct atttgggttc taatcgggcc 180
 tccggggtcc ctgacaggtt cagtggcagt ggatcaggca cagattttac actgaaaatc 240
 agcagagtgg aggctgagga tttttttttt tattactgca tgcaagctct acaaactcct 300
 ctcactttcg gcggaggac 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 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

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

<400> SEQUENCE: 313

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caggttcagc tggtgcaagtc tggacctgag gtgaagaacc ctggggctc agtgaaggc       60
tcctgcagg cttctggta caccttacc acctatggta tcagttgggt acgcacaggcc      120
cctggacaag ggcttgatgg gatgggatgg atcagcggtt acaatggta aacaaacgat      180
gcacagaagt tccaggacag agtcgccatg accacagaca catccacgag cacagctac      240
atggagctga ggagcctgag atctgacgac acggccattt attactgttc gagagatcgt     300
ttagtagtac cacctgcctt taattattcc tactacgtta tggacgtctg gggccaaggg     360
accacggta cccgtctccctc 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

ggttacacct 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			

-continued

<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

<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 cttattttt 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 ctgcgggtca cccttgac gcccgtcc 60

atctcctgca ggtctagtca aagcctcgta tacagtatg gaaacaccta cttgaattgg 120

tctcagcaga ggccagggtca atctccaagg cgccataattt ataagggttc taaccggac 180

tctggggtcc cagacagatt cagcggcgtt gggtcaggca ctgatttcac actgaaaatc 240

agcagggtgg aggctgagga tgggggtt tattactgca tgcaaggtaa acactggccg 300

tacacttttgc cccaggggac caagctggag atcaaa 336

<210> SEQ ID NO 322
<211> LENGTH: 112
<212> TYPE: PRT

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<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	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 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

-continued

<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 327

atgcaggta 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

<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 tggtgcatgc tggacctgag gtgaagaacc ctggggcctc agtgaaggc	60
tccctgcaagg cttctggta cacctttacc acctatggta tcagttgggt acgcacaggcc	120
cctggacaag ggcttgatgc gatggatgg atcagcggtt acaatggtaa aacaaacgat	180
gcacagaagt tccaggacag agtcgcccatt accacagaca catccacgag cacagctac	240
atggagctga ggagccttag atctgacgac acggccattt attactgttc gagagatcgt	300
ttagtagtac cacctgcct taattattcc tactacgtta tggacgtctg gggccaagg	360
accacggta ccgtctccca 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 15Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr
20 25 30Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45Gly Trp Ile Ser Gly Tyr Asn Gly Lys Thr Asn Asp Ala Gln Lys Phe
50 55 60Gln Asp Arg Val Ala Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Ile Tyr Tyr Cys
85 90 95Ser 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

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115

120

125

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<210> SEQ ID NO 331
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 331

gatgttgtga tgactcagtc tccactctcc ctgccccgtca cccttggaca gccggcctcc      60
atctcctgca ggtctagtca aaggcctcgta tacagtgtat gaaacacacta cttgaatttgg      120
tctcagcaga ggccagggtca atctccaagg cgccctaattt ataagggttca taaccgggac      180
tctggggtcc cagacagatt cagcggcagt gggtcaggca ctgatttcc actgaaaatc      240
agcagggtgg aggctgagga tttttttttt tattactgca tgcaaggta acactggccg      300
tacacttttg gccaggggac caagctggag atcaaa                                336

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<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 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

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<210> SEQ ID NO 333
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 333

caggttcagtc tgggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc      60
tcctgcaagg cttctggta caccttacc acctatggta tcagctgggt gcgcacaggcc      120
cctggacaag ggcttgcgtg gatggatgg atcagcggtt acaatggtaa aacaaactat      180
gcacagaagc tccaggccag agtcaccatg accacagaca catccacgag cacagctac      240
atggagctga ggagcctgag atctgacgac acggccgtgt attactgttc gagagatcgt      300
tttagtagtac cacctgcctc taattattcc tactacgtta tggacgtctg gggcaaggg      360
accacggta ccgtctcctc a                                         381

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<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																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	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	ctgccccgtca	cccttggaca	gccggcctcc		60
atctcctgca	ggtctagtca	aaggcctcgta	tacagtgtatg	gaaacaccta	cttgaattgg		120
tttcagcaga	ggccaggcca	atctccaagg	cgcctaattt	ataaggtttc	taaccgggac		180
tctggggtcc	cagacagatt	cagcggcagt	gggtcaggca	ctgatttac	actgaaaatc		240
agcaggggtgg	aggctgagga	tgttggggtt	tattactgca	tgcaaggtag	acactggccg		300
tacacttttg	gccaggggac	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																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
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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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

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gaggtgcagc tggggaggc ctggtcaagc ctgggggtc cctgagactc      60
tcctgtgcag cctctggatt cacctcagt agctatagca tggactgggt ccgcaggct    120
ccagggaaagg ggctggagtg ggtctcatcc attagtagta gtatgttata cataactac    180
gcagactctg tgaaggcccg attcaccatc tccagagaca ccgccaagaa ctcactgtat    240
ctgcaaatga acagcctgag agacgaggac acggctgttt attactgtgc gagagaggc    300
agttagcagac ttttacta ctggggccag ggaaccctgg tcaccgtctc ctca      354

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<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
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<210> SEQ ID NO 340
<211> LENGTH: 8

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<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
<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 ctgttaggaga cagagtccacc	60
atcaacttgcgc gggccagtca gagtatttagt agctggttgg cctggtatca gcagagacca	120
ggaaagcccc ctaagctct gatctataag gctgtctagtt tagaaggtagg agtcccacca	180
aggttcagcg gcagtggtac tgggacagaa ttcactctca ccatcagcag cctgcagcct	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			

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 347
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 347

cagagtattt gtagctgg

18

<210> SEQ ID NO 348
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 348

Gln	Ser	Ile	Ser	Ser	Trp
1		5			

<210> SEQ ID NO 349
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 349

aaggcggtct

9

<210> SEQ ID NO 350
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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-continued

<400> SEQUENCE: 350

Lys Ala Ser

1

<210> SEQ ID NO 351
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 351

caacagttata atagttattt gttttttttt

27

<210> SEQ ID NO 352
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 352

Gln Gln Tyr Asn Ser Tyr Trp Tyr Thr
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

gagggtgcagc	tgggtggagtc	tggggggggc	ctgggtcaagc	ctgggggggtc	cctgagactc	60
tcctgtgcag	cctctggatt	caccttcagt	agctatacgca	tggactgggt	ccgcccaggct	120
ccagggaaagg	ggctggagtg	ggtctcatcc	attagtagta	gtatgtat	cataatactac	180
gcagactctg	tgaaggggccg	attcaccatc	tccagagaca	ccgccaagaa	ctcactgtat	240
ctgcaaatga	acagcctgag	agacgaggac	acggctgttt	attactgtgc	gagagagggc	300
agttagcagac	tttttgacta	ctggggccag	ggaaccctgg	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 Leu Val Lys Pro Gly Gly
1 5 10 15Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30Ser Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45Ser Ser Ile Ser Ser Ser Ser Tyr Ile Tyr Tyr Ala Asp Ser Val
50 55 60Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ala Lys Asn Ser Leu Tyr
65 70 75 80Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95**220**

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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 ctgtaggaga cagagtccacc	60
atcaactgcc gggccagtcgaa gagtatttagt agctggttgg cctggtatca gcagagacca	120
gggaaagccc ctaagctcct gatctataag gctgtcttagtt tagaaggtagg agtcccattca	180
aggttcagcg gcagtggatc tgggacagaaa ttcaactctca ccatcagcag cctgcagcct	240
gaggattttg caacttatta ctgccaacag tataatagtt attggtagacac ttttggccag	300
gggaccaagc tggagatcaa a	321

<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

gaggtgcagc tgggtggagtc tggggggaggc ctggtcaagc ctggggggtc cctgagactc	60
tcctgtgcag cctctggatt caccttcagt agctatagca tgaactgggt ccggccaggct	120
ccagggagg ggctggagtg ggtctcatcc attagtagta gtatgtatca cataatactac	180
gcagactcag tgaaggggccg attcaccatc tccagagaca acgccaagaa ctcactgtat	240
ctgcaaatga acagcctgag agccgaggac acggctgtgtt attactgtgc gagagaggc	300

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agtagcagac ttttgacta ctggggccaa ggaaccctgg tcaccgtctc 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 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

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 cagagtacc 60

atcacattgcc gggccagtcg agtattatgt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctct gatctataag gcgtctagtt tagaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tggacagaa ttcaactctca ccatcagcag cctgcagcct 240

gatgattttg caaccttatta ctgccaacag tataatagtt attggatcac 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

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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	tgggtggagtc	tgggggaggc	ttgggtcaagc	ctggagggtc	cctgagactc	60
tcctgtgcag	cctctggatt	cacccatcgt	gaccactaca	tgagctggat	ccgcccaggct	120
ccagggaaagg	ggctggagtg	gatttcatac	attagtaatg	atgggtgtac	caaatactat	180
gtggactctg	tggagggcgc	attcatcatt	tccagggaca	acgccaagaa	ctcattgtat	240
ctacatatga	acagcctcag	agccgacgac	acggccgtgt	attactgtgc	gagagatcag	300
ggatataattg	gctacgactc	gtattattac	tattcctacg	gtatggacgt	ctggggccaa	360
gggaccacgg	tcaccgtcg	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	Ley	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	Ley	Glu	Trp	Ile
	35				40						45				
Ser	Tyr	Ile	Ser	Asn	Asp	Gly	Gly	Thr	Lys	Tyr	Tyr	Val	Asp	Ser	Val
	50			55					75		80				
Glu	Gly	Arg	Phe	Ile	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Ley	Tyr
	65				70				75		80				
Ley	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

-continued

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
<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 agggatata 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

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```

aaaattgtgt tgacgcagtc tccaggcacc ctgcctttgt ttccagggga aagagccacc      60
ctctcctgtt gggccaggtca gagtgtaaac aacaaattct tagcctgtt ccagcagaaaa      120
tctggccagg ctcccaggtt cctcatctat ggtgcattca gcagggccac tggcatcccc      180
gacaggttca gtggcagtgg gtctgggacc gacttcactc tcaccatcg cggaactggag      240
cctgaagatt ttgaagtgtt ttattgtcaa gtatatggta actcactcac tctcggcgga      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									10						15

Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Asn	Asn	Lys
									25						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									55						60

Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Gly	Leu	Glu
65									70						80

Pro	Glu	Asp	Phe	Glu	Val	Tyr	Tyr	Cys	Gln	Val	Tyr	Gly	Asn	Ser	Leu
								85						95	

Thr	Leu	Gly	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

cagagtgtt aacaacaaatt 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

-continued

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

<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 tgggtggagtc tggggggaggc ttgggtcaagc ctggagggtc cctgagactc	60
tcctgtgcag cctctggatt caccttcaact gaccactaca tgagctggat ccgccaggct	120
ccagggaaagg ggctggagtg gatttcataac attagtaatg atgggtgtac caaatactat	180
gtggactctg tggaggggccg attcatcatt tccaggggaca acggcaagaa ctcattgtat	240
ctacatatga acagcctcag agccgacgac acggccgtgt attactgtgc gagagatcag	300
ggatatattt gctacgactc gtattttac tatttcatacg 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 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	

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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

```
gaaaattgtgt tgacgcagtc tccaggcacc ctgcctttgt ttccagggga aagagccacc     60
ctctccctgta gggccagtc gagtgttaac aacaaattct tagcctggta ccagcagaaaa     120
tctggccagg ctcaggcgtc cctcatctat ggtgcattca gcagggccac tggcatccca     180
gacagggttca gtggcagtgg gtctgggacc gacttcactc tcaccatcg cggactggag     240
cctgaagatt ttgaagtgtta ttattgtcaa gatatggta actcactcac tctcggcggaa     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 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

-continued

<400> SEQUENCE: 381

```
caggtgcagc tggtgaggc tgggtcaagc ctggagggtc cctgagactc      60
tcctgtcag cctctggatt cacccatcg gaccactaca tgagctggat ccgccaggct    120
ccagggaaagg ggctggagtg ggtttcatac attagtaatg atgggtggtaa caaatactac    180
gcagactctg tgaaggggcg attcaccatc tccagggaca acgccaagaa ctcactgtat    240
ctgcaaatga acagccttag agccgaggac acggccgtgt attactgtgc gagagatcag    300
ggatatattt gctacgactc gtattattac tattcctacg gtatggacgt ctggggcaa    360
gggaccacgg 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	Lys	Val	Pro	Gly	Gly				
1													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 383

<211> LENGTH: 321

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 383

```
gaaatttgtt tgacgcagtc tccaggcacc ctgtcttgtt ctccagggaa aagagccacc      60
ctctcctgca gggccagtca gagtgttaac aacaaattct tagcctggta ccagcagaaa    120
cctggccagg cttcccaggct cctcatctat ggtgcattca gcagggccac tggcatcccc    180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag    240
cctgaagatt ttgcagtgtt ttactgtcaa gtatatggta actcactcac ttccggcggaa    300
gggaccacagg tggagatcaa a                                         321
```

<210> SEQ ID NO 384

<211> LENGTH: 107

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 384

Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly
1									10						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	Pro	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	Arg	Leu	Glu
65															80

Pro	Glu	Asp	Phe	Ala	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 385

<211> LENGTH: 360

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 385

gaggtgcaga	agggtggagtc	tggggggaggc	ctggtaaagc	cggggggggc	cctgagactc		60
tccctgtacag	cctctggatt	cacccatcg	acttataaca	tgaattgggt	ccgccaggct		120
ccagggaaagg	gactggagtg	ggtctcatcc	attaggagta	gttagtaatta	cataactac		180
gcagactcag	tgaagggccg	attcaccatc	tccagagaca	acgccaagaa	ttcaactgtat		240
ctgcaaatga	acagcctgag	agccgatgac	acggctgtgt	attactgtgc	gagagatggc		300
agcagtttgt	acgactactc	tgactactgg	ggccagggaa	ccctggcac	cgtctccctca		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	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
100															110

Gly Thr Leu Val Thr Val Ser Ser

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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

attagagta gtagtaatta cata

24

<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

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<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 393

```
gacatccaga tgaccaggc tccttccacc ctgtctgcat ctgttaggaga cagagtacc       60
atcaacttgc gggccaggta gagtatttagt agctggttgg cctggtatca acagatacca     120
ggaaagccc ctaaactctt gatctataag gcgtcttagtt tagaaaatgg ggtcccatca     180
aggttcagcg gcagtggtatc tgggacagaa ttcaactctca tcatcagcag cctgcagcct    240
gatgattttg caacttatta 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			

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

cagagtatta gtagctgg 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

-continued

<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

caacagtata ttagttatttc tcggacg

27

<210> SEQ ID NO 400
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<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 tgggtggagtc tggggggaggc ctggtaagc cgggggggtc cctgagactc 60
tcctgtacag cctctggatt caccttcagt acttataaca tgaattgggt ccgccaggct 120
ccagggaaagg gactggagtg ggtctcatcc attaggagta gttagtaatta catataactac 180
gcagactcag tgaaggcccg attcaccatc tccagagaca acgccaagaa ttcaactgtat 240
ctgcaaatga acagcctgag agccgatgac acggctgtgtt attactgtgc gagagatggc 300
agcagtttgtt acgactactc tgactactgg ggccaggaa ccctggtcac cgtctctca 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

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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
atcaacttgcc	gggccagtca	gagtattagt	agctggttgg	cctggtatca	acagatacca	120
ggaaagcccc	ctaaaactcct	gatctataag	gcgtctagtt	tagaaaatgg	ggtcccatca	180
aggttcagcg	gcagtggatc	tgggacagaa	ttcactctca	tcatcagcag	cctgcagcct	240
gatgattttg	caacttatta	ctgccaacag	tatattagtt	attctcgac	gttcggccaa	300
gggaccaagg	tggaaatcaa	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

-continued

<211> LENGTH: 360
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 405

```

gaggtgcagc tggtggagtc tgggggaggc ctggtaaagc ctgggggtc cctgagactc      60
tcctgtcagc cctctggatt caccttcagt acttataaca tgaactgggt ccgccaggct     120
ccagggaaagg ggctggagtg ggtctcatcc attaggagta gtagtaatta cataatactac    180
gcagactcag tgaaggcccg attcaccatc tccagagaca acgccaagaa ctcactgtat    240
ctgcaaatga acagcctgag agccgaggac acggctgtgtt attactgtgc gagagatggc   300
agcagtttgtt acgactactc tgactactgg ggccaaggaa ccctggtcac cgtctcccta   360

```

<210> SEQ ID NO 406
<211> LENGTH: 120
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 406

```

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 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

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 cagagtccacc    60
atcaacttgcg gggccagtcgca gagtattagt agctgggtgg cctggtatca gcagaaaacca 120
ggaaagcccc ctaagctcct gatctataag gcgtctagtt tagaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcaactctca ccatcagcag cctgcagcct 240
gatgattttg caacttatta ctgccaacag tatatttagtt attctcgac gttcggccaa 300
gggaccaagg tggaaatcaa a                                         321

```

<210> SEQ ID NO 408
<211> LENGTH: 107

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<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															
														15	

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

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

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	tgggtcaagc	cgggggggtc	cctgagactc	60
tccctgtacag	cctctggatt	cacccatcgat	acttataaca	tgaattgggt	120
ccagggaaagg	gactggagtg	ggtctcatcc	attaggagta	gtagtaatta	180
gcagactcgag	tgaaggccgc	attcaccatc	tccagagaca	acgccaagaa	240
ctgcaaatga	acagcctgag	agccgatgac	acggctgtgt	attactgtgc	300
agcagtttgt	acgactactc	tgactactgg	ggccagggaa	ccctggtcac	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	Ley	Val	Lys	Pro	Gly	Gly
1														
														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	Ley	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	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
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

250

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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 gttagtaatta cata

24

<210> SEQ ID NO 414
<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

-continued

<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 cagagtacc 60
atcacttgcc gggccagtc gagtattagt agctggttgg cctggtatca acagatacca 120
ggaaagccc ctaaaactctt gatctataag gcgtctagtt tagaaaatgg ggtccccatca 180
aggttcagcg gcagtggtatc tgggacagaa ttcaactctca tcatcagcag cctgcagcct 240
gatgatttttgc caacttatta ctgccaacag tatatttagtt 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

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

```

cagagtatta gtagctgg 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

```

-continued

<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 ttagttattc 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

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 tggtgagtc tgggggaggc ctggtaaagc cgggggggtc cctgagactc	60
tccctgtacag cctctggatt cacttcagt acttataaca tgaattgggt ccgccaggct	120
ccagggaaagg gactggagtg ggtctcatcc attaggagta gttagtaatta cataatactac	180
gcagacttag tgaagggccg attcaccatc tccagagaca acgccaagaa ttcaactgtat	240
ctgcaaatga acagcctgag agccgatgac acggctgtgt attactgtgc gagagatggc	300
agcagtttgtt acgactactc tgactactgg ggccaggaa ccctggtcac cgtctcctca	360

<210> SEQ ID NO 426
<211> LENGTH: 120
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<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 tggtgaggc tgggtcaagc ctgggggtc cctgagactc      60
tcctgtcag cctctggatt caccttca gttataaca tgaactgggt ccgcaggct    120
ccagggaaagg ggctggaggc ggtctcatcc attaggagta gtatataattt cataactac    180
gcagacttag tgaaggggcg attcaccatc tccagagaca acgccaagaa ctcactgtat    240
ctgcaaatga acagccttag agccgaggac acggctgtgtt attactgtgc gagagatggc    300
agcagtttgtt acgactactc tgactactgg ggccaaaggaa ccctggtcac cgtctctca    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	Gly	Leu	Val	Lys	Pro	Gly	Gly
1															
Ser	Leu	Arg	Leu	Ser	Cys	Ala	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	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
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	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															
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 ctgtctgcat ctgtaggaga cagagtacc      60
atcaacttgcgccc gggccagtcgca gaggattttttt agctgggtgg cctggatca gcagaaacca    120
gggaaagccc ctaagctctt gatctataag gcgtcttagtt tagaaatgg ggtcccatca    180
aggttcagcg gcagttggatc tgggacagaa ttcaactctca ccatcagcag cctgcagcct    240
gatgatttttgc caacttattttt ctgccaaacag tatattttttt attctcgac gttcgccaa    300
gggaccaagg tggaaatcaa a                                         321

```

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<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	tggtgaggc	tgggggaggc	ctggtaagc	cgggggggtc	cctgagactc	60
tccctgtacag	cctctggatt	caccttcagt	acttataaca	tgaattgggt	ccgcccaggct	120
ccaggaaagg	gactggagtg	ggtctcatcc	attaggagta	gttagtaatta	cataactac	180
gcagactcag	tgaagggecg	attcaccatc	tccagagaca	acgccaaagag	ttcaactgtat	240
ctgcaaatga	acagcctgag	agccgaggac	acggctgtgt	attactgtgc	gagagatggc	300
agcagtttgt	acgactactc	tgactactgg	ggccaggaa	ccctggtcac	cgtctctca	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	Ley	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
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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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

attagaggta gtagtaatta cata

24

<210> SEQ ID NO 438
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 438

Ile Arg 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

-continued

```

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 cagagtacc 60
atcacttgcc gggccagtca gagtattagt agctggttgg cctggtatca acaggttacca 120
ggaaagccc ctaaaactcct gatctataag gcgtctagtt tagaaaatgg ggtcccatca 180
aggttcagcg gcagtggatc tggcacagaa ttcaactctca tcatcagcag cctgcagcct 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

```

```

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

```

cagagtatta 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

267

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-continued

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

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

```
<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 ttagttattc 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

<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 tggggggaggc ctggtaagc cggggggggtc cctgagactc 60

tcctgtacaq cctctqqatt caccttcaqt acttataaca tqaattqqqt ccqcccaqqct 120

ccaggaaacq gactggatq ggtctcatcc attaggatq gtatgttaattt catataactac 180

atggccatgtc acggggatggg aaaaaaaaggaa accggatgtatc attatgtatggc gggggatggc 300

aggacttatac aggacttatac tgaatctatca aaaaaaaaacaa acatgtatccaa ctttgtatca 362

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<210> SEQ ID NO 45

<211> LENGTH: 1

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	tgggtcaagc	ctggggggtc	cctgagactc	60
tcctgtgcag	cctctggatt	cacccatcgat	acttataaca	tgaactgggt	120
ccagggaaagg	ggctggagtg	ggtctcatcc	attaggagta	gttagtaatta	180
gcagactcag	tgaagggccg	attcaccatc	tccagagaca	acgccaagaa	240
ctgcaaatga	acagcctgag	agccgaggac	acggctgtgt	attactgtgc	300
agcagtttgt	acgactactc	tgactactgg	ggccagggaa	ccctggtcac	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 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

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	ctgttaggaga	cagagtccacc	60
atcaacttgc	ggcccagtca	gagtattagt	agctggttgg	cctggtatca	gcagaaacca	120
ggaaaagccc	ctaagctct	gatctataag	gcgtctagtt	tagaaagtgg	ggtcccacca	180
aggttcagcg	gcagtggatc	tgggacagaa	ttcactctca	ccatcagcag	cctgcagcct	240
gatgattttg	caacttatta	ctgccaacag	tatattagtt	attctcgac	gttcggccaa	300

-continued

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															
															15

Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Ser	Ser	Trp
															30
Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
															45
Tyr	Lys	Ala	Ser	Ser	Leu	Glu	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
															60
Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
															80
Asp	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Tyr	Ile	Ser	Tyr	Ser	Arg
															95
Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys					
															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

gagggtcagc	tggtggagtc	tgggggaggc	ctggtcaagc	cgggggggtc	cctgagactc		60	
tcctgtacag	cctctggatt	caccttcagt	acttataaca	tgaattgggt	ccgccaggct			120
ccagggaaagg	gactggagtg	ggtctcatcc	attaggatga	gtagtaatta	cataactac			180
gcagactcag	tgaaggccg	attcaccatc	tccagagaca	acgccaagaa	ttcactgtat			240
ctgcaaatga	acagcctgag	agccgatgac	acggctgtgt	attactgtgc	gagagatggc			300
agcagtttgt	acgactactc	tgactactgg	ggccaggaa	ccctggcac	cgtctcccta			360

<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	Ley	Val	Lys	Pro	Gly	Gly	
1															
															15
Ser	Leu	Arg	Leu	Ser	Cys	Thr	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Thr	Tyr
															30
Asn	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Leu	Glu	Trp	Val	
															45
Ser	Ser	Ile	Arg	Ser	Ser	Asn	Tyr	Ile	Tyr	Tyr	Ala	Asp	Ser	Val	
															60
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr

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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 459
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 459

ggattcacct tcagtaactta 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

<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:

-continued

<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	tgacccagtc	tccttccacc	ctgtctgcat	ctgttaggaga	cagagtccacc	60
atcacttgcc	gggccagtc	gaggattagt	agctggttgg	cctggtatca	acagatacca	120
gggaaagccc	ctaaactcct	gatctataag	gcgtctagtt	tagaaaatgg	ggtcccattca	180
aggttcagcg	gcagtggatc	tgggacagaa	ttcaactctca	tcatcagcag	cctgcagcct	240
gatgattttg	caacttatta	ctgccaacag	tatatttagtt	attctcggac	gttcggccaa	300
gggaccaagg	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	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 467

<211> LENGTH: 18

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 467

cagagtatta gtagctgg 18

<210> SEQ ID NO 468

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

-continued

<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 ttagttattc 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

```
<211> LENGTH: 360
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
```

<400> SEQUENCE: 473

```
gaggtgcagc tggtggagtc tggggggaggc ctggtaaagc cgggggggtc cctgagactc      60
tcctgtacag cctctggatt caccttcagt acttataaca tgaattgggt ccgccaggct      120
ccagggaaagg gactggagtg ggtctcatcc attaggagta gtatgtatca cataactac      180
gcagactcag tgaaggggcg attcaccatc tccagagaca acgccaagaa ttcaactgtat      240
ctgcaaatga acagcctgag agccgatgac acggctgtgt attactgtgc gagagatggc      300
agcagtttgtt acgactactc tgactactgg ggccaggaa ccctggcac cgctctctca      360
```

-continued

<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					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 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	cagagtccacc	60
atcacttgc	gggcacgtca	gagtattagt	agctggttgg	cctggtatca	acagatacca	120
ggaaagcccc	ctaaactct	gatctataag	gcgtctagtt	tagaaaatgg	ggtcccatca	180
aggttcageg	gcagtggatc	tggcacagaa	ttcactctca	tcatcagcag	cctgcagcct	240
gatgattttg	caaccttata	ctgccaacag	tatatttagtt	attctcgac	gttcggccaa	300
gggaccaagg	tggaaatcaa	a				321

<210> SEQ ID NO 476
<211> LENGTH: 107
<212> TYPE: PRT
<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

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Asp	Asp	Phe	Ala
Thr	Tyr	Tyr	Cys
85		90	
Gln	Gln	Tyr	Ile
		Ser	Ser
		Tyr	Arg
		95	

Thr	Phe	Gly
Gln	Gly	Thr
100		105
Lys		

<210> SEQ ID NO 477
<211> LENGTH: 360
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 477

gaggtgcagc	tggtgtggagtc	tggggggaggc	ctgggtcaagc	ctgggggggtc	cctgagactc	60
tccctgtgcag	cctctggatt	cacccatcgat	acttataaca	tgaactgggt	ccggccaggct	120
ccagggaaagg	ggctggagtg	ggtctcatcc	attaggagta	gtagtaatta	cataatactac	180
gcagactcag	tgaagggccg	attcaccatc	tccagagaca	acggccaagaa	ctcactgtat	240
ctgcaaatga	acagcctgag	agccgaggac	acggctgtgt	attactgtgc	gagagatggc	300
agcagtttgt	acgactactc	tgactactgg	ggccaaaggaa	ccctggtcac	cgtctctca	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	Ley	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	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	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 479
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 479

gacatccaga	tgacccagtc	tccttccacc	ctgtctgcat	ctgttaggaga	cagagtacc	60
atcacttgcc	gggccagtca	gagtattagt	agctggttgg	cctggtatca	gcagaaacca	120
gggaaagccc	ctaagctct	gatctataag	gcgtctagtt	tagaaagtgg	ggtccccatca	180

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aggttcagcg gcagtggatc tgggacagaa ttcaactctca ccatcagcag cctgcagcct	240
gatgattttg caaccttatta ctgccaacag tatatttagtt attctcgac gttcggccaa	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
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 481
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 481

gagggtcaac tagtggagtc tggggggaggc ttggtagacgc ctggggggtc cctgagactc	60
tccctgttag tctctggatt caccttcggt gactacgaca tgcactgggt ccgtcaagct	120
acaggaagag gtctggagtg ggtctcaggat attgctccctg ctggtgacac atcctataca	180
ggctccgtga agggccgatt caccatctcc agagagaatg ccaagaactc cttgcacatctt	240
caaataaca gcctgacaac cggggacacg gctatatatt attgtgttag agaggatata	300
gcagtgcctg gtttgattta ctggggccag ggaaccctgg tcaccgtctc ctca	354

<210> SEQ ID NO 482
<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 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			

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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

<400> SEQUENCE: 485

attgctcctg ctggtgacac a 21

<210> SEQ ID NO 486
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 486

Ile Ala Pro Ala Gly Asp Thr
 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 atatacgagt gcctggttt gattac 36

<210> SEQ ID NO 488
<211> LENGTH: 12

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<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

gaaatagtga	tgacgcagtc	tccagccacc	ctgtctgtgt	ctccagggga	acgaggcacc	60
ctctcctgca	gggccagtca	gagtgttagc	agcaacttag	cctggtagcca	gcagaaacct	120
ggccaggctc	ccagactct	catctatggt	gcatccacga	gggccactgg	cttcccagcc	180
aggttcagtg	gcagttggtc	tgggacagag	ttcaactctca	ccatcagcag	cctgcagtc	240
gaagattttg	cagtttatta	ctgtcagcag	tataataagt	ggcctccgtt	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 15

Glu Arg Gly 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 Phe 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 Phe Lys
100 105

<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

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<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

ggtgtcatcc

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 tccgttcaact

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

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 497

gagggtgcaac tagtggagtc tgggggaggc ttggtagacgc ctggggggtc cctgagactc

60

tcctgtgtat tctctggatt cacccctcggt gactacgaca tgcactgggt ccgtcaagct

120

acaggaagag gtctggagtg ggtctcaggat attgctccctg ctgggtgacac atccatataca

180

ggctccgtga agggccgatt caccatctcc agagagaatg ccaagaactc cttgcatctt

240

caaatgaaca gcctgacaac cggggacacg gctatatatt attgtgctag agaggatata

300

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gcagtgcctg gtttgattt 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 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 499
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 499

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccaggggga acgaggcacc 60

ctctcctgca gggccagtc gagtgtttagc agcaacttag cctggtagcca gcagaaacct 120

ggccaggctc ccagactct catctatggt gcatccacga gggccactgg cttcccagcc 180

aggttcagtg cgactgggtc tgggacagag ttcaactctca ccatcagcag cctgcagtc 240

gaagattttg cagtttatta ctgtcagcag tataataagt ggcctccgtt cactttcgcc 300

cctgggacca aagtggatat caaa 324

<210> SEQ ID NO 500
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 500

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

Glu Arg Gly 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 Phe Pro Ala Arg Phe Ser Gly
50 55 60

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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 501
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 501

gagggtgcagc tgggtggagtc tgggtacagc ctggggggtc cctgagactc 60
 tcctgtgcag cctctggatt caccttcggt gactacgaca tgcactgggt ccgccaagct 120
 acaggaaaaag gtctggagtg ggtctcagct attgctccctg ctggtgacac atactatcca 180
 ggctccgtga agggccgatt caccatctcc agagaaaatg ccaagaactc cttgtatctt 240
 caaatgaaca gcctgagagc cggggacacg gctgtgtatt actgtgttag agaggatata 300
 gcagtgcctg gtttgatta ctggggccaa ggaaccctgg tcaccgtctc ctca 354

<210> SEQ ID NO 502
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 502

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 Gly Asp 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 Ala Pro Ala 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 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 503
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 503

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggaa aagagccacc 60
 ctctcctgca gggccagtca gagtgttagc agcaacttag cctggtagca gcagaaacct 120

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ggccaggctc ccaggctct catctatggt gcatccacca	gggccactgg tatcccagcc	180
aggttcagtgc cagtggttc tgggacagag ttcaactctca	ccatcagcag cctgcagtct	240
gaagatttttgc agtttata ctgtcagcag tataataagt	ggcctccgtt cactttcgcc	300
cctgggacca aagtggatata 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 gtgaaggagc ctggggcctc agtgaaggtc	60
tcctgcaagg cttctggta cacctttacc aactacgcta tcagctgggt gcgcacaggc	120
cctggacaag ggcttgatgt gatggatgg gtcagcgctt acaatggtca cacaactat	180
gcacatgaag tccaggcag agtcaccatg accacagaca catccacgac cacagctac	240
atggagctga ggagcctgag atctgacgac acggccatgt attactgtgc gagaggggt	300
gtagtcgtgc cagttgtcc ccacttctac aacggtatgg acgtctgggg ccaaggacc	360
acggtcaccc tctccctca	378

<210> SEQ ID NO 506
<211> LENGTH: 126
<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	

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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 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 24

<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 acaatggta caca 24

<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

<210> SEQ ID NO 511
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 511

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gcgagaggggg gtgttagtcgt gccagttgct ccccaacttct 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

gatatttgta	tgactcaggta	tccactctcc	ctgccccgtca	cccctggaga	gccggcctcc	60
atcttcctgca	ggtcttagtca	gaggctcttg	catattaatg	aataacaacta	tttggattgg	120
tacccaaaga	agccaggggca	gtctccacag	ctcctgatct	atttgggttt	taatcggggcc	180
tccggggtcc	ctgacagggtt	cagtggcagt	ggatcaggca	cagattttac	actgaaaatc	240
agcagagtgg	aggctgagga	tgttggggtc	tattactgca	tgcaagctct	tcaaactccg	300
tggacgttag	gccaagggac	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					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 515
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 515

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

<400> SEQUENCE: 521

cagggtcagc tgggtgcagtc tggacctgag gtgaaggagc ctggggcctc agtgaaggc 60

tcctgcaagg cttctggta caccttacc aactacgcta tcagctgggt gcgacaggtc 120

-continued

cctggacaag ggcttgagtg gatggatgg gtcagcgctt acaatggtca cacaactat	180
gcacatgaag tccaggcag agtcaccatg accacagaca catccacgac cacagctac	240
atggagctga ggagccttag atctgacgac acggccatgt attactgtgc gagaggggt	300
gtagtcgtgc cagttgcctcc ccacttctac aacggtatgg acgtctgggg ccaaggacc	360
acggtcaccg tctcctca	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 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 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 gccggctcc	60
atctcctgca ggtcttagtca gagcctcctg catattaatg aataacaacta tttggattgg	120
tacctaaaga agccaggca gtctccacag ctcctgatct atttgggttt taatggggcc	180
tccggggtcc ctgacaggtt cagtggcagt ggatcaggca cagattttac actgaaaatc	240
agcagagtggtt aggctgagga tttttttttt tattactgca tgcaagctct tc当地actccg	300
tggacgttag gccaaggac caaggtggaa atcaaa	336

<210> SEQ ID NO 524
<211> LENGTH: 112
<212> TYPE: PRT
<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

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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 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

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caggttcagc tggtgcaagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc      60
tcctgcaagg cttctggta caccttacc aactacgccta tcagctgggt gcgacaggcc      120
cctggacaag ggcttgatgt gatggatgg gtcagcgctt acaatggtca cacaactat      180
gcacagaagc tccaggcag agtcaccatg accacagaca catccacgag cacagctac      240
atggagctga ggagcctgag atctgacgac acggccgtgt attactgtgc gagaggggt      300
gtatcgatgc cagttgcgtcc ccacttctac aacggtatgg acgtctgggg gcaaggacc      360
acggtcacccg tctccctca                                         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
 100 105 110

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

<210> SEQ ID NO 527

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

<400> SEQUENCE: 527

```
gatattgtga tgactcagtc tccactctcc ctgccccgtca cccctggaga gccggcctcc      60
atctcctgtca ggtcttagtca gagcctctcg catattaatg aataacaacta tttggattgg     120
tacctgcaga agccaggggca gtctccacag ctcctgatct atttgggttc taatcgggcc     180
tccgggggtcc ctgacagggtt cagtggcagt ggatcaggca cagattttac actgaaaatc     240
agcagagtggtt aggctgagga tgttgggtt tattactgca tgcaagctct tc当地actccg     300
tggacgttccg gccaaggggac caaggtggaa atcaaa                                336
```

<210> SEQ 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

```
gaggtgcagc tgggtggagtc tgggtacagc ctggggggtc cctgagactc      60
tcctgtgcag cctctggatt cacccctaagt agctacgaca tgcactgggt ccgccaagca    120
acaggaaaaag gtctggagtg ggtctcagct attggcagta ctggtgacac atactataca    180
ggctccgtga tggggccgatt caccatctcc agagacgctg ccaaaaaactc cttctatctt    240
gaaatgaaca gcctgagagt cggggacacg ggtgtatatt actgtgoag agagggaaata    300
agaacacccct atgattatttggggccaggaa gcccgggtca ccgtctccctc a            351
```

<210> SEQ ID NO 530
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

-continued

<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				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 ctgggtacac 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

Ile	Gly	Ser	Thr	Gly	Asp	Thr									
1							5								

-continued

<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 ctccaggaga aagagccacc	60
ctctcctgca gggccagtca gagtgtagc agcaatgtag cctggtagcca gcagaaacct	120
ggccaggctc ccaggctct catctatggt gcatccacca gggccactgg tatcccagcc	180
aggttcagtg gcagtgggtc tgggacagaa ttcaactctca cc当地cagcag cctgcagct	240
gaagatttttgc cagtttatta ctgtcagcag tataataatt ggcctccatt cactttcgcc	300
cctggggacca aagtggatata 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 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

<210> SEQ ID NO 539

-continued

<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 tccattcact

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
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

-continued

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 545

gagggtgcagc	tgggtggagtc	tgggggaggc	ttggcacagc	ctggggggtc	cctgagactc	60
tcctgtgcag	cctctggatt	caccctaagt	agctacgaca	tgcactgggt	ccgccaagca	120
acaggaaaag	gtctggagtg	ggtctcagct	atggcagta	ctggtgacac	atactataca	180
ggctccgtga	tgggccgatt	caccatctcc	agagacgctg	ccaaaaactc	cttctatctt	240
gaaatgaaca	gcctgagagt	cggggacacg	gctgtatatt	actgtgcaag	agagggata	300
agaacacccct	atgattattg	gggccaggga	accctggtca	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	Ley	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	Ley	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 547

<211> LENGTH: 324

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 547

gaaatagtga	tgacgcagtc	tccagccacc	ctgtctgtgt	ctccaggggc	aagagccacc	60
ctctcctgca	gggccagtc	gagtgttagc	agcaatgtag	cctggtagca	gcagaaacct	120
ggccaggctc	ccaggctct	catctatggt	gcatccacca	gggccactgg	tatcccagcc	180
aggttcagtg	gcagtggc	tgggacagaa	ttcactctca	ccatcagcag	cctgcagtc	240
gaagatttg	cagtttatta	ctgtcagcag	tataataatt	ggcctccatt	cactttccgc	300
cctgggacca	aagtggat	caa				324

<210> SEQ ID NO 548

<211> LENGTH: 108

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

-continued

<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 tgggtacagc ctgggggtc cctgagactc      60
tcctgtcagc cctctggatt caccctaagt agctacgaca tgcactgggt ccgccaagct 120
acaggaaaag gtctggagtg ggtctcagct attggcagta ctggtgacac atactatcca 180
ggctccgtga agggccgatt caccatctcc agagaaaatg ccaagaactc cttgttatctt 240
caaatgaaca gcctgagagc cggggacacg gctgtgtatt actgtgcaag agagggata 300
agaacaccct atgattattt gggccaaggaa accctggtca ccgtctccct 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
 115

```

-continued

<210> SEQ ID NO 551
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 551

```

gaaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccaggggaa aagagccacc      60
cttcctgca gggccagtca gagtgtttagc agcaatttag cctggtacca gcagaaacct      120
ggccaggctc ccaggctct catctatggt gcatccacca gggccactgg tatcccagcc      180
aggttcagtg gcagttgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct      240
gaagattttgc agtttattat ctgtcagcag tataataatt ggctccatt cactttcgcc      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

```

gagggtgcagc tgggtggagtc tggggggaggc ttggtagacgc ctggggggtc cctgagactc      60
tcctgtgcag cctctggatt caccctaagt agctacgaca tgcactgggt ccgccaagca      120
acaggaaaaag gtctggagtg ggtctcagct attggcagta ctggtagacac atactataca      180
ggctccgtga tgggccgatt caccatctcc agagacgctg ccaaaaactc cttcttatctt      240
gaaatgaaca gcctgagagt cggggacacg gctgtatatt actgtgcaag agagggaaata      300
agaacaccct atgattatttgc gggccaggaa gccccgggtca ccgtctccctc a             351

```

<210> SEQ ID NO 554
<211> LENGTH: 117

-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 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 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

 attggcagta 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

-continued

1 5

<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 gagtgtttagc agcaatgttag cctggtagcca gcagaaaacct 120
ggccaggctc ccaggctct catctatggt gcatccacca gggccactgg tatcccagcc 180
aggttcagtg gcagtggttc tgggacagaa ttcaactctca ccatcagcag cctgcagtc 240
gaagattttg cagtttatta ctgtcagcag tataataatt ggcctccatt cactttcgcc 300
cctgggacca aagtggatat 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

ggtgcatcc

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

-continued

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

<400> SEQUENCE: 569

```

gagggtgcagc tgggtggagtc tggggggagc ttgggtacagc ctggggggtc cctgagactc      60
tcctgtgcag cctctggatt cacccatagt agctacgaca tgcactgggt ccgc当地ca      120
acaggaaaaag gtctggagtg ggtctcgactt attggcagta ctgggtacac atactataca      180
ggctccgtga tggggccgatt caccatctcc agagacgctg ccaaaaactc ctttatctt      240
gaaatgaaca gcctgagagt cggggacacg gctgtatatt actgtgcaag agagggaaata      300
agaacaccct atgattattt gggccagggaa accctggtca ccgtctccctc 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 ctccagggaa aagagccacc      60
ctctcctgca gggccagtca gagtgtagc agcaatgtag cctggtagca gcagaaacct      120
ggccaggctc ccaggctct catctatggt gcatccacca gggccactgg tatcccagcc      180
aggttcagtg gcagtgggtc tgggacagaa ttcaacttca ccatcagcag cctgcgtct      240
gaagattttc cagtttatta ctgtcagcag tataataatt ggcctccatt cactttccgc      300
cctggacca aagtggatata caaa                                         324

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<210> SEQ ID NO 572
<211> LENGTH: 108
<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 572

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 573

<211> LENGTH: 351

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 573

gaggtgcagc	tgggtggagtc	tggggggaggc	ttggtagacgc	ctggggggtc	cctgagactc	60
tcctgtgcag	cctctggatt	caccctaagt	agctacgaca	tgcactgggt	ccgccaagct	120
acaggaaaag	gtctggagtg	ggtctcagct	atggcagta	ctggtgacac	atactatcca	180
ggctccgtga	agggccgatt	caccatctcc	agagaaaatg	ccaagaactc	cttgtatctt	240
caaatgaaca	gcctgagagc	cggggacacg	gctgtgtatt	actgtgcaag	agagggaaata	300
agaacacccct	atgattattg	gggccaagga	accctggtca	ccgtctccctc	a	351

<210> SEQ ID NO 574

<211> LENGTH: 117

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 574

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Ley	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				

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Val Thr Val Ser Ser
115

<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	ctccaggaga	aagagccacc	60
ctctcctgca	gggccagtca	gagtgttagc	agcaatttag	cctggtagcca	gcagaaacct	120
ggccaggctc	ccaggctct	catctatggt	gcatccacca	gggccactgg	tatcccagcc	180
aggttcagtg	gcagtgggtc	tgggacagag	ttcaactctca	ccatcagcag	cctgcagtc	240
gaagattttg	cagtttatta	ctgtcagcag	tataataatt	ggcctccatt	cactttcgcc	300
cctgggacca	aagtggatata	caaa				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

gaagtgcagc	tgggggaggc	tgggtacagc	ctggcaggtc	cctgagactc	60
tcctgtgcag	cctctggatt	cacctttgtat	gattatgcac	tgcactgggt	120
ccaggaaagg	gcctggagtg	ggtctcaggat	attaattgga	acagtggtag	180
gcggactctg	tgaaggggccg	attcaccatc	tccagagaca	acggcaagca	240
ctgcaaata	acagtctgag	acctgaggac	acggccttgt	attactgtgt	300
actacggat	actactacgg	tatggacgac	tggggccaag	ggaccacgg	360

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tca

363

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<210> SEQ ID NO 578
<211> LENGTH: 121
<212> TYPE: PRT
<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

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<210> SEQ ID NO 579
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 579

ggattcacct ttgatgatta tgcc

24

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<210> SEQ ID NO 580
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<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

attnaatttggaa acagttggtag cata

24

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<210> SEQ ID NO 582
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 582

Ile Asn Trp Asn Ser Gly Ser Ile
1 5

<210> SEQ ID NO 583

<211> LENGTH: 42

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 583

gtaaaaagagg 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 tgacctcgtc tccatccttc ctgtctgcat ctgttaggaga cagagtacc	60
atcaacttgc gggccagtc gggcatttc agttatattag cctggtatca gaaaaaaacca	120
gggaaagccc ctaacctcct gatctatgat gcatccactt tgcaaagtgg ggtcccatca	180
aggttcagcg gcagtggatc tgggacagaaa ttcaactctca cactcagcag cctgcagcct	240
gaagattttgc caacttattta ctgtcaacag cttaatattt acccattcac ttccggccct	300
gggaccaaag tggatataaa 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 80

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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 587
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 587

cagggcatttatgcagttat 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 attcaat 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

-continued

1 5

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<210> SEQ ID NO 593
<211> LENGTH: 363
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 593

gaagtgcagc tgggtggagtc tgggggaggc ttggcacgc ctggcaggc cctgagactc      60
tcctgtgcag cctctggatt cacctttat gattatgcc a tgcactgggt ccggcaagct      120
ccagggaaagg gcctggagtg ggtctcaggat attaatttgg a acagtggtag cataggctat      180
gcggactctg tgaaggcccg attcaccatc tccagagaca acgccaagca ctccctgtat      240
ctgcaa atga acagtctgag acctgaggac acggccttgtt attactgtgt aaaagaggtg      300
actacggat actactacgg tatggacgctc tggggccaag ggaccacggt caccgtctcc      360
tca                                              363

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<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 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

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<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 cagagtacc      60
atcacttgc gggccagtc gggcattagc agttat tag cctggtatca gaaaaaacca      120
ggaaagccc ctaacctct gatctatgat gatccac ttgcaaaatgg ggtcccatca      180
aggttcagcg gcagtggtac tgggacagaa ttcactctca cactcagcag cctgcagcct      240
gaagat ttttgc caacttatta ctgtcaacag cttaatatcc acccattcac ttccggccct      300

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gggaccaaag tggatatcaa a 321

<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 ttgggtacagc ctggcaggc cctgagactc 60
tcctgtgcag cctctggatt cacctttgtt gattatgcca tgcactgggt ccggcaagct 120
ccagggaaagg gcctggagtg ggtctcaggat attaattgga acagtggtag cataggctat 180
gcggactctg tgaaggcccg attcaccatc tccagagaca acgccaagaa ctcccgttat 240
ctgcaaatga acagtctgag agctgaggac acggccttgtt attactgtgt aaaagaggtg 300
actacgggat actactacgg tatggacgtc tggggggcaag ggaccacggt caccgtctcc 360
tgg 363

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<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 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

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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95
 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 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
atcaacttgcc gggccagtcgaa gggcatttgc agttattttag cctggtatca gcaaaaacca 120
ggaaagcccc ctaagctctt gatctatgtat gcatccactt tgcaaagtgg ggtcccatca 180
aggttcagcg gcagtggata tgggacagaa ttcaactctca caatcagcag octgcagcct 240
gaagattttgc caacttatta ctgtcaacag cttaatattt acccattcac tttcggccct 300
gggacccaaag tggatatcaa a 321

<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 tggtggagtc tgggggaggc ttggtagcgc ctgggggtc cctgagactc 60
tcctgtgcag cctctggatt cacgttttagt agctatgccat tgaactgggt ccggccaggct 120

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ccagggaaagg ggctggattg ggtctcaggt atcagtggta atggtggttag cacctactac	180
gcagactccg tgaaggggccg gttcaccatc tccagagaca tttccaagaa cacgctgtat	240
gtgcaaatgc acagcctgag agtcgaggac acggccgtt actactgtgc gaaagccgt	300
tattacgatt tttggggggg gaatttcgat ctctggggcc gtggcaccca ggtcaactgtc	360
tcctca	366

<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 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 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 tttagtagcta tgcc	24
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<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

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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

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 ggaaatttcg 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 ctccaggggg aagagcacc 60
ctctcctgca gggccagtca gagtgttagc atcaggtact tagcctggta tcagcagaaa 120
cctggccagg cttccaggct cttcatctat ggtgcatacca gcagggccac tggcatccca 180
gacaggttca gtgtcagtgt gtctggaca gacttcactc tcaccatcac tagactggag 240
cctgaagatt ttgcagtcta ttactgtcag caatatggta gttcaccgct cactttccgc 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

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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	Gly	Thr	Lys	Val	Glu	Ile	Lys				
	100					105									

<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 gcatcaggta 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 gtatccacc gctcact 27

<210> SEQ ID NO 616

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

<400> SEQUENCE: 617

gaggtgcagt	tgttggagtc	tgggggaggc	ttggtagacgc	cgggggggtc	cctgagactc	60
tcctgtgcag	cctctggatt	cacgttttagt	agctatgcca	tgaactgggt	ccggccaggct	120
ccagggaaagg	ggctggattt	ggtctcaggt	atcagtggta	atggtggttag	cacctactac	180
gcagactccg	tgaagggccg	gttcaccatc	tccagagaca	tttccaagaa	cacgctgtat	240
gtgcaaatgc	acagcctgag	agtcgaggac	acggccgttt	actactgtgc	gaaagcccgt	300
tattacgatt	tttggggggg	gaatttcgat	ctctggggcc	gtggcacccct	ggtcactgtc	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	Ley	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	Ley	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	Ley	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	Ley	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

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gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc	60
ctctcctgca gggccagtca gagtgttagc atcaggtact tagcctggta tcagcagaaa	120
cctggccagg ctcaggct cctcatctat ggtgcattca gcagggcac tggcatccca	180
gacaggttca gtgtcagtgt gtctggaca gacttcactc tcaccatcac tagactggag	240
cctgaagatt ttgcagtcata ttactgttag caatatggta gttcaccgct cactttcgcc	300
ggagggacca aggtggagat caaa	324

<210> SEQ ID NO 620

<211> LENGTH: 108

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 620

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	

<210> SEQ ID NO 621

<211> LENGTH: 366

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 621

gaggtgcagc tggggggaggc ttggtagc ctggggggtc cctgagactc	60
tccctgtcagc cctctggatt cacgttagt agctatgcca tgagctgggt ccggcaggct	120
ccagggaaagg ggctggagtg ggtctcagct atcagtggtt atgggttag cacctactac	180
gcagactccg tgaaggcccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagccgt	300
tattacgatt tttgggggg gaatttcgat ctctggggcc gtggcacccct ggtcactgtc	360
tcctca	366

<210> SEQ ID NO 622

<211> LENGTH: 122

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 622

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

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

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

Ser Ala Ile Ser Gly Asn Gly Gly Ser 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 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 623
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 623

```
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc      60
ctctccctgca gggccagtca gagtgtttagc atcaggtact tagcctggta ccagcagaaa     120
cctggccagg cttcccaggct cctcatctat ggtgcattcca gcagggccac tggcatcccc     180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag     240
cctgaagatt ttgcagtgtta ttactgttag caatatggta gttcaccgct cactttcgcc     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 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

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 Gly Thr Lys Val Glu Ile Lys
 100 105

<210> SEQ ID NO 625
<211> LENGTH: 381
<212> TYPE: DNA

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

<400> SEQUENCE: 625

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caggttcagc tggtgcaagtc tggacctgag gtgaagaacc ctggggctc agtgaaggc 60
tcctgcagg cttctggta cacctttacc acctatggta tcagttgggt acgcacaggcc 120
cctggacaag ggcttgatgg gatgggatgg atcagcggtt acaatggta aacaaacgat 180
gcacagaagt tccaggacag agtcgccatg accacagaca catccacgag cacagctac 240
atggagctga ggagcctgag atctgacgac acggccattt attactgttc gagagatcgt 300
ttagtagtac cacctgcctt ttattattcc tactacgtta tggacgtctg gggccaaggg 360
accacggta ccgtctctc a 381
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<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				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 627
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 627

ggttacacctt ttaccaccta tggt 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			

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<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

<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 ctttatttattt cctactacgt 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 15Val 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 ctgcgggtca cccttgac gcccgtcc 60

atctcctgca ggtctagtca aagcctcgta tacagtatg gaaacaccta cttgaattgg 120

tttcagcaga ggccagggtca atctccaagg cgccataattt ataagggttc taaccgggac 180

tctggggtcc cagacagatt cagcggcagt gggtcaggca ctgatttcac actgaaaatc 240

agcagggtgg aggctgagga tgttgggtt tattactgca tgcaaggtagt acactggccg 300

tacacttttgc gccaggggac caagctggag atcaaa 336

<210> SEQ ID NO 634
<211> LENGTH: 112
<212> TYPE: PRT

-continued

<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	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 635

<211> LENGTH: 33

<212> TYPE: DNA

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

<400> SEQUENCE: 635

caaaggctcg tatacagtga tggaaacacc tac 33

<210> SEQ ID NO 636

<211> LENGTH: 11

<212> TYPE: PRT

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

<400> SEQUENCE: 636

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

<210> SEQ ID NO 637

<211> LENGTH: 9

<212> TYPE: DNA

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

<400> SEQUENCE: 637

aaggtttct 9

<210> SEQ ID NO 638

<211> LENGTH: 3

<212> TYPE: PRT

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

<400> SEQUENCE: 638

Lys	Val	Ser
1		

<210> SEQ ID NO 639

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<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 639

atgcaggta cacactggcc gtacact

27

<210> SEQ ID NO 640
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 640

Met Gln Gly Thr His Trp Pro Tyr Thr
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

caggttcagc tggcggcgtc tggacacctgag gtgaagaacc ctggggcctc agtgaaggc	60
tccgtcaagg cttctggta cacctttacc acctatggta tcagttgggt acgcacaggcc	120
cctggacaag ggcttgatgt gatggatgg atcagcggtt acaatggtaa aacaaacgat	180
gcacagaagt tccaggacag agtcgcccatt accacagaca catccacgag cacagctac	240
atggagctga ggagccttagt atctgacgac acggccattt attactgttc gagagatcgt	300
ttagtagtac cacctgcctt ttattattcc tactacgtta tggacgtctg gggccaagg	360
accacggta ccgtctccca 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 15Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr
20 25 30Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45Gly Trp Ile Ser Gly Tyr Asn Gly Lys Thr Asn Asp Ala Gln Lys Phe
50 55 60Gln Asp Arg Val Ala Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Ile Tyr Tyr Cys
85 90 95Ser 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

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115

120

125

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<210> SEQ ID NO 643
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 643

gatgttgtga tgactcagtc tccactctcc ctgccccgtca cccttggaca gccggcctcc      60
atctcctgca ggtctagtca aaggcctcgta tacagtgtat gaaacacacta cttgaatttgg      120
tttcagcaga ggccagggtca atctccaagg cgccctaattt ataagggttca taaccgggac      180
tctgggggtcc cagacagatt cagcggcagt gggtcaggca ctgatttcc actgaaaatc      240
agcagggtgg aggctgagga tttttgggtt tattactgca tgcaaggtagt acactggccg      300
tacacttttg gccaggggac caagctggag atcaaa                                336

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<210> SEQ ID NO 644
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 644

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

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<210> SEQ ID NO 645
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 645

caggttcagtc tgggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc      60
tcctgcaagg cttctggta caccttacc acctatggta tcagctgggt gcgcacaggcc      120
cctggacaag ggcttgatgt gatggatgg atcagcggtt acaatggtaa aacaaactat      180
gcacagaagc tccaggccag agtcaccatg accacagaca catccacgag cacagctac      240
atggagctga ggagcctgag atctgacgac acggccgtgt attactgttc gagagatcgt      300
tttagtagtac cacctgccct ttattattcc tactacgtta tggacgtctg gggcaaggg      360
accacggtca ccgtctcctc a                                         381

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<210> SEQ ID NO 646
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 646

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala	
1																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	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	gccggcctcc		60
atctcctgca	ggtctagtca	aaggcctcgta	tacagtgtatg	gaaacaccta	cttgaattgg		120
tttcagcaga	ggccaggcca	atctccaagg	cgcctaattt	ataaggtttc	taaccgggac		180
tctggggtcc	cagacagatt	cagcggcagt	gggtcaggca	ctgatttac	actgaaaatc		240
agcaggggtgg	aggctgagga	tgttggggtt	tattactgca	tgcaaggtag	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																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
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

-continued

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

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cagggttcagc tgggtgcagtc tggacacctgag gtgaagaacc ctggggcctc agtgaaggc 60
tcctgcaagg cttctggta cacctttacc acctatggta tcagttgggt acgcacaggcc 120
cctggacaag ggcttgagtg gatgggatgg atcagcggtt acaaatggtaa aacaaacgat 180
gcacagaagt tccaggacag agtcgcccatt accacagacata catccacgag cacagcctac 240
atggagctga ggagcctgag atctgacgac acggccattt attactgttc gagagatcgt 300
tttagtagtac cacctggccct taattattac tactacgtta tggacgtctg gggccaagg 360
accacggtca ccgtctccctc 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 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 651

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 651

ggttacacct ttaccaccta tggt

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<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

<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 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 cccttgacca gccggcctcc 60

atctcctgca ggtcttagtca aaggctcgta tacagtgtat gaaacaccta cttgaattgg 120

-continued

tttcagcaga ggccaggta atctccaagg cgcctaattt ataaggtttc taaccgggac	180
tctgggggtcc cagacagatt cagcggcagt gggtcaggca ctgatttcac actgaaaatc	240
agcagggtgg aggctgagga tgggggtt tattactgca tgcaaggtag acactggccg	300
tacacttttgc cagggggac 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	
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

<210> SEQ ID NO 662
<211> LENGTH: 3

-continued

<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
<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 tggtgccagtc tggacctgag gtgaagaacc ctggggcctc agtgaaggc 60
tcctgcagg cttctggta cacctttacc acctatggta tcagttgggt acgcacaggcc 120
cctggacaag ggcttgagtg gatggatgg atcagcggtt acaatggtaa aacaacat 180
gcacagaagt tccaggacag agtcgccatg accacagaca catccacgag cacagctac 240
atggagctga ggagcctgag atctgacgac acggccattt attactgttc gagagatcgt 300
tttagtagtac cacctgcct taattattac tactacgta tggacgtctg gggccaagg 360
accacggta ccgtctcc 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

-continued

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

gatgttgtga	tgactcagtc	tccactctcc	ctgccccgtca	cccttggaca	gccggcctcc	60
atctcctgc	aaggctcgta	aaggctcgta	tacagtgtat	gaaacacacta	cttgaattgg	120
tttcagcaga	ggccagggtca	atctccaagg	cgcctaattt	ataaggtttc	taaccgggac	180
tctggggtcc	cagacagatt	cagcggcagt	gggtcaggca	ctgatttcac	actgaaaatc	240
agcagggtgg	aggctgagga	tgttggggtt	tattactgca	tgcaaggtag	acactggccg	300
tacactttt	gccaggggac	caagctggag	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	tggagctgag	gtgaagaagc	ctggggcctc	agtgaaggtc	60
-------------	-------------	------------	------------	------------	------------	----

-continued

tcctgcaagg cttctggta caccttacc acctatggta tcagctgggt gcgacaggcc	120
cctggacaag ggcttgagtg gatgggatgg atcagcggtt acaaactat	180
gcacagaagc tccagggcag agtcaccatg accacagaca catccacgag cacagoctac	240
atggagctga ggagcctgag atctgacgac acggccgtgt attactttc gagagatcgt	300
ttagtagtac cacctgcct taattattac tactacgtta tggacgtctg gggcaaggg	360
accacggtca 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			
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 ctgcccgtca cccttggaca gccggctcc	60
--	----

atctcctgca ggtctagtca aagcctcgta tacagtgtat gaaacaccta cttgaattgg	120
---	-----

tttcagcaga ggcaggcga atctccaagg cgccataattt ataaggttca tAACCGGGAC	180
---	-----

tctgggtcc cagacagatt cagcggcagt gggtcaggca ctgatttac actgaaaatc	240
---	-----

agcagggtgg aggctgagga ttttttttttattactgca tgcaaggta acactggccg	300
--	-----

tacacttttgc cccaggggac 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

-continued

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 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 tgggtcagtc tggacctgag gtgaagaacc ctggggcctc agtgaaggtc      60
tcctgcaagg cttctggta cacctttacc acctatggta tcagttgggt acgcacaggcc    120
cctggacaag ggcttgagtg gatgggatgg atcagcggtt acaatggtaa aacaaacgat    180
gcacagaagt tccaggacag agtcgcccatt accacagaca catccacgag cacagcctac   240
atggagctga ggagcctgag atctgacgac acggccattt attactgttc gagagatcgt   300
tttagtagtac cacctgcctt ttattattac tactacgtta tggacgtctg gggccaaggg   360
accacggtca ccgtctccctc 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

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

-continued

<210> SEQ ID NO 675
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 675

ggttacacct ttaccaccta tggt

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

<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 accacacctgcc ctttattattt 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

-continued

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

<400> SEQUENCE: 681

```

gatgttgtga tgactcagtc tccactctcc ctgcggcgta cccttggaca gccggcctcc      60
atctcctgca ggtctagtca aaggcctcgta tacagtgtat gaaacaccta cttgaattgg     120
tttcagcaga ggccagggtca atctccaagg cgccataattt ataaggtttc taaccgggac    180
tctggggtcc cagacagatt cagcggcagt gggtcaggca ctgatttcac actgaaaatc     240
agcagggtgg aggctgagga tttttttttt tattactgca tgcaagggtac 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			
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 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

-continued

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<400> SEQUENCE: 685

aaggtttct

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

<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 tgggtcgagtc tggacctgag gtgaagaacc ctggggcctc agtgaaggc 60
tcctgcaagg cttctggta caccttacc acctatggta tcagttgggt acgacaggcc 120
cctggacaag gggtttagtg gatggatgg atcagcggtt acaatggtaa aacaacgat 180
gcacagaagt tccaggacag agtcgccatg accacagaca catccacgag cacagctac 240
atggagctga ggagcctgag atctgacgac acggccattt attactgttc gagagatcgt 300
tttagtagtac cacctgcctt ttattattac tactacgtta tggacgtctg gggccaagg 360
accacggta ccgtctcctc a 381

<210> SEQ ID NO 690
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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391**392**

-continued

<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 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

<400> SEQUENCE: 691

```

gatgttgtga tgactcagtc tccactctcc ctgccccgtca cccttggaca gccggcctcc      60
attcctcgca ggtctagtca aaggcctcgta tacagtgtatc gaaacaccta cttgaattgg     120
tttcagcaga ggcagggtca atctccaagg cgccctaattt ataagggttc taaccgggac     180
tctggggtcc cagacagatt cagcggcagt gggtcaggca ctgatttcac actgaaaatc     240
agcagggtgg aggctgagga tttttttttt tattactgca tgcaaggtagt acactggccg     300
tacacttttg gccaggggac caagctggag atcaaa                                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

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<210> SEQ ID NO 693
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 693

cagggttcagc	tgggtgcagtc	tggagctgag	gtgaagaagc	ctggggcctc	agtgaaggtc	60
tcctgcaagg	cttctggta	caccttacc	acctatggta	tcagctgggt	gcgacaggcc	120
cctggacaag	ggcttgatgt	gatgggatgg	atcagcggtt	acaatggtaa	aacaaactat	180
gcacagaagc	tccagggcag	agtcaccatg	accacagaca	catccacgag	cacagctac	240
atggagctga	ggagcctgag	atctgacgac	acggccgtgt	attactgttc	gagagatcgt	300
ttagtagtac	cacctgcct	ttattattac	tactacgtta	tggacgtctg	ggggcaaggg	360
accacggta	ccgtctcctc	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
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	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	
	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

gatgttgta	tgactcagtc	tccactctcc	ctgccccgtca	cccttggaca	gccggcctcc	60
atctcctgca	ggtctagtca	aaggcctcgta	tacagtgtat	gaaacaccta	cttgaattgg	120
tttcagcaga	ggccaggcca	atctccaagg	cgcctaattt	ataaggttcc	taaccgggac	180
tctggggtcc	cagacagatt	cagcggcagt	gggtcaggca	ctgatttcac	actgaaaatc	240
agcagggtgg	aggctgagga	tgttgggtt	tattactgca	tgcaaggta	acactggccg	300
tacacttttgc	ccaggggac	caagctggag	atcaaa			336

-continued

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

<400> SEQUENCE: 697

caggtgcacc	tggggaggc	tgggtcaagc	ctggagggtc	cctgagactc	60	
tcctgtgcag	cctctggatt	cacccatcgat	gaccactaca	tgagctggat	ccggcaggct	120
ccagggaaagg	ggctggagtg	gatttcatac	attagtaatg	atgggtggat	caaatactat	180
gtggactctg	tggaggggccg	attcatcatt	tccagggaca	acgccaagaa	ctcattgtat	240
ctacatatga	acagcctcag	agccgacgac	acggccgtgt	attactgtgc	gagagatcag	300
ggatatatty	gctacgactc	gtatttattac	tattcctacg	gtatggacgt	ctggggccaa	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	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

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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 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

<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 atgggtgtac 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

-continued

<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	ctgcctttgt	ttccagggga	aagagccacc	60
ctctccctgta	gggccagtca	gagtgttaac	aacaaattct	tagcctgta	ccagcagaaaa	120
tctggccagg	cctcccaggct	cctcatctat	ggtgcatcca	gcagggccac	tggcatccca	180
gacaggttca	gtggcagtgg	gtctgggacc	gacttcactc	tcaccatcg	cggaactggag	240
cctgaagatt	ttgaagtgtta	ttattgtcaa	gtatatggta	actcactcac	tttcggcgga	300
gggaccaagg	tggagatcaa	g				321

<210> SEQ ID NO 706

<211> LENGTH: 107

<212> TYPE: PRT

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

<400> SEQUENCE: 706

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
			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	Phe	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys						
				100		105									

<210> SEQ ID NO 707

<211> LENGTH: 21

<212> TYPE: DNA

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

<400> SEQUENCE: 707

cagagtgtta acaacaatt c

<210> SEQ ID NO 708

-continued

<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 708

Gln Ser Val Asn Asn Lys Phe
1 5

<210> SEQ ID NO 709
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 709

ggtgtcatcc

9

<210> SEQ ID NO 710
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 710

Gly Ala Ser
1

<210> SEQ ID NO 711
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 711

caagttatgt 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

cagggtgcagc	tggtggagtc	tgggggaggc	ttggtaaagc	ctggagggtc	cctgagactc	60
tcctgtgcag	cctctggatt	cacccatcgt	gaccactaca	tgagctggat	ccgccaggct	120
ccagggaaagg	ggctggagtg	gatttcatac	attagtaatg	atgggtgtac	caaatactat	180
gtggactctg	tggagggccg	attcatcatt	tccagggaca	acgccaagaa	ctcattgtat	240

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ctacatatga acagccttag	agccgacgac	acggccgtgt	attactgtgc	gagagatcag	300
ggatatattg gctacgactc	gtattattac	tattcctacg	gtatggacgt	ctggggccaa	360
gggaccacgg tcaccgttc	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	Ley	Val	Lys	Pro	Gly	Gly	
1														15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Asp	His
20														30	
Tyr	Met	Ser	Trp	Ile	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Ley	Glu	Trp	Ile
35														45	
Ser	Tyr	Ile	Ser	Asn	Asp	Gly	Gly	Thr	Lys	Tyr	Tyr	Val	Asp	Ser	Val
50														60	
Glu	Gly	Arg	Phe	Ile	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr
65														80	
Leu	His	Met	Asn	Ser	Leu	Arg	Ala	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
85														95	
Ala	Arg	Asp	Gln	Gly	Tyr	Ile	Gly	Tyr	Asp	Ser	Tyr	Tyr	Tyr	Ser	
100														110	
Tyr	Gly	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser
115														125	

<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	ctgcctttgt	ttccagggga	aagagccacc	60
ctctccctgta	gggccagtca	gagtgttaac	aacaaattct	tagcctgta	ccagcagaaaa	120
tctggccagg	cctccaggct	cctcatctat	ggtgcatcca	gcagggccac	tggcatccca	180
gacaggttca	gtggcagtgg	gtctggacc	gacttcactc	tcaccatcg	cggaactggag	240
cctgaagatt	ttgaagtgtta	ttattgtcaa	gtatatggta	actcactcac	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

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405**406**

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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 Phe 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

caggtgcagc	tgggtggagtc	tgggggaggc	ttggtcaagc	ctggagggtc	cctgagactc	60
tcctgtgcag	cctctggatt	cacccatcgt	gaccactaca	tgagctggat	ccgcccaggct	120
ccagggaaagg	ggctggagtg	ggtttcatac	attagtaatg	atgggtgtac	caaatactac	180
gcagactctg	tgaaggggccg	attcaccatc	tccagggaca	acgccaagaa	ctcactgtat	240
ctgcaaatga	acagcctgag	agccgaggac	acggccgtgt	attactgtgc	gagagatcag	300
gatatatttgc	gtacgactc	gtattattac	tattcctacg	gtatggacgt	ctggggcaa	360
gggaccacgg	tcaccgtctc	ctca				384

<210> SEQ ID NO 718
 <211> LENGTH: 128
 <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	Ley	Val	Lys	Pro	Gly	Gly	
1																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	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 ctgtcttgt ctccaggaga aagagocacc      60
ctctcctgca gggccagtca gagtgtaaac aacaaattct tagcctggta ccagcagaaa     120
cctggccagg ctcaggatc ctcatctat ggtgcattca gcagggccac tggcatccc     180
gacagggtca gtggcagtgg gtctggaca gacttcactc tcaccatcg cagactggag     240
cctgaagatt ttgcagtgtta ttactgtcaa gtatatggta actcactcac ttccggcgg     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

Thr Phe 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 tggacctgag gtgaaggagc ctggggcctc agtgaaggtc      60
tcctgcaagg cttctggta caccttacc aactacgcta tcagctgggt gcgacaggc      120
cctggacaag ggcttgatgt gatggatgg gtcagcgctt acaatggta cacaaactat     180
gcacatgaag tccaggcag agtcaccatg accacagaca catccacgac cacagctac     240
atggagctga ggacgctgag atctgacgac acggccatgt attactgtgc gagaggggt     300
gtatgcgtgc cagttgctcc ccacttctac aacggtatgg acgtctgggg ccaagggacc     360
acggtcaccc ttcctca                                         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

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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 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 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:
<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 acaatggta 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

```

-continued

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

<400> SEQUENCE: 727

gcgagagggg gtgttagtcgt gccagttgct 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

gatatttgtga	tgactcagtt	tccactctcc	ctgccccgtca	cccctggaga	gccgggctcc	60
atctcctgtca	ggtctctgtca	gagcctcctcg	catattaatg	aataacaacta	tttggattgg	120
tacctaaaga	agccaggggca	gtctccacag	ctcctgtatct	atttgggttt	taatcgggcc	180
tccgggggtcc	ctgacagggtt	cagtggcagt	ggatcaggca	cagattttac	actgaaaaatc	240
agcagagtg	aggctgagga	tgttggggtc	tattactgca	tgcaagctct	tcaaactccg	300
tggacgttccg	gccaaggggac	caaggtggaa	atcaaa			336

<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

-continued

<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
 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

-continued

<400> SEQUENCE: 737

```
caggttcagc tgggtcagtc tggacacctgag gtgaaggagc ctggggctc agtgaaggtc      60
tcctgcagg cttctggta caccttacc aactacgcta tcagctgggt gcgacaggc      120
cctggacaag ggcttgagtg gatgggatgg gtcagcgctt acaatggtca cacaactat      180
gcacatgaag tccaggcag agtcaccatg accacagaca catccacgac cacagctac      240
atggagctga ggagcctgag atctgacgac acggccatgt attactgtgc gagagggggt      300
gtagtcgtgc cagttgtcc ccacttctac aacggtatgg acgtctgggg ccaagggacc      360
acggtcaccg tctcctca                                         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			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	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 739

<211> LENGTH: 336

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 739

```
gatattgtga tgactcagtc tccactctcc ctgcgggtca cccctggaga gccggctcc      60
atctcctgca ggtctagtca gagcctcctg catattaatg aataacaacta tttggattgg      120
tacctaaaga agccaggcgtc gtctccacag ctccctgatct atttgggttt taatcgggccc     180
tccgggtcc ctgacagggtt cagttggcgtt ggatcaggca cagattttac actgaaaatc     240
agcagagtgg aggctgagga ttttttttttattactgca 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:

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-continued

<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

cagggtcagc	tgggtgcagtc	tggagctgag	gtgaagaagc	ctggggcctc	agtgaaggtc	60
tcctgcaagg	cttctggta	caccttacc	aactacgcta	tcaagctgggt	gcgacaggcc	120
cctggacaag	ggcttgatgt	gatggatgg	gtcagcgctt	acaatggtca	cacaactat	180
gcacagaagc	tccagggcag	agtcaccatg	accacagaca	catccacgag	cacagctac	240
atggagctga	ggagcctgag	atctgacgac	acggccgtgt	attactgtgc	gagaggggt	300
gtagtcgtgc	cagttgctcc	ccacttctac	aacggatgg	acgtctgggg	gcaagggacc	360
acggtcaccc	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						

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

<210> SEQ ID NO 743
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 743

gatattgtga	tgactcagtc	tccactctcc	ctgccccgtca	cccctggaga	gccggcctcc	60
atctcctgca	ggtcttagtca	gagcctccctg	catattaatg	aataacaacta	tttggattgg	120
tacactgcaga	agccaggggca	gtctccacag	ctcctgatct	atttgggttc	taatcgggcc	180
tccgggggtcc	ctgacagggtt	cagtggcagt	ggatcaggca	cagattttac	actgaaaatc	240
agcagagtgaa	aggctgagga	tgttgggggtt	tattactgca	tgcaagctct	tcaaactccg	300
tggacgttcg	gccaaggggac	caaggtggaa	atcaaa			336

<210> SEQ ID NO 744
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<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						

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 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							
1				5			

<210> SEQ ID NO 746
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

-continued

<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

<210> SEQ ID NO 749
 <211> LENGTH: 3
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic
 <220> FEATURE:
 <221> 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:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: (1)...(9)
 <223> OTHER INFORMATION: Xaa = Any amino acid

<400> SEQUENCE: 750

-continued

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

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

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<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 Ser Leu Gly Thr Lys Thr
65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro
100 105 110

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
115 120 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
130 135 140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145 150 155 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
165 170 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
180 185 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
195 200 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
210 215 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225 230 235 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
245 250 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
260 265 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
275 280 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
290 295 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305 310 315 320

Leu Ser Leu Ser Leu Gly Lys
325

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<210> SEQ ID NO 753
<211> LENGTH: 327
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<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 Gln Phe
 165 170 175
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 180 185 190
 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
 195 200 205
 Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 210 215 220
 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
 225 230 235 240
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 245 250 255
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 260 265 270
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 275 280 285
 Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
 290 295 300
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 305 310 315 320
 Leu Ser Leu Ser Leu Gly Lys
 325

<210> SEQ ID NO 754

<211> LENGTH: 2076

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 754

atgggcaccc tcagctccag gcggtcttgg tggccgctgc cactgctgtc gctgctgtc 60
 ctgctcctgg gtccccgggg cgcccggtcg caggaggacg aggacggcga ctacgaggag 120
 ctgggtctag ctttgcttc cgaggaggac ggctggccg aagcacccga gcacggaaacc 180

428

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acagccacct tccaccgctg cgccaaggat ccgtggaggt tgcctggcac ctacgtggtg	240
gtgctgaagg aggagaccca cctctcgca gtcagagegca ctgcccgccg cctgcaggcc	300
caggctgccc gccggggata cctcaccaag atcctgeatg tcttccatgg ccttcttct	360
ggcttcctgg tgaagatgag tggcgacctg ctggagctgg ccttgaagtt gccccatgtc	420
gactacatcg aggaggactc ctctgtctt gcccagagca tcccgtggaa cctggagccg	480
attacccctc caeggtaecg ggcggtgaaa taccageccc ccgacggagg cagcctggtg	540
gaggtgtatc tcctagacac cagcatacag agtgaccacc gggaaatcga gggcagggtc	600
atggtcaccc acttcgagaa tgtgcccggag gaggacggga cccgcttcca cagacaggcc	660
agcaagtgtg acagtcatgg caccacccctg gcaggggtgg tcagcggccg ggatgcccgc	720
gtggccaagg gtgccagcat ggcgagcctg cgcgtgetca actgccaagg gaaggccacg	780
gttagcggca ccctcatagg cctggagttt attcgaaaa gccagctggt ccagectgtg	840
ggccactgg tgggtctgct gccccctggcg ggtgggtaca gccgcgtctt caacgcggcc	900
tgcccagcgc tggcgaggggc tggggctcgat ctggtcaccc ctgcccggcaa ctccgggac	960
gatgcctgccc tctactcccc agcctcagct cccgagggtca tcacagttgg ggccaccaat	1020
gcccaggacc agccgggtgac cctggggact ttggggacca actttggccg ctgtgtggac	1080
ctcttgcacc caggggagga catcattggt gcctccagcg actgcagcac ctgttttgt	1140
tcacagagtg ggacatcaca ggctgctgccc cacgtggctg gcattgcagc catgatgctg	1200
tctggccgagc cggagctcac cctggccggat ttgaggcaga gactgatcca cttctctgccc	1260
aaagatgtca tcaatgagcc ctgggttccct gaggaccagc gggtaactgac ccccaacctg	1320
gtggccgccc tgccccccag caccatggg gcagggttggc agctgttttgc caggactgt	1380
tggtcagcac actcggggcc tacacggatg gccacagcc tcgcccgtcg cgccccagat	1440
gaggagctgc tgagctgctc cagtttctcc aggagtggaa agcggcgcccc cgagcgcatt	1500
gaggcccaag gggcaagct ggtctgcccgg gcccacaacg cttttgggggg tgaggggtgc	1560
tacgcccattt ccagggtgtcg cctgctaccc caggccaaact gcagcgttcca cacagcttcca	1620
ccagctgagg ccagcatggg gaccctgtc cactgcacc accagggcca cgtcctcaca	1680
ggctgcagct cccactggga ggtggaggac ctggcaccc acaagccccc tggctgagg	1740
ccacgaggctc agcccaacca gtgcgtggcc cacaggagg ccagcatcca cgttctctgc	1800
tgccatgccc caggtctggaa atgcaaagtc aaggagcatg gaatcccccc ccctcaggag	1860
caggtgaccg tggcctgctggaa ggagggtgg accctgactg gctgcagtc cctccctggg	1920
acctccccacg tcctggggcc ctacgcgttca gacaacacgt gtgtagtcag gagccgggac	1980
gtcagacta caggcagcac cagcgaagag gccgtgacag ccgttgcctt ctgtgcggg	2040
agccggcacc tggcgccaggc ctcccaaggag ctcccaag	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									10			15			

Leu	Leu	Leu	Leu	Leu	Leu	Gly	Pro	Ala	Gly	Ala	Arg	Ala	Gln	Glu
													30	
20									25					

Asp Glu Asp Gly Asp Tyr Glu Glu Leu Val Leu Ala Leu Arg Ser Glu

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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
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
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
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
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 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
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

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-continued

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 Gly Lys Leu Val Cys Arg Ala His
 500 505 510
 Asn Ala Phe Gly Gly Glu Gly 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
 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

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130	135	140
Glu Asp Ser Ser Val Phe Ala Gln Ser Ile Pro Trp Asn Leu Glu Arg		
145	150	155
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
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
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
Ser Ala Glu Pro Glu Leu Thr Leu Ala Glu Leu Arg Gln Arg Leu Ile		
405	410	415
His Phe Ser Ala 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 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 Gly 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		

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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 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

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

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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 Gln Leu Leu Cys Arg Thr Val Trp			
450	455	460	
Ser Ala His Ser Gly Pro Thr Arg 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 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	
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	

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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 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

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

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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			
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

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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

Gln Gly Leu Ser Pro Trp Tyr Ala Glu Lys Cys Ser Ser Thr Leu Ala
340 345 350

Thr Ser Tyr Ser Ser Gly Asp Tyr Thr Asp Gln Arg Ile Thr Ser Ala
355 360 365

Asp Leu His Asn Asp Cys Thr Glu Thr His Thr Gly Thr Ser Ala Ser
370 375 380

Ala Pro Leu Ala Ala Gly Ile Phe Ala Leu Ala Leu Glu Ala Asn Pro
385 390 395 400

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

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465	470	475	480
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

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 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			

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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		
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	480
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	

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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
 545 550 555 560
 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
 625 630 635 640
 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 Gly Thr Glu Leu
 705 710 715 720
 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
 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

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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
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
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 Thr Ala Ala Gly Asn Phe Arg Asp		
305	310	315
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
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 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
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

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Asn Ala Phe Gly Gly Glu Gly 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 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
 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

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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
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
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
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
Ala Arg Cys Ala Pro Gly Glu Leu Leu Ser Cys Ser Ser Phe Ser		
485	490	495
Arg Ser Gly 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
Thr Pro Ala Ala Arg Thr Ser Leu Glu Thr His Ala His Cys His Gln		
545	550	555
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

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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 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 Glu Asp Ser Ser Pro Asp Gly Ser
 165 170 175

Ser Gln Val Glu Val Tyr 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

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 Pro Leu

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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 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 Arg Gly
 485 490 495

Asp Arg Ile Glu Ala Ile Gly Gln Gln Val Cys Lys Ala Leu Asn
 500 505 510

Ala Phe 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
 645 650 655

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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:
a) a heavy chain complementarity determining region 1 (HCDR1) comprising an amino acid sequence that is at least 95% identical to SEQ ID NO: 76; 15
b) a heavy chain complementarity determining region 2 (HCDR2) comprising an amino acid sequence that is at least 95% identical to SEQ ID NO: 78; 20
c) a heavy chain complementarity determining region 3 (HCDR3) comprising an amino acid sequence that is at least 95% identical to SEQ ID NO: 80;
d) a light chain complementarity determining region 1 (LCDR1) comprising an amino acid sequence that is at least 95% identical to SEQ ID NO: 84; 25
e) a light chain complementarity determining region 2 (LCDR2) comprising an amino acid sequence that is at least 95% identical to SEQ ID NO: 86; and 30
f) a light chain complementarity determining region 3 (LCDR3) comprising an amino acid sequence that is at least 95% identical to SEQ ID NO: 88.

2. The antibody or antigen-binding fragment of an antibody of claim 1, wherein the antibody or antigen-binding fragment of the antibody binds an epitope comprising amino acid residue 238 of hPCSK9 (SEQ ID NO:755).

3. The antibody or antigen-binding fragment of an antibody of claim 1, wherein the antibody or antigen-binding fragment of the antibody binds a human PCSK9 with GOF mutation D374Y ("hPCSK9(D374Y)").

4. An antibody or antigen-binding fragment of an antibody that specifically binds hPCSK9, comprising a heavy chain variable region comprising an amino acid sequence that is at least 95% identical to SEQ ID NO:90; and a light chain variable region comprising an amino acid sequence that is at least 95% identical to SEQ ID NO:92. 45

5. The antibody or antigen-binding fragment of an antibody of claim 4, wherein the antibody or antigen-binding fragment of the antibody binds an epitope comprising amino acid residue 238 of hPCSK9 (SEQ ID NO:755). 50

6. The antibody or antigen-binding fragment of an antibody of claim 4, wherein the antibody or antigen-binding fragment of the antibody binds a human PCSK9 with GOF mutation D374Y ("hPCSK9(D374Y)"). 55

7. An antibody or antigen-binding fragment of an antibody that specifically binds hPCSK9, comprising:
a) a heavy chain complementarity determining region 1 (HCDR1) comprising an amino acid sequence that is at least 98% identical to SEQ ID NO: 76; 60
b) a heavy chain complementarity determining region 2 (HCDR2) comprising an amino acid sequence that is at least 98% identical to SEQ ID NO: 78;
c) a heavy chain complementarity determining region 3 (HCDR3) comprising an amino acid sequence that is at least 98% identical to SEQ ID NO: 80; 65

(LCDR1) comprising an amino acid sequence that is at least 98% identical to SEQ ID NO: 84;

e) a light chain complementarity determining region 2 (LCDR2) comprising an amino acid sequence that is at least 98% identical to SEQ ID NO: 86; and

f) a light chain complementarity determining region 3 (LCDR3) comprising an amino acid sequence that is at least 98% identical to SEQ ID NO: 88.

8. The antibody or antigen-binding fragment of an antibody of claim 7, wherein the antibody or antigen-binding fragment of the antibody binds an epitope comprising amino acid residue 238 of hPCSK9 (SEQ ID NO:755).

9. The antibody or antigen-binding fragment of an antibody of claim 7, wherein the antibody or antigen-binding fragment of the antibody binds a human PCSK9 with GOF mutation D374Y ("hPCSK9(D374Y)").

10. An antibody or antigen-binding fragment of an antibody that specifically binds hPCSK9, comprising a heavy chain variable region comprising an amino acid sequence that is at least 98% identical to SEQ ID NO:90; and a light chain variable region comprising an amino acid sequence that is at least 98% identical to SEQ ID NO:92.

11. The antibody or antigen-binding fragment of an antibody of claim 10, wherein the antibody or antigen-binding fragment of the antibody binds an epitope comprising amino acid residue 238 of hPCSK9 (SEQ ID NO:755).

12. The antibody or antigen-binding fragment of an antibody of claim 10, wherein the antibody or antigen-binding fragment of the antibody binds a human PCSK9 with GOF mutation D374Y ("hPCSK9(D374Y)").

13. An antibody or antigen-binding fragment of an antibody that specifically binds hPCSK9, comprising:
a) a heavy chain complementarity determining region 1 (HCDR1) comprising an amino acid sequence that is at least 99% identical to SEQ ID NO: 76;
b) a heavy chain complementarity determining region 2 (HCDR2) comprising an amino acid sequence that is at least 99% identical to SEQ ID NO: 78;
c) a heavy chain complementarity determining region 3 (HCDR3) comprising an amino acid sequence that is at least 99% identical to SEQ ID NO: 80;
d) a light chain complementarity determining region 1 (LCDR1) comprising an amino acid sequence that is at least 99% identical to SEQ ID NO: 84;
e) a light chain complementarity determining region 2 (LCDR2) comprising an amino acid sequence that is at least 99% identical to SEQ ID NO: 86; and
f) a light chain complementarity determining region 3 (LCDR3) comprising an amino acid sequence that is at least 99% identical to SEQ ID NO: 88.

14. The antibody or antigen-binding fragment of an antibody of claim 13, wherein the antibody or antigen-binding fragment of the antibody binds an epitope comprising amino acid residue 238 of hPCSK9 (SEQ ID NO:755).

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15. The antibody or antigen-binding fragment of an antibody of claim **13**, wherein the antibody or antigen-binding fragment of the antibody binds a human PCSK9 with GOF mutation D374Y (“hPCSK9(D374Y)”).

16. An antibody or antigen-binding fragment of an antibody that specifically binds hPCSK9, comprising a heavy chain variable region comprising an amino acid sequence that is at least 99% identical to SEQ ID NO:90; and a light chain variable region comprising an amino acid sequence that is at least 99% identical to SEQ ID NO:92. ⁵

17. The antibody or antigen-binding fragment of an antibody of claim **16**, wherein the antibody or antigen-binding fragment of the antibody binds an epitope comprising amino acid residue 238 of hPCSK9 (SEQ ID NO:755). ¹⁰

18. The antibody or antigen-binding fragment of an antibody of claim **16**, wherein the antibody or antigen-binding fragment of the antibody binds a human PCSK9 with GOF mutation D374Y (“hPCSK9(D374Y)”). ¹⁵

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