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(54) **Title:**
HUMAN ANTIBODIES TO HUMAN DELTA LIKE LIGAND 4

(57) **Abstract:**

HUMAN ANTIBODIES TO HUMAN DELTA LIKE LIGAND 4 Abstract An isolated human antibody or a fragment of a human antibody which specifically binds to human delta-like ligand 4 (hDll4) and blocks hDll4 binding to a Notch receptor. The human anti hDll4 antibody or antibody fragment binds hDll4 with an affinity of [err] 500 pM, as measured by surface plasmon resonance.

HUMAN ANTIBODIES TO HUMAN DELTA LIKE LIGAND 4

Abstract

An isolated human antibody or a fragment of a human antibody which specifically binds to human delta-like ligand 4 (hDll4) and blocks hDll4 binding to a Notch receptor. The human anti-hDll4 antibody or antibody fragment binds hDll4 with an affinity of ≤ 500 pM, as measured by surface plasmon resonance.

HUMAN ANTIBODIES TO HUMAN DELTA LIKE LIGAND 4

BACKGROUND

[0001] The Notch-signaling pathway is a system for cell-to-cell communication used by a wide range of eukaryotes for many biological processes, such as differentiation, proliferation, and homeostasis. Delta like 4 (Dl4) or delta-like ligand 4 (Dll4) (hereinafter "Dll4") is a member of the Delta family of Notch ligands which exhibits highly selective expression by vascular endothelium (Shutter et al. (2000) Genes Develop. 14:1313-1318). Dll4 is a ligand for Notch receptors, including Notch1 and Notch 4. The nucleic acid and amino acid sequences for human Dll4 are shown in SEQ ID NO:1-2, respectively.

[0002] Methods to produce antibodies useful as human therapeutics include generation of chimeric antibodies and humanized antibodies (see, for example, U.S. 6,949,245). See, for example, WO 94/02602 (Abgenix) and U.S. 6,596,541 (Regeneron Pharmaceuticals) describing methods of generating nonhuman transgenic mice capable of producing human antibodies.

[0003] Japanese patent application 2003/047470A2 (Asahi Kasei Kogyo) describes antibodies to the extracellular portion of human Notch ligand protein.

BRIEF SUMMARY OF THE INVENTION

[0004] In a first aspect, the invention provides human antibodies, preferably recombinant human antibodies, that specifically bind human delta-like ligand 4 (hDll4). These antibodies are characterized by binding to hDll4 with high affinity and by the ability to neutralize Dll4 activity. The antibodies of the invention are capable of blocking Dll4 binding to its Notch receptor(s), and thus inhibit signaling by Dll4. The antibodies can be full-length (for example, an IgG1 or IgG4 antibody) or may comprise only an antigen-binding portion (for example, a Fab, $F(ab')_2$ or scFv fragment), and may be modified to effect functionality, e.g., to eliminate residual effector functions (Glu which eliminates residual effector functions (Reddy et al. (2000) J. Immunol. 164:1925-1933).

[0005] In one embodiment, the antibody of the invention comprises a heavy chain variable region (HCVR) selected from the group consisting of SEQ ID NO:4, 20, 36, 52, 68, 84, 100, 116, 132, 148, 164, 180, 196, 212, 228, 244, 260, 276, 292, 308, 324, 340, 356, 372, 397, 413, 429, 445, 461, 477, 493, 509, 525, 541, 557, 573, 589, 605, 621, 637, 653, 669, 685, 701, 717, 733, 749, 765, 781, 797, 813, 893, 897, 901, 905, 909, 913, 917, 921, 925, 935, 939, 943, and 947 or a substantially identical sequence thereof. In a preferred embodiment, the HCVR is the amino acid sequence of SEQ ID NO:429 or 901.

[0006] In one embodiment, the antibody of the invention comprises a light chain variable region (LCVR) selected from the group consisting of SEQ ID NO:12, 28, 44, 60, 76, 92, 108, 124, 140, 156, 172, 188, 204, 220, 236, 252, 268, 284, 300, 316, 332, 348, 364, 380, 405, 421, 437, 453, 469, 485, 501, 517, 533, 549, 565, 581, 597, 613, 629, 645, 661, 677, 693, 709, 725, 741, 757, 773, 789, 805, 821, 895, 899, 903, 907, 911, 915, 919, 923, 927, 937, 941, 945, and 949 or a substantially identical sequence thereof. In a preferred embodiment, the LCVR is the amino acid sequence of SEQ ID NO:437 or 903.

[0007] In one embodiment, the antibody of the invention comprises a HCVR selected from the group consisting of SEQ ID NO: 4, 20, 36, 52, 68, 84, 100, 116, 132, 148, 164, 180, 196, 212, 228, 244, 260, 276, 292, 308, 324, 340, 356, 372, 397, 413, 429, 445, 461, 477, 493, 509, 525, 541, 557, 573, 589, 605, 621, 637, 653, 669, 685, 701, 717, 733, 749, 765, 781, 797, 813, 893, 897, 901, 905, 909, 913, 917, 921, 925, 935, 939, 943, and 947 or a substantially identical sequence thereof, and a LCVR selected from the group consisting of SEQ ID NO:12, 28, 44, 60, 76, 92, 108, 124, 140, 156, 172, 188, 204, 220, 236, 252, 268, 284, 300, 316, 332, 348, 364, 380, 405, 421, 437, 453, 469, 485, 501, 517, 533, 549, 565, 581, 597, 613, 629, 645, 661, 677, 693, 709, 725, 741, 757, 773, 789, 805, 821, 895, 899, 903, 907, 911, 915, 919, 923, 927, 937, 941, 945, and 949 or a substantially identical sequence thereof. In a preferred embodiment, the HCVR/LCVR are the amino acid sequence pairs SEQ ID NO:429/437or 901/903.

[0008] In one embodiment, the invention features a human antibody or antibody fragment comprising a heavy chain complementary determining region 1 (CDR1) selected from the group consisting of SEQ ID NO:6, 22, 38, 54, 70, 86, 102, 118, 134, 150, 166, 182, 198, 214, 230, 246, 262, 278 294, 310, 326, 342, 358, 374, 399, 415, 431, 447, 463, 479, 495, 511, 527, 543, 559, 575, 591, 607, 623, 639, 655, 671, 687, 703, 711119, 735, 751, 767, 783, 799, 815, 831, 847, 863 and 879, or a substantially identical sequence thereof.

[0009] In one embodiment, the invention features a human antibody or antibody fragment comprising a heavy chain CDR2 selected from the group consisting of SEQ ID NO:8, 24, 40, 56, 72, 88, 104, 120, 136, 152, 168, 184, 200, 216, 232, 248, 264, 280, 296, 312, 328, 344, 360, 376, 401, 417, 433, 449, 465, 481, 497, 513, 529, 545, 561, 577, 593, 609, 625, 641, 657, 673, 689, 705, 721, 737, 753, 769, 785, 801, 817, 833, 849, 865 and 881, or a substantially identical sequence thereof.

[0010] In one embodiment, the invention features a human antibody or antibody fragment comprising a heavy chain CDR3 selected from the group consisting of SEQ ID NO:10, 26, 42, 58, 74, 90, 106, 122, 138, 154, 170, 186, 202, 218, 234, 250, 266, 282, 298, 314, 330, 346, 362, 378, 403, 419, 435, 451, 467, 483, 499, 515, 531, 547, 563, 579, 595, 611, 627, 643, 659, 675, 691, 707, 723, 739, 755, 771, 787, 803, 819, 835, 851, 867 and 883, or a substantially identical sequence thereof.

[0011] In one embodiment, the invention features a human antibody or antibody fragment comprising a heavy chain CDR1 selected from the group consisting of SEQ ID NO: 6, 22, 38, 54, 70, 86, 102, 118, 134, 150, 166, 182, 198, 214, 230, 246, 262, 278 294, 310, 326, 342, 358, 374, 399, 415, 431, 447, 463, 479, 495, 511, 527, 543, 559, 575, 591, 607, 623, 639, 655, 671, 687, 703, 711119, 735, 751, 767, 783, 799, 815, 831, 847, 863 and 879, or a substantially identical sequence thereof; a heavy chain CDR2 selected from the group consisting of SEQ ID

NO: 8, 24, 40, 56, 72, 88, 104, 120, 136, 152, 168, 184, 200, 216, 232, 248, 264, 280, 296, 312, 328, 344, 360, 376, 401, 417, 433, 449, 465, 481, 497, 513, 529, 545, 561, 577, 593, 609, 625, 641, 657, 673, 689, 705, 721, 737, 753, 769, 785, 801, 817, 833, 849, 865 and 881, or a substantially identical sequence thereof; and a heavy chain CDR3 selected from the group consisting of SEQ ID NO: 10, 26, 42, 58, 74, 90, 106, 122, 138, 154, 170, 186, 202, 218, 234, 250, 266, 282, 298, 314, 330, 346, 362, 378, 403, 419, 435, 451, 467, 483, 499, 515, 531, 547, 563, 579, 595, 611, 627, 643, 659, 675, 691, 707, 723, 739, 755, 771, 787, 803, 819, 835, 851, 867 and 883, or a substantially identical sequence thereof. In a preferred embodiment, the antibody or antibody fragment comprises heavy chain CDR1, CDR2 and CDR3 selected from the group consisting of SEQ ID NO:431/433/435; 374/376/378; 783/785/787; and 799/801/803.

[0012] In one embodiment, the invention features a human antibody or antibody fragment comprising a light chain CDR1 selected from the group consisting of SEQ ID NO: 14, 30, 46, 62, 78, 94, 110, 126, 142, 158, 174, 190, 206, 222, 238, 254, 270, 286, 302, 318, 334, 350, 366, 382, 407, 423, 439, 455, 471, 487, 503, 519, 535, 551, 567, 583, 599, 615, 631, 647, 663, 679, 695, 711, 727, 743, 759, 775, 791, 807, 823, 839, 855, 871 and 887, or a substantially identical sequence thereof.

[0013] In one embodiment, the invention features a human antibody or antibody fragment comprising a light chain CDR2 selected from the group consisting of SEQ ID NO:16, 32, 48, 64, 80, 96, 112, 128, 144, 160, 176, 192, 208, 224, 240, 256, 272, 288, 304, 320, 336, 352, 368, 384, 409. 425, 441, 457, 473, 489, 505, 521, 537, 553, 569, 585, 601, 617, 633, 649, 665, 681, 697, 713, 729, 745, 761, 777, 793, 809, 825, 841, 857, 873 and 889, or a substantially identical sequence thereof.

[0014] In one embodiment, the invention features a human antibody or antibody fragment comprising a light chain CDR3 selected from the group consisting of SEQ ID NO:18, 34, 50, 66, 82, 98, 11, 130, 146, 162, 178, 194, 210, 226, 242, 258, 274, 290, 306, 322, 338, 354, 370, 386, 411, 427, 443, 459, 475, 491, 507, 523, 539, 555, 571, 587, 603, 619, 635, 651, 667, 683, 699, 715, 731, 747, 763, 779, 795, 811, 827, 843, 859, 875 and 891, or a substantially identical sequence thereof.

[0015] In one embodiment, the invention features a human antibody or antibody fragment comprising a light chain CDR1 selected from the group consisting of SEQ ID NO: 14, 30, 46, 62, 78, 94, 110, 126, 142, 158, 174, 190, 206, 222, 238, 254, 270, 286, 302, 318, 334, 350, 366, 382, 407, 423, 439, 455, 471, 487, 503, 519, 535, 551, 567, 583, 599, 615, 631, 647, 663, 679, 695, 711, 727, 743, 759, 775, 791, 807, 823, 839, 855, 871 and 887, or a substantially identical sequence thereof; a light chain CDR2 selected from the group consisting of SEQ ID NO: 16, 32, 48, 64, 80, 96, 112, 128, 144, 160, 176, 192, 208, 224, 240, 256, 272, 288, 304, 320, 336, 352, 368, 384, 409. 425, 441, 457, 473, 489, 505, 521, 537, 553, 569, 585, 601, 617, 633, 649, 665, 681, 697, 713, 729, 745, 761, 777, 793, 809, 825, 841, 857, 873 and 889, or a substantially identical sequence thereof; and a light chain CDR3 selected from the group consisting of SEQ

ID NO: 18, 34, 50, 66, 82, 98, 11, 130, 146, 162, 178, 194, 210, 226, 242, 258, 274, 290, 306, 322, 338, 354, 370, 386, 411, 427, 443, 459, 475, 491, 507, 523, 539, 555, 571, 587, 603, 619, 635, 651, 667, 683, 699, 715, 731, 747, 763, 779, 795, 811, 827, 843, 859, 875 and 891, or a substantially identical sequence thereof. In a preferred embodiment, the antibody or antibody fragment comprises the light chain CDR1, CDR2 and CDR3 selected from the group consisting of SEQ ID NO:439/441/443; 382/384/386; 791/793/795; and 807/809/811.

[0016] In a second aspect, the invention provides nucleic acid molecules encoding the antibodies, or antigen-binding portions, of the invention. Recombinant expression vectors carrying the antibody-encoding 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 making the antibodies of the invention by culturing the host cells of the invention.

[0017] In one embodiment, the antibody of the invention comprises a HCVR encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO:3, 19, 35, 51, 67, 83, 99, 115, 131, 147, 163, 179, 195, 211, 227, 243, 259, 275, 291, 307, 323, 339, 355, 371, 396, 412, 428, 444, 460, 476, 492, 508, 524, 540, 556, 572, 588, 604, 620, 636, 652, 668, 684, 700, 716, 732, 748, 764, 780, 796, 812, 892, 896, 900, 904, 908, 912, 916, 920, 924, 934, 938, 942, and 946 or a substantially similar sequence having at least 95% homology thereof.

[0018] In one embodiment, the antibody of the invention comprises a LCVR encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO:11, 27, 43, 59, 75, 91, 107, 123, 139, 155, 171, 187, 203, 219, 235, 251, 267, 283, 299, 315, 331, 347, 363, 379, 404, 420, 436, 452, 468, 484, 500, 516, 532, 548, 564, 580, 596, 612, 628, 644, 660, 676, 692, 708, 724, 740, 756, 772, 788, 804, 820, 894, 898, 902, 906, 910, 914, 918, 922, 926, 936, 940, 944, and 948 or a substantially similar sequence having at least 95% homology thereof.

[0019] In one embodiment, the antibody of the invention comprises a HCVR encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 3, 19, 35, 51, 67, 83, 99, 115, 131, 147, 163, 179, 195, 211, 227, 243, 259, 275, 291, 307, 323, 339, 355, 371, 396, 412, 428, 444, 460, 476, 492, 508, 524, 540, 556, 572, 588, 604, 620, 636, 652, 668, 684, 700, 716, 732, 748, 764, 780, 796, 812, 892, 896, 900, 904, 908, 912, 916, 920, 924, 934, 938, 942, and 946 or a substantially similar sequence having at least 95% homology thereof, and a LCVR encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 11, 27, 43, 59, 75, 91, 107, 123, 139, 155, 171, 187, 203, 219, 235, 251, 267, 283, 299, 315, 331, 347, 363, 379, 404, 420, 436, 452, 468, 484, 500, 516, 532, 548, 564, 580, 596, 612, 628, 644, 660, 676, 692, 708, 724, 740, 756, 772, 788, 804, 820, 894, 898, 902, 906, 910, 914, 918, 922, 926, 936, 940, 944, and 948 or a substantially similar sequence having at least 95% homology thereof.

[0020] In one embodiment, the invention features a human antibody or antibody fragment comprising a heavy chain CDR1 encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO:5, 21, 37, 53, 69, 85, 101, 117, 133, 149, 165, 181, 197, 213, 229, 245, 261, 277, 293, 309, 325, 341, 357, 373, 398, 414, 430, 446, 462, 478, 494, 510, 526, 542, 558, 574, 590, 606, 622, 638, 654, 670, 686, 702, 718, 734, 750, 766, 782, 798, 814, 830, 846, 862 and 878, or a substantially similar sequence having at least 95% homology thereof.

[0021] In one embodiment, the invention features a human antibody or antibody fragment comprising a heavy chain CDR2 encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO:7, 23, 39, 55, 71, 87, 103, 119, 135, 151, 167, 183, 100, 215, 231, 247, 263, 279, 295, 311, 327, 343, 359, 375, 400, 416, 432, 448, 464, 480, 496, 512, 528, 544, 560, 576, 592, 608, 624, 640, 656, 672, 688, 704, 720, 736, 752, 768, 784, 800, 816, 832, 848, 864 and 880, or a substantially similar sequence having at least 95% homology thereof.

[0022] In one embodiment, the invention features a human antibody or antibody fragment comprising a heavy chain CDR3 encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO:9, 25, 41, 57, 73, 89, 105, 121, 137, 153, 169, 185, 201, 217, 233, 249, 265, 281, 297, 313, 329, 345, 361, 377, 402, 418, 434, 450, 466, 482, 498, 514, 530, 546, 562, 578, 594, 610, 626, 642, 658, 674, 690, 706, 722, 738, 754, 770, 786, 802, 818, 834, 850, 866 and 882, or a substantially similar sequence having at least 95% homology thereof.

[0023] In one embodiment, the invention features a human antibody or antibody fragment comprising a heavy chain CDR1 encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO:5, 21, 37, 53, 69, 85, 101, 117, 133, 149, 165, 181, 197, 213, 229, 245, 261, 277, 293, 309, 325, 341, 357, 373, 398, 414, 430, 446, 462, 478, 494, 510, 526, 542, 558, 574, 590, 606, 622, 638, 654, 670, 686, 702, 718, 734, 750, 766, 782, 798, 814, 830, 846, 862 and 878, or a substantially similar sequence having at least 95% homology thereof; a heavy chain CDR2 encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO:7, 23, 39, 55, 71, 87, 103, 119, 135, 151, 167, 183, 100, 215, 231, 247, 263, 279, 295, 311, 327, 343, 359, 375, 400, 416, 432, 448, 464, 480, 496, 512, 528, 544, 560, 576, 592, 608, 624, 640, 656, 672, 688, 704, 720, 736, 752, 768, 784, 800, 816, 832, 848, 864 and 880, or a substantially similar sequence having at least 95% homology thereof; and a heavy chain CDR3 encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 9, 25, 41, 57, 73, 89, 105, 121, 137, 153, 169, 185, 201, 217, 233, 249, 265, 281, 297, 313, 329, 345, 361, 377, 402, 418, 434, 450, 466, 482, 498, 514, 530, 546, 562, 578, 594, 610, 626, 642, 658, 674, 690, 706, 722, 738, 754, 770, 786, 802, 818, 834, 850, 866 and 882, or a substantially similar sequence having at least 95% homology thereof. In a preferred embodiment, the antibody or antibody fragment comprises heavy chain CDR1, CDR2 and CDR3 encoded b a nucleic acid sequence selected from the group consisting of SEQ ID NO:430/432/434; 373/375/377; 782/784/786; and 798/800/802.

[0024] In one embodiment, the invention features a human antibody or antibody fragment comprising a light chain CDR1 encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO:13, 29, 45, 61, 77, 93, 109, 125, 141, 157, 173, 189, 205, 221, 237, 253, 269, 285, 301, 317, 333, 349, 365, 381, 406, 422, 438, 454, 470, 486, 502, 518, 534, 550, 566, 582, 598, 614, 630, 646, 662, 678, 694, 710, 726, 742, 758, 774, 790, 806, 822, 838, 854, 870 and 886, or a substantially similar sequence having at least 95% homology thereof.

[0025] In one embodiment, the invention features a human antibody or antibody fragment comprising a light chain CDR2 encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO:15, 31, 47, 63, 79, 95, 111, 127, 143, 159, 175, 191, 207, 223, 239, 255, 271, 287, 303, 319, 335, 351, 367, 383, 408, 424, 440, 456, 472, 488, 504, 520, 536, 552, 568, 584, 600, 616, 632, 648, 664, 680, 696, 712, 728, 744, 760, 776, 792, 808, 824, 840, 856, 872, and 888, or a substantially similar sequence having at least 95% homology thereof.

[0026] In one embodiment, the invention features a human antibody or antibody fragment comprising a light chain CDR3 encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO:17, 33, 49, 65, 81, 97, 113, 129, 145, 161, 177, 193, 209, 225, 241, 257, 273, 289, 305, 321, 337, 353, 369, 385, 410, 426, 442, 458, 474, 490, 506, 522, 538, 554, 570, 586, 602, 618, 634, 650, 666, 682, 698, 714, 730, 746, 762, 778, 794, 810, 826, 842, 858, 874 and 890, or a substantially similar sequence having at least 95% homology thereof.

[0027] In one embodiment, the invention features a human antibody or antibody fragment comprising a light chain CDR1 encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO:13, 29, 45, 61, 77, 93, 109, 125, 141, 157, 173, 189, 205, 221, 237, 253, 269, 285, 301, 317, 333, 349, 365, 381, 406, 422, 438, 454, 470, 486, 502, 518, 534, 550, 566, 582, 598, 614, 630, 646, 662, 678, 694, 710, 726, 742, 758, 774, 790, 806, 822, 838, 854, 870 and 886, or a substantially similar sequence having at least 95% homology thereof; a light chain CDR2 encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 15, 31, 47, 63, 79, 95, 111, 127, 143, 159, 175, 191, 207, 223, 239, 255, 271, 287, 303, 319, 335, 351, 367, 383, 408, 424, 440, 456, 472, 488, 504, 520, 536, 552, 568, 584, 600, 616, 632, 648, 664, 680, 696, 712, 728, 744, 760, 776, 792, 808, 824, 840, 856, 872, and 888, or a substantially similar sequence having at least 95% homology thereof; and a light chain CDR3 encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 17, 33, 49, 65, 81, 97, 113, 129, 145, 161, 177, 193, 209, 225, 241, 257, 273, 289, 305, 321, 337, 353, 369, 385, 410, 426, 442, 458, 474, 490, 506, 522, 538, 554, 570, 586, 602, 618, 634, 650, 666, 682, 698, 714, 730, 746, 762, 778, 794, 810, 826, 842, 858, 874 and 890, or a substantially similar sequence having at least 95% homology thereof. In a preferred embodiment, the antibody or antibody fragment comprises the light chain CDR1, CDR2 and CDR3 encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO:438/440/442; 381/383/385; 790/792/794; and 806/808/810.

[0028] In a third aspect, the invention features an isolated antibody or antibody fragment that specifically binds hDll4, comprising a CDR 1, 2 and 3 selected from the group consisting of (a) a heavy chain CDR1 region comprising an amino acid sequence of the formula $X^1 - X^2 - X^3 - X^4 - X^5 - X^6 - X^7 - X^8$ (SEQ ID NO:928), wherein X^1 is Gly; X^2 is Phe or Tyr; X^3 is Thr; X^4 is Phe; X^5 is Ser, Thr or Asn; X^6 is Ser, Asn or Tyr; X^7 is Tyr or Phe; and X^8 is Gly or Ala; (b) a heavy chain

CDR2 region comprising an amino acid sequence of the formula . $X^1 - X^2 - X^3 - X^4 - X^5 - X^6 - X^7 - X^8$ (SEQ ID NO:929), wherein X^1 is Ile or Leu; X^2 is Trp or Ser; X^3 is Tyr, Ala or Gly; X^4 is Asp, Ser or Tyr; X^5 is Gly or Asp; X^6 is Ser, Gly, Thr or Val; X^7 is Asn or Asp; and X^8 is Lys or Arg; (c) a heavy chain CDR3 region comprising an amino acid sequence of the formula $X^1 - X^2 - X^3 - X^4 - X^5 - X^6 - X^7 - X^8 - X^9 - X^{10} - X^{11} - X^{12} - X^{13} - X^{14} - X^{15} - X^{16}$ (SEQ ID NO:930), wherein X^1 is Ala or Ser; X^2 is Arg or Lys; X^3 is Asp or Tyr; X^4 is Ser, Gly or His; X^5 is Asp, Ala or Trp; X^6 is Asn, or Phe; X^7 is Tyr, Arg or Lys; X^8 is His or Ser; X^9 is Gly or Trp; X^{10} is Tyr or Phe; X^{11} is Glu or Asp; X^{12} is Gly, His or Pro; X^{13} is Tyr, Trp or absent; X^{14} is Phe or absent; X^{15} is Asp or absent; and X^{16} is Pro or absent.

[0029] In a preferred embodiment, the antibody or antibody fragment comprises heavy chain CDR 1, 2 and 3 selected from the group consisting of (a) a heavy chain CDR1 region comprising an amino acid sequence of the formula $X^1 - X^2 - X^3 - X^4 - X^5 - X^6 - X^7 - X^8$ (SEQ ID NO:928), 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 Phe; and X^8 is Gly or Ala; (b) a heavy chain CDR2 region comprising an amino acid sequence of the formula $X^1 - X^2 - X^3 - X^4 - X^5 - X^6 - X^7 - X^8$ (SEQ ID NO:929), wherein X^1 is Ile or Leu; X^2 is Trp or Ser; X^3 is Tyr or Gly; X^4 is Asp or Ser; X^5 is Gly; X^6 is Ser, Thr or Val; X^7 is Asn or Asp; and X^8 is Lys or Arg; (c) a heavy chain CDR3 region comprising an amino acid sequence of the formula $X^1 - X^2 - X^3 - X^4 - X^5 - X^6 - X^7 - X^8 - X^9 - X^{10} - X^{11} - X^{12} - X^{13} - X^{14} - X^{15} - X^{16}$ (SEQ ID NO:930), wherein X^1 is Ala or Ser; X^2 is Arg or Lys; X^3 is Asp; X^4 is Gly or His; X^5 is Asp or Ala; X^6 is Phe; X^7 is Tyr or Arg; X^8 is Ser; X^9 is Gly; X^{10} is Tyr; X^{11} is Glu; X^{12} is Gly or His; X^{13} is Tyr or Trp; X^{14} is Phe or absent; X^{15} is Asp or absent; and X^{16} is Pro or absent.

[0030] In a further embodiment, the isolated antibody or antibody fragment further comprises (d) a light chain CDR1 region comprising an amino acid sequence of the formula $X^1 - X^2 - X^3 - X^4 - X^5 - X^6 - X^7$ (SEQ ID NO:931), wherein X^1 is Gln; X^2 is Ser; X^3 is Val; X^4 is Arg, Ser or Thr; X^5 is Ser or Gly; X^6 is Ser or Tyr; and X^7 is Tyr or absent; (e) a light chain CDR2 region comprising an amino acid sequence of the formula $X^1 - X^2 - X^3$ (SEQ ID NO:932), wherein X^1 is Gly or Asp; X^2 is Ala or Thr; and X^3 is Ser; and (f) a light chain CDR3 region comprising 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:933), wherein X^1 is Gln; X^2 is Gln or His; X^3 is Tyr, Arg or Ser; X^4 is Gly, Ser or Ala; X^5 is Ser, Asn or Phe; X^6 is Trp or Ser; X^7 is Pro; X^8 is Trp, Pro or Arg; and X^9 is Thr.

[0031] In a preferred embodiment, the isolated antibody or antibody fragment further comprises (d) a light chain CDR1 region comprising an amino acid sequence of the formula $X^1 - X^2 - X^3 - X^4 - X^5 - X^6 - X^7$ (SEQ ID NO:931), wherein X^1 is Gln; X^2 is Ser; X^3 is Val; X^4 is Arg or Ser; X^5 is Ser; X^6 is Ser or Tyr; and X^7 is Tyr or absent; (e) a light chain CDR2 region comprising an amino acid sequence of the formula $X^1 - X^2 - X^3$ (SEQ ID NO:932), wherein X^1 is Gly or Asp; X^2 is Ala or Thr; and X^3 is Ser; and (f) a light chain CDR3 region comprising 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:933), wherein X^1 is Gln; X^2 is Gln or His; X^3 is Tyr or Arg; X^4 is Gly or Ser; X^5 is Ser or Asn; X^6 is Trp or Ser; X^7

is Pro; X^8 is Pro or Arg; and X^9 is Thr.

[0032] In a fourth aspect, the invention features a fully human antibody or antibody fragment which binds hDll4 with an IC_{50} of less than about 10 nM, as measured in *in vitro* assay or ELISA-based Dll4 blocking assay (described below). In a preferred embodiment, the antibody of the invention exhibits an IC_{50} of about 500 pM or less. In an even more preferred embodiment, the antibody of the invention exhibits an IC_{50} of about 100 pM or less.

[0033] In one embodiment, the invention provides a fully human monoclonal antibody which specifically binds and inhibits human Dll4 and exhibits an IC_{50} of less than or equal to about 150 pM, 100 pM, 75 pM, or 50 pM, as measured by Notch-inducible luciferase bioassay with hDll4-Fc. As shown in the experimental section below, the anti-hDll4 antibodies of the invention do not cross-react with closely related delta proteins, such as hDll1 and hDll3.

[0034] In one embodiment, the invention provides an isolated human antibody, or an antigen-binding portion thereof, that binds hDll4 with a K_D of less than about 500 pM, preferably less than about 300 pM, even more preferably less than about 100 pM, less than about 50 pM, less than about 10 pM, as determined by surface plasmon resonance (BIACORE™), for example, using dimeric hDll4 (Table 2).

[0035] The invention encompasses anti-hDll4 antibodies having a modified glycosylation pattern. In some applications, modification to remove undesirable glycosylation sites may be useful, or an antibody lacking a fucose moiety present on the oligosaccharide chain, for example, to increase antibody dependent cellular cytotoxicity (ADCC) function (see Shield et al. (2002) JBC 277:26733). In other applications, modification of a galactosylation can be made in order to modify complement dependent cytotoxicity (CDC).

[0036] The invention includes anti-hDll4 antibodies which bind specific epitopes of hDll4 and are capable of blocking the biological activity of hDll4. The extracellular domain of Dll4 is composed of an N-terminal domain, a Delta/Serrate/Lag-2 (DSL) domain, and a tandem of eight epidermal growth factor (EGF)-like repeats. Generally, the EGF domains are recognized as occurring at about amino acid residues 218-251 (domain 1), 252-282 (domain 2), 284-322 (domain 3), 324-360 (domain 4), and 362-400 (domain 5), with the DSL domain at about amino acid residues 173-217 and the N-terminal domain at about amino acid residues 27-172 of hDll4 (SEQ ID NO:2).

[0037] In one embodiment, a blocking antibody of the invention binds within amino acids residues 27 to 524 of SEQ ID NO:2. In a more specific embodiment, a blocking antibody of the invention binds an epitope within the N-terminus-DSL domains 27-217 of SEQ ID NO:2; in an even more specific embodiment, the blocking antibody binds an epitope within about amino acid residues 27-172 (N-terminal domain) or 173-217 (DSL domain). In another embodiment, a blocking antibody of the invention binds the EGF-2 epitope within about amino acids residues 252-282 of SEQ ID NO:2.

[0038] In a fifth aspect, the invention features a composition comprising a recombinant human anti-human Dll4 antibody and an acceptable carrier. Further included in the invention are vectors and host cells comprising vectors which contain nucleic acid molecules encoding the human anti-hDll4 antibody of the invention, as well as methods of producing these novel antibodies, comprising growing a host cell comprising nucleic acid encoding the anti-hDll4 antibody of the invention or an antibody fragment, under conditions permitting production of the protein and recovering the protein so produced.

In a sixth aspect, the invention features methods for inhibiting hDll4 activity using an antibody, or antigen-binding portion thereof, of the invention. In one embodiment, the method comprises contacting hDll4 with the instant antibody or antigen-binding portion thereof, such that hDll4 is inhibited from binding to Notch receptor, for example Notch-1. In another embodiment, the method comprises administering an antibody or antibody fragment of the invention, to a human subject suffering from a disorder which is ameliorated by inhibition of Dll4 activity. The disorder treated is a disease or condition which is improved, ameliorated, inhibited or prevented by removal, inhibition or reduction of Dll4 activity, for example, pathological vascularization associated with tumor angiogenesis and cancer, immunodeficiency diseases, transplant rejection, or inflammation; and neurodegenerative conditions, e.g., associated with prion disease. The invention also provides for the use of an antibody or antigen-binding fragment of an antibody, as described above, in the manufacture of a medicament for use to attenuate or inhibit a Dll4-mediated disease or disorder in a human.

[0039] Other objects and advantages will become apparent from a review of the ensuing detailed description.

DETAILED DESCRIPTION

[0040] 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.

[0041] As used in this specification and the appended claims, the singular forms "a", "an", and "the" include plural references unless the context clearly dictates otherwise. Thus for example, a reference to "a method" includes one or more methods, and/or steps of the type described herein and/or which will become apparent to those persons skilled in the art upon reading this disclosure.

[0042] 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, the preferred methods and materials are now described.

Definitions

[0043] "Delta-like ligand 4", "Dll4", "hDll4" are used interchangeably to refer to the protein encoded by the nucleic acid sequence of SEQ ID NO:1 and the protein having the amino acid sequence of SEQ ID NO:2.

[0044] 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 (abbreviated herein as HCVR or VH) and a heavy chain constant region. The heavy chain constant region is comprised of three domains, CH1, CH2 and CH3. Each light chain is comprised of a light chain variable region (abbreviated herein as LCVR or VL) and a light chain constant region. The light chain constant region is comprised of one domain, CL. The VH and VL regions can be further subdivided into regions of hypervariability, termed complementary determining regions (CDR), interspersed with regions that are more conserved, termed framework regions (FR). Each VH and VL is composed of three CDRs and four FRs, arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4.

[0045] The term "high affinity" antibody refers to those antibodies having a binding affinity to hDll4 of at least 10^{-8} M; preferably 10^{-9} M; even more preferably 10^{-10} M, as measured by surface plasmon resonance, e.g., BIACORE™ or solution-affinity ELISA.

[0046] By the term "slow off rate" or "Koff" is meant an antibody that dissociates from hDll4 with a rate constant of $1 \times 10^{-3}\ s^{-1}$ or less, preferably $1 \times 10^{-4}\ s^{-1}$ or less, as determined by surface plasmon resonance, e.g., BIACORE™.

[0047] A "neutralizing" or "blocking" antibody, is intended to refer to an antibody whose binding to Dll4 results in inhibition of the biological activity of Dll4. This inhibition of the biological activity of Dll4 can be assessed by measuring one or more indicators of Dll4 biological activity. These indicators of Dll4 biological activity can be assessed by one or more of several standard *in vitro* or *in vivo* assays known in the art (see examples below). Preferably, the ability of an antibody to neutralize Dll4 activity is assessed by inhibition of Dll4 binding to a Notch receptor.

[0048] The term "antigen-binding portion" of an antibody (or simply "antibody portion" or "antibody fragment"), as used herein, refers to one or more fragments of an antibody that retain the ability to specifically bind to an antigen (e.g., hDll4). It has been shown that the antigen-binding function of an antibody can be performed by fragments of a full-length antibody. Examples of binding fragments encompassed within the term "antigen-binding portion" of an antibody include (i) a Fab fragment, a monovalent fragment consisting of the VL, VH, CL and CH1 domains; (ii) a $F(ab')_2$ fragment, a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region; (iii) a Fd fragment consisting of the VH and CH1 domains; (iv) a Fv fragment consisting of the VL and VH domains of a single arm of an antibody, (v) a dAb fragment (Ward et al. (1989) Nature 241:544-546), which consists of a VH domain;

and (vi) an isolated CDR. Furthermore, although the two domains of the Fv fragment, VL and VH, are coded for by separate genes, they can be joined, using recombinant methods, by a synthetic linker that enables them to be made as a single protein chain in which the VL and VH regions pair to form monovalent molecules (known as single chain Fv (scFv); see e.g., Bird et al. (1988) Science 242:423-426; and Huston et al. (1988) Proc. Natl. Acad. Sci. USA 85:5879-5883). Such single chain antibodies are also intended to be encompassed within the term "antigen-binding portion" of an antibody. Other forms of single chain antibodies, such as diabodies are also encompassed. Diabodies are bivalent, bispecific antibodies in which VH and VL domains are expressed on a single polypeptide chain, but using a linker that is too short to allow for pairing between the two domains on the same chain, thereby forcing the domains to pair with complementary domains of another chain and creating two antigen binding sites (see e.g., Holliger et al. (1993) Proc. Natl. Acad Sci. USA 90:6444-6448; Poljak et al. (1994) Structure 2:1121-1123).

[0049] Still further, an antibody or antigen-binding portion thereof may be part of a larger immunoadhesion molecule, formed by covalent or noncovalent association of the antibody or antibody portion with one or more other proteins or peptides. Examples of such immunoadhesion molecules include use of the streptavidin core region to make a tetrameric scFv molecule (Kipriyanov et al. (1995) Human Antibodies and Hybridomas 6:93-101) and use of a cysteine residue, a marker peptide and a C-terminal polyhistidine tag to make bivalent and biotinylated scFv molecules (Kipriyanov et al. (1994) Mol. Immunol. 31:1047-1058). Antibody portions, such as Fab and $F(ab')_2$ fragments, can be prepared from whole antibodies using conventional techniques, such as papain or pepsin digestion, respectively, of whole antibodies. Moreover, antibodies, antibody portions and immunoadhesion molecules can be obtained using standard recombinant DNA techniques, as described herein.

[0050] The term "human antibody", as used herein, is intended to include antibodies having variable and constant regions derived from human germline immunoglobulin sequences. The human antibodies of the invention may include amino acid residues not encoded by human germline immunoglobulin sequences (e.g., mutations introduced by random or site-specific mutagenesis in vitro or by somatic mutation in vivo), for example in the CDRs and in particular CDR3. However, the term "human antibody", as used herein, is not intended to include antibodies in which CDR sequences derived from the germline of another mammalian species, such as a mouse, have been grafted onto human framework sequences.

[0051] The term "recombinant human antibody", as used herein, is intended to include all human antibodies that are prepared, expressed, created or isolated by recombinant means, such as antibodies expressed using a recombinant expression vector transfected into a host cell (described further below), antibodies isolated from a recombinant, combinatorial human antibody library (described further below), antibodies isolated from an animal (e.g., a mouse) that is transgenic for human immunoglobulin genes (see e.g., Taylor et al. (1992) Nucl. Acids

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

[0052] An "isolated antibody", as used herein, is intended to refer to an antibody that is substantially free of other antibodies having different antigenic specificities (e.g., an isolated antibody that specifically binds hDll4 is substantially free of antibodies that specifically bind antigens other than hDll4). An isolated antibody that specifically binds hDll4 may, however, have cross-reactivity to other antigens, such as hDll4 molecules from other species. Moreover, an isolated antibody may be substantially free of other cellular material and/or chemicals.

[0053] 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.).

[0054] The term "K_D", as used herein, is intended to refer to the dissociation constant of a particular antibody-antigen interaction.

[0055] The term "epitope" includes any determinant, preferably a polypeptide determinant, capable of specific binding to an immunoglobulin or T-cell receptor. In certain embodiments, epitope determinants include 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. An epitope is a region of an antigen that is bound by an antibody. In certain embodiments, an antibody is said to specifically bind an antigen when it preferentially recognizes its target antigen in a complex mixture of proteins and/or macromolecules. In preferred embodiments, an antibody is said to specifically bind an antigen when the equilibrium dissociation constant is less than or equal to 10^{-8} M, more preferably when the equilibrium dissociation constant is less than or equal to 10^{-9} M, and most preferably when the dissociation constant is less than or equal to 10^{-10} M.

[0056] A protein or polypeptide is "substantially pure," "substantially homogeneous" or "substantially purified" when at least about 60 to 75% of a sample exhibits a single species of polypeptide. The polypeptide or protein may be monomeric or multimeric. A substantially pure polypeptide or protein will typically comprise about 50%, 60, 70%, 80% or 90% W/W of a protein sample, more usually about 95%, and preferably will be over 99% pure. Protein purity or homogeneity may be indicated by a number of means well known in the art, such as polyacrylamide gel electrophoresis of a protein sample, followed by visualizing a single polypeptide band upon staining the gel with a stain well known in the art. For certain purposes, higher resolution may be provided by using HPLC or other means well known in the art for purification.

[0057] The term "polypeptide analog or variant" as used herein refers to a polypeptide that is comprised of a segment of at least 25 amino acids that has substantial identity to a portion of an amino acid sequence and that has at least one of the following properties: (1) specific binding to hDll4 under suitable binding conditions, or (2) ability to block Dll4 binding to a Notch receptor. Typically, polypeptide analogs or variants comprise a conservative amino acid substitution (or insertion or deletion) with respect to the naturally-occurring sequence. Analogs typically are at least 20 amino acids long, preferably at least 50, 60, 70, 80, 90, 100, 150 or 200 amino acids long or longer, and can often be as long as a full-length naturally-occurring polypeptide.

[0058] Preferred amino acid substitutions are those which: (1) reduce susceptibility to proteolysis, (2) reduce susceptibility to oxidation, (3) alter binding affinity for forming protein complexes, (4) alter binding affinities, and (4) confer or modify other physicochemical or functional properties of such analogs. Analogs can include various mutations of a sequence other than the naturally-occurring peptide sequence. For example, single or multiple amino acid substitutions (preferably conservative amino acid substitutions) may be made in the naturally-occurring sequence (preferably in the portion of the polypeptide outside the domain(s) forming intermolecular contacts. A conservative amino acid substitution should not substantially change the structural characteristics of the parent sequence (e.g., a replacement amino acid should not tend to break a helix that occurs in the parent sequence, or disrupt other types of secondary structure that characterizes the parent sequence). Examples of art-recognized polypeptide secondary and tertiary structures are described in Proteins, Structures and Molecular Principles (Creighton 1984 W. H. Freeman and Company, New York; Introduction to Protein Structure (Brànden & Tooze, eds., 1991, Garland Publishing, NY); and Thornton et al. 1991 Nature 354:105.

[0059] Non-peptide analogs are commonly used in the pharmaceutical industry as drugs with properties analogous to those of the template peptide. These types of non-peptide compound are termed "peptide mimetics" or "peptidomimetics" (see, for example, Fauchere (1986) J. Adv. Drug Res. 15:29; and Evans et al. (1987) J. Med. Chem. 30:1229. Systematic substitution of one or more amino acids of a consensus sequence with a D-amino acid of the same type (e.g., D-lysine in place of L-lysine) may also be used to generate more stable peptides. In addition, constrained peptides comprising a consensus sequence or a substantially identical consensus sequence variation may be generated by methods known in the art (Rizo et al. (1992) Ann. Rev. Biochem. 61:387), for example, by adding internal cysteine residues capable of forming intramolecular disulfide bridges which cyclize the peptide.

[0060] The term "percent sequence identity" in the context of nucleic acid sequences refers to the residues in two sequences which are the same when aligned for maximum correspondence. The length of sequence identity comparison may be over a stretch of at least about nine nucleotides or more, usually at least about 18 nucleotides, more usually at least about 24 nucleotides, typically at least about 28 nucleotides, more typically at least about 32 nucleotides, and preferably at least about 36, 48 or more nucleotides. There are a number of different algorithms known in the art which can be used to measure nucleotide sequence identity. For instance, polynucleotide sequences can be compared using FASTA, Gap or Bestfit, which are programs in Wisconsin Package Version 10.0, Genetics Computer Group (GCG), Madison, Wis. FASTA, which includes, e.g., the programs FASTA2 and FASTA3, provides alignments and percent sequence identity of the regions of the best overlap between the query and search sequences (Pearson (1990) Methods Enzymol. 183:63-98 and (2000) Methods Mol. Biol. 132:185-219). Unless otherwise specified, default parameters for a particular program or algorithm are used. For instance, percent sequence identity between nucleic acid sequences can be determined using FASTA with its default parameters (a word size of 6 and the NOPAM factor for the scoring matrix) or using Gap with its default parameters as provided in GCG Version 6.1.

[0061] A reference to a nucleic acid sequence encompasses its complement unless otherwise specified. Thus, a reference to a nucleic acid molecule having a particular sequence should be understood to encompass its complementary strand, with its complementary sequence. Generally, the art uses the terms "percent sequence identity", "percent sequence similarity" and "percent sequence homology" interchangeably. In this application, these terms shall have the same meaning with respect to nucleic acid sequences.

[0062] The term "substantial similarity", or "substantial sequence similarity," 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%, preferably at least about 95%, and more preferably at least about 96%, 97%, 98% or 99% of the nucleotide bases, as measured by any well-known algorithm of sequence identity, such as FASTA, BLAST or Gap, as discussed above.

[0063] As applied to polypeptides, the term "substantial identity" or "substantially identical" means that two peptide sequences, when optimally aligned, such as by the programs GAP or BESTFIT using default gap weights, share at least 80% sequence identity, preferably at least 90% or 95% sequence identity, even more preferably at least 98% or 99% sequence identity. Preferably, residue positions which are not identical differ by conservative amino acid substitutions. A "conservative amino acid substitution" is one in which an amino acid residue is substituted by another amino acid residue having a side chain (R group) with similar chemical properties (e.g., charge or hydrophobicity). In general, a conservative amino acid substitution will not substantially change the functional properties of a protein. In cases where two or more amino acid sequences differ from each other by conservative substitutions, the percent sequence identity or degree of similarity may be adjusted upwards to correct for the conservative nature of the substitution. Means for making this adjustment are well-known to those of skill in the art. See, e.g., Pearson (1994) Methods Mol. Biol. 24: 307-331. Examples of groups of amino acids that have side chains with similar chemical properties include 1) aliphatic side chains: glycine, alanine, valine, leucine and isoleucine; 2) aliphatic-hydroxyl side chains: serine and threonine; 3) amide-containing side chains: asparagine and glutamine; 4) aromatic side chains: phenylalanine, tyrosine, and tryptophan; 5) basic side chains: lysine, arginine, and histidine; and 6) sulfur-containing side chains are cysteine and methionine. Preferred conservative amino acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, glutamate-aspartate, and asparagine-glutamine. Alternatively, a conservative replacement is any change having a positive value in the PAM250 log-likelihood matrix disclosed in Gonnet et al. (1992) Science 256: 1443 45. A "moderately conservative" replacement is any change having a nonnegative value in the PAM250 log-likelihood matrix.

[0064] Sequence similarity for polypeptides, which is also referred to as sequence identity, is typically measured using sequence analysis software. Protein analysis software matches similar sequences using measures of similarity assigned to various substitutions, deletions and other modifications, including conservative amino acid substitutions. For instance, GCG contains programs such as "Gap" and "Bestfit" which can be used with default parameters to determine sequence homology or sequence identity between closely related polypeptides, such as homologous polypeptides from different species of organisms or between a wild type protein and a mutein thereof. See, e.g., GCG Version 6.1. Polypeptide sequences also can be compared using FASTA using default or recommended parameters, a program in GCG Version 6.1. FASTA (e.g., FASTA2 and FASTA3) provides alignments and percent sequence identity of the regions of the best overlap between the query and search sequences (Pearson (2000) *supra*). Another preferred algorithm when comparing a sequence of the invention to a database containing a large number of sequences from different organisms is the computer program BLAST, especially blastp or tblastn, using default parameters. See, e.g., Altschul et al. (1990) J. Mol. Biol. 215: 403 410 and Altschul et al. (1997) Nucleic Acids Res. 25:3389 402.

[0065] The length of polypeptide sequences compared for homology will generally be at least about 16 amino acid residues, usually at least about 20 residues, more usually at least about 24 residues, typically at least about 28 residues, and preferably more than about 35 residues. When searching a database containing sequences from a large number of different organisms, it is preferable to compare amino acid sequences.

Preparation of Human Antibodies

[0066] Methods for generating human antibodies include, for example, VELOCIMMUNE® (Regeneron Pharmaceuticals), XENOMOUSE™ technology (Abgenix), the "minilocus" approach, and phage display. The VELOCIMMUNE® technology (U.S. 6,596,541) encompasses a method of generating a high specificity fully human antibody to a select antigen. This 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.

[0067] The XENOMOUSE™ technology (Green et al. (1994) Nature Genetics 7:13-21) generates a mouse having both human variable and constant regions from both the heavy chain and kappa light chain loci. In an alternative approach, others have utilized a 'minilocus" approach in which an exogenous Ig locus is mimicked through inclusion of individual genes from the Ig locus (see, for example, U.S. 5,545,807). The DNA encoding the variable regions can be isolated with or without being operably linked to the DNA encoding the human heavy and light chain constant region.

[0068] Other methods of generating human antibodies, including isolation from a human donor, are known. See, for example, U.S. 6,787,637.

[0069] 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 CDC. The constant region of an antibody is important in the ability of an antibody to fix complement and participate in CDC or direct cell killing through antibody-dependent cellular cytoxicity (ADCC). Thus, the isotype of an antibody may be selected on the basis of the desirability for the antibody to fix complement.

[0070] Human immunoglobulins can exist in two forms that are associated with hinge heterogeneity. In one form, an immunoglobulin molecule comprises a stable four chain construct of approximately 150-160 kDa in which the dimers are held together by an interchain heavy chain disulfide bond. In a second form, the dimers are not linked via inter-heavy chain disulfide bonds and a molecule of about 75-80 kDa is formed composed of a single light and heavy chain. These forms have been difficult to separate, even after affinity purification.

[0071] 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. In fact, a single amino acid substitution in the hinge region of the human IgG4 hinge can significantly reduce the appearance of the second form (Angal et al. 1993 Molecular

Immunology 30:105) to levels typically observed using a human IgG1 hinge. The instant invention encompasses antibodies having one or more mutations in the hinge, CH2 or CH3 region which may be desirable, for example, in production to improve the yield, or modulate effector functions.

[0072] Antibodies of the invention are preferably prepared with the use of VELOCIMMUNE® technology. A transgenic mouse in which the endogenous immunoglobulin heavy and light chain variable regions are replaced with the corresponding human variable regions is challenged with the antigen of interest, and lymphatic cells (such as B-cells) recovered from the mice that express antibodies. The lymphatic cells may be fused with a myeloid-type 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 may be isolated directly from antigen-specific lymphocytes. In various embodiments, the transgenic mouse comprises 12 functional human variable heavy chain genes and 11 functional human variable kappa light chain genes; 25 to 30 human variable heavy chain genes and from 18 to 20 human variable kappa light chain genes; 43 to 48 human variable heavy chain genes and 20 to 22 human variable kappa light chain genes; or about 80 human variable heavy chain genes and about 40 human variable kappa light chain genes.

[0073] In general, the antibodies of the instant invention possess very high affinities, typically possessing K_D of from about 10^{-9} through about 10^{-11} M, when measured by binding to antigen either immobilized on solid phase or in solution phase. The mouse constant regions are replaced with desired human constant regions to generate the fully human antibodies of the invention, for example wild-type or modified IgG1 or IgG4 (for example, SEQ ID NO:950, 951, or 952). While the constant region selected may vary according to specific use, high affinity antigen-binding and target specificity characteristics reside in the variable region.

[0074] Cancer, infectious diseases, autoimmunity, immunodeficiency, transplants, inflammation, injury and degenerative conditions can be treated by modulation of the immune system. In cases of disease due to inappropriate function or hyperactivity of the immune system, such as autoimmunity or inflammation, can be ameliorated through inhibition of immune cell function or reduction of immune cell numbers. This can be accomplished by blockade of positive signals or stimulation of negative signals on immune cell populations critical to the disease process, such as T, B or NK cells, neutrophils, macrophages, antigen presenting cells, mast cells or other cell types. Overactivity can also be inhibited through elimination of various immune cell populations by stimulation of apoptosis, targeting of specific surface receptors with depleting antibodies or antibody-drug conjugates, or the blockade or alteration of the differentiation of immune cell lineages or specific cell types. Inefficient or reduced immune function can cause or exacerbate disorders such as cancer, infectious disease, and other immunodeficiencies. Hypoactivity of the immune system can be improved through activation of immune cells by stimulation of positive signals by crosslinking or agonistic antibodies or blockade of negative signals. Immune cell populations can be increased by stimulation of development of some or all immune cell lineages, prevention of apoptosis, or elimination of inhibitory signals. In a specific application, the antibodies of the invention are useful for treatment, inhibition or amelioration of a condition or disease such as, for example, cancer, immunodeficiency, transplant rejection, or inflammation.

Epitope Mapping and Related Technologies

[0075] To screen for antibodies which 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 in Harlow and Lane (1990) *supra* can be performed. Other methods include alanine scanning mutants, peptide blots (Reineke (2004) Methods Mol Biol 248:443-63), 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).

[0076] 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.

[0077] 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 (U.S. patent Publication No. 2004/0101920). Each category may reflect a unique epitope either distinctly different from or partially overlapping with epitope represented by another category. This technology allows rapid filtering of genetically identical antibodies, such that characterization can be focused on genetically distinct antibodies. When applied to hybridoma screening, MAP may facilitate identification of rare hybridoma clones that produce mAbs having the desired characteristics. MAP may be used to sort the hDll4 antibodies of the invention into groups of antibodies binding different epitopes.

[0078] Agents useful for altering the structure of the immobilized antigen are enzymes, such as, for example proteolytic enzymes, for example, trypsin, endoproteinase Glu-C, endoproteinase Asp-N, chymotrypsin, etc. Agents useful for altering the structure of the immobilized antigen may also be chemical agents, such as, succinimidyl esters and their derivatives, primary amine-containing compounds, hydrazines and carbohydrazines, free amino acids, etc.

[0079] The antigen protein may be immobilized on either biosensor chip surfaces or polystyrene beads. The latter can be processed with, for example, an assay such as multiplex LUMINEX™ detection assay (Luminex Corp., Austin, TX). Because of the capacity of LUMINEX™ to handle multiplex analysis with up to 100 different types of beads, LUMINEX™ provides almost unlimited antigen surfaces with various modifications, resulting in improved resolution in antibody epitope profiling over a biosensor assay.

Therapeutic Administration and Formulations

[0080] The administration of therapeutic entities 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 (15th ed, 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. Any of the foregoing mixtures may be appropriate in treatments and therapies in accordance with the present invention, provided that the active ingredient in the formulation is not inactivated by the formulation and the formulation is physiologically compatible and tolerable with the route of administration. See also Powell et al. "Compendium of excipients for parenteral formulations" PDA (1998) J Pharm Sci Technol. 52:238-311 and the citations therein for additional information related to excipients and carriers well known to pharmaceutical chemists.

EXAMPLES

Example 1. Generation of Human Antibodies to Human Dll4.

[0081] Mice may be immunized by any method known in the art (see, for example, Harlow and Lane *supra*). In one embodiment, hDll4 antigen is administered directly to VELOCIMMUNE® mice comprising DNA loci encoding human Ig heavy chain variable regions and kappa light chain variable regions, with an adjuvant to stimulate the immune response. Such an adjuvant includes complete and incomplete Freund's adjuvant, MPL+TDM adjuvant system (Sigma), or RIBI (muramyl dipeptides) (see O'Hagan 2000 Vaccine Adjuvant, by Human Press, Totawa, NJ). The antibody immune response is monitored by standard antigen specific immunoassay. When a desired immune response is achieved, antibody-expressing B cells were harvested and fused with mouse myeloma cells to preserve their viability, forming hybridoma cell lines. Such hybridoma cell lines are screened and selected to identify cell lines that produce antigen-specific antibodies using assays as described below.

[0082] Alternatively, antigen-specific hybridoma cells may be isolated by flow cytometry.

Briefly, after fusion to myeloma cells, pooled hybridoma cells were grown for 10 days in HAT medium. The cells were then harvested and stained with biotin-labeled Dll4 at 2 mg/ml for one hour, followed by addition of phycoerythrin-streptavidin. The fluorescence-labeled cells were sorted by flow cytometry (single cell per well into 96 well plates containing hybridoma growth medium), cultured for 8-10 days, and conditioned media screened for the presence of functionally desirable monoclonal antibodies, as described below.

[0083] Anti-hDll4 antibodies generated via direct isolation of splenocytes. Antigen-specific antibodies may also be isolated directly from antigen-immunized B cells without fusion to myeloma cells, as described in U.S. Patent Publication 2007/0280945A1. Stable recombinant antibody-expressing CHO cell lines were established from the isolated proper recombinants.

Example 2. Antigen Binding Affinity Determination.

[0084] Equilibrium dissociation constants (K_D values) for antigen binding to the selected antibodies described above were determined by surface kinetics on a real-time biosensor surface plasmon resonance assay (BIACORE™ 2000). The antibody was captured on a goat anti-mouse IgG polyclonal antibody surface created through direct chemical coupling to a BIACORE™ chip to form a captured antibody surface. Varying concentrations of monomeric hDll4 or dimeric hDll4-hFc were injected over the captured antibody surfaces, and antigen-antibody binding and dissociation monitored in real time. Kinetic analysis was performed to calculate K_D, dissociation rate constants, and half-life of antigen/antibody complex dissociation (Table 1). A similar method was applied to measure single B cell-derived monoclonal antibodies modified to contain a human IgG constant domain. Antibodies were presented by goat anti-hFc polyclonal antibody reagent (Jackson Immuno Research Lab) immobilized on BIACORE™ chip, and exposed to either dimeric Dll4-mFc or monomeric Dll4 protein (Table 2).

[0085] Antibody-antigen binding affinity may also be assessed using an ELISA based solution competition assay. Briefly, on a 96-well microtiter plate, antibodies (purified proteins or in conditioned medium) were premixed with serial dilutions of antigen protein (monomeric or dimeric) ranging from 0 to 10 μg/ml with a constant concentration of antibody. After a 2 hr incubation of antigen with antibody, the solutions were transferred to a microtiter plate precoated with antigen for measurement of free antibody (MAXISORB™, VWR, West Chester, PA). The plate was coated with 1 μg/ml hDll4-hFc protein in PBS solution overnight at 4° C and nonspecific binding sites blocked with BSA for 2 hrs. After a 1 hr incubation following transfer, the plate was washed and the plate-bound antibodies were detected with an HRP-conjugated goat anti-mouse IgG polyclonal antibody reagent (Jackson Immuno Laboratory) and developed using colorimetric substrates (OPTEIA™; BD Biosciences Pharmingen, San Diego, CA). The enzymatic reaction was stopped with 1 M phosphoric acid, optical absorptions at 450 nm were recorded and the data were analyzed using a sigmoidal dose-response model and an IC_{50} values were reported (Table 1).

TABLE 1

Antibody	K_D Dll4 (nM)	K_D Dll4-Fc (nM)	IC_{50} Dll4-Fc (nM)
13B6	2.79	0.188	0.06
15E10	0.55	0.023	0.58
22G12	1.29	0.076	0.03
24C8	0.52	0.047	0.01
VAV 2H4-19	1.51	0.611	0.10
VAV 4H10-9	13.70	0.662	0.30
VAV 7B9-9	0.88	0.021	0.27
VAW 10E4-9	89.00	0.468	0.06
VAW 10G11-2	31.30	1.430	1.66
VAW 1C6-1	45.60	0.092	0.25
VAW 1G2-4	83.80	0.035	0.40
VAW 1H2-2	67.00	0.148	0.30
VAW 2H3-2	0.30	0.150	0.26
VAW 3A7-2	1.64	0.162	0.02
VAW 3A9-5	NA	2.510	16.00
VAW 3F12-8	8.12	0.648	0.07
VAW 6B8-12	0.69	0.060	0.43
VAW 6C6-2	91.70	0.092	0.50
VAW 6G12-10	3.74	0.527	0.19
VAW 7C10-11	17.10	0.653	0.28
VAW 8A10-14	1.41	0.648	0.08
VAW 8G1-12	6.09	8.300	8.60
VAW 9B11-2	62.20	0.048	0.00
VAW 9F12-6	16.00	1.350	0.02
VAW 9G10-1	56.10	0.555	0.10

TABLE 2

Antibody	K_D Dll4 (nM)	K_D Dll4-Fc (nM)
314266-06F12-B7	2.17	0.075
318518-01A04-D5	0.237	0.244
318518-01A10-D8	0.399	0.016
318518-01B09-C3	0.833	0.180
318518-01B11-D4	0.382	0.088
318518-01E07-H2	0.165	0.238
318518-01G04-F3	0.501	0.107

318518-01G05-B5	1.06	0.196
318518-02A07-B3	0.208	0.148
318518-02B06-E2	2.15	0.193
318518-02B08-F7	N/A	N/A
318518-02C04-D1	0.478	0.331
318518-02F05-D10	1.28	0.035
318518-02G03-F2	1.31	0.042
318518-02G04-B11	0.813	0.048
318518-02G08-F11	N/A	N/A
318518-03A03-B2	0.136	0.124
318518-03C10-F2	1.18	0.131
318518-03D04-B5	0.904	0.136
318518-03D07-G11	3.74	0.163
318518-03F04-A6	0.501	0.088
318518-03F06-A3	0.556	0.037
318518-03H03-F3	6.89	0.084
318518-14A06-E7	4.54	0.282
318518-14A07-C4	0.235	0.035
318518-14D08-G1	0.541	0.046
318518-14H08-A2	6.67	0.128
318518-1H08-E9	0.225	0.050

Example 3. Inhibition of Dll4 and Notch Interaction

[0086] The ability of the antibodies to block Dll4 binding to Notch was evaluated with an ELISA-based immunoassay. Briefly, Notch-hFc recombinant protein was coated on a 96-well plate in PBS buffer overnight at 4°C at 1 mg/ml, and the nonspecific binding sites were blocked with BSA. This plate was used to measure free biotin-Dll4-hFc from antibody titration sample solutions. To make the antibody titration samples, a constant amount of biotin-Dll4-hFc at 25 pM was pre-mixed with varied amounts of antibody, either in crude hybridoma condition medium or as purified antibody protein, ranging from 0 to ~50 nM in serial dilutions, followed by 2 hr incubation at room temperature to allow antibody-antigen binding to reach equilibrium. The equilibrated sample solutions were then transferred to the Notch-hFc coated plates for the measurement of free biotin-Dll4-hFc. After 1 hour binding, the plate was washed and bound biotin-Dll4-hFc was detected using HRP conjugated streptavidin (Poly HRP streptavidin, Pierce Endogen), and developed using TMB substrate (BD Pharmigen). Data was analyzed using GraphPad Prism software and IC_{50} values were determined as the amount of antibody required to achieve 50% reduction of biotin-Dll4-hFc bound to the plate-coated Notch-Fc (Table 3) (*conditioned media).

TABLE 3

Antibody	IC_{50} (nM)
VAV 2H4-19	0.01
VAW 3A7-2	0.017
VAW 9G10-1	0.019
VAW 10E4-9	0.032
VAW 8A10-11	0.04
VAW 9F12-6	0.059
VAW 3F12-8	0.066
VAW 1C6-1	0.086
VAW 1G2-4	0.11
VAW 6C6-2	0.119
VAV 7B9-4	0.123
VAW 1H2-2	0.154
VAW 2H3-2	0.168
VAW 6B8-12	0.255
VAW 6G12-10	0.257
VAW 7C10-11	0.273
VAV 4H10-9	0.599
VAW 10G11-2	0.931
VAW 3A9-5	3.8
VAW 8G1-12	10.7
VAW 9B11-2	0.069
15E10*	0.04
22G12	0.10
13B6	0.11
24C8	0.031
314266-06F12-B7	0.07
318518-01A04-D5	0.11
318518-01A10-D8	0.05
318518-01B09-C3	0.03
318518-01B11-D4	0.03
318518-01E07-H2	1.17
318518-01G04-F3	0.02
318518-01G05-B5	1.08
318518-02A07-B3	0.03

318518-02B06-E2	0.09
318518-02B08-F7	N/A
318518-02C04-D1	0.60
318518-02F05-D10	0.16
318518-02G03-F2	0.07
318518-02G04-B11	1.09
318518-02G08-F11	N/A
318518-03A03-B2	0.57
318518-03C10-F2	0.12
318518-03D04-B5	0.04
318518-03D07-G11	0.45
318518-03F04-A6	0.01
318518-03F06-A3	0.02
318518-03H03-F3	0.17
318518-14A06-E7	0.04
318518-14A07-C4	0.02
318518-14D08-G1	0.14
318518-14H08-A2	0.25
318518-1H08-E9	0.03

[0087] The ability of selected purified anti-hDll4 antibodies to block Dll4 binding to Notch was also evaluated with the ELISA-based immunoassay described above, modified by replacing 25 pM of biotin-Dll4-hFc with 30 pM of biotin-Dll4-hFc, and reducing antibody-antigen incubation duration from 2 hrs to 1 hr. For convenience, antibody 318518-01A10-D8 was renamed "REGN281" (HCVR/LCVR SEQ ID NOs:429/437 and hIgG1 SEQ ID NO:950). Derived antibodies tested included REGN421 (HCVR/LCVR SEQ ID NO:901/903, hIgG1 SEQ ID NO:950); and REGN422 (HCVR/LCVR SEQ ID NO:901/903, with modified hIgG4 SEQ ID NO:952). Results are shown in Table 4.

TABLE 4

Antibody	IC_{50} (nM)
REGN281	0.042
REGN421	0.045
REGN422	0.039

[0088] Ability of antibody to neutralize Dll4 mediated cellular function was also tested *in vitro* using Dll4 expressing human umbilical vein endothelial cells (HUVEC). Inhibition of Notch mediated hHes1 and EphB2 gene expression in HUVEC with the derived antibodies was monitored as follows: low passage HUVEC were cultured in MCDB-131 media (Vec Technologies). One day prior to analysis, HUVEC cells were seeded at a density of 2 x 10^5 cells/well in 24-well plates in 1 ml total media volume. The test antibody or other inhibitor was added directly to the individual sample wells in triplicate followed by 5-hour culture at 37°C. At the end of the culture period, media was removed and total RNA was isolated using QIAZOL™ and the RNEASY™ lipid tissue kit (Qiagen). mRNA level quantification was performed by the use of PCR and the fluorogenic 5' nuclease assay (TAQMAN® assay, Appied Biosystems). For each sample, cDNA was synthesized from 1-2 mg of total RNA. cDNA generated from an equivalent amount of starting RNA (typically 25 ng) was loaded in triplicate on ABI PRISM™ optical reaction plates. For each RNA sample a "no RT" control was also run in which no reverse transcriptase was added to allow for subtraction of any potential genomic DNA contributions to the signal. 2x Mastermix (TAQMAN® 2x PCR Mastermix; ABI) was added to each reaction to a final concentration of 1x. Additionally, TAQMAN® probe and primers for the gene of interest were added to each reaction. Each primer was used at a final concentration of 900 nM and the probe was added at a final concentration of 200 nM. Human genomic DNA was used as a standard. The assays were performed under standard TAQMAN® conditions on a ABI 7900HT instrument. Levels of Hes1 and EphrinB2 were measured and normalized to an endogenous control gene (cyclophilin) (Table 5). Probes and primers: human Hes1 probe (SEQ ID NO:387); Oligos: hHes1-869F (SEQ ID NO:388); hHes1-940R (SEQ ID NO:389), human ephrinB2 probe: hEphB2-773T (SEQ ID NO:390); Oligos: hEphB2-752F (SEQ ID NO:391) hEphB2-812R (SEQ ID NO:392); human cyclophilin: probe: hCyclophilin-343T (SEQ ID NO:393); Oligos: hCyclophilin-323F (SEQ ID NO:394); hCyclophilin-389R (SEQ ID NO:395).

TABLE 5

Antibody	EphrinB2 Expression IC_{50} (nM)	Hes1 Expression IC_{50} (nM)
22G12	0.379	0.381
15E10	2.56	4.49
VAW 3A7-2	0.409	0.533
314266-06F12-B7	0.239	0.405
318518-01A10-D8	0.305	0.329
318518-01G04-F3	0.088	0.172
318518-01H08-E9	0.413	0.548
318518-02A07-B3	0.398	0.128
318518-03F04-A6	0.158	0.115
318518-03F06-A3	0.304	0.692
318518-014A07-C4	0.175	0.312
318518-014D08-G1	0.510	0.568
hDll4-hFc	0.843	0.974

[0089] HUVEC Proliferation Assay. The ability of antibody to block Dll4 mediated growth inhibition of Human umbilical vein endothelial cells (HUVEC) cells was tested in an *in vitro* cell proliferation assay. Low passage HUVEC cells were obtained and cultured in MCDB-131 media (Vec Technologies). One day prior to analysis 12-well tissue culture plates were coated with hDll4-hFc in PBS at 4°C overnight (0.2 µg/ml; 0.5 ml PBS/well). Plates were washed 1x with PBS and HUVEC cells were seeded at a density of $4x10^3$ cells/well in 1.0 ml total media volume. Immediately following addition of cells anti-hDll4 antibodies were added in 0.5 ml total volume over a range of concentrations to generate an inhibition curve. Cells were grown for 96-hours at 37°C. Cell number was quantitated using the CCK-8 reagent (Dojindo). All assays were run in triplicate. (Table 6, NB, not blocking).

TABLE 6

Antibody	IC_{50} (nM)
15E10	0.284
VAW9B11-2	1.868
VAW8D8-12	NB
13B6	5.01
VAW2H4-19	NB
VAW3A7-2	0.198
VAW8A10-14	0.214
22G12	0.888
318518-06F12-B7	2.067
318518-01A10-D8	0.096
318518-01G04-F3	0.106
318518-01H08-E9	0.188
318518-02A07-B3	0.200
318518-03F04-A8	0.184
318518-03F06-A3	0.188
318518-014A07-C4	0.159
318518-014D08-G1	0.165

[0090] Notch-Inducible Luciferase Assay. A bioassay was developed to determine the ability of selected purified antibodies to neutralize Dll4-mediated cellular function *in vitro* using an engineered HEK293 cell line (ATCC) that constitutively expresses human Notch 1 and contains a Notch-responsive promoter driving luciferase. Inhibition of Notch-inducible luciferase activity was determined as follows: 1 day prior to assay, each well of an opaque 96 well tissue culture plate was coated with 100 µl of either 1 nM or 1.5 nM hDll4-hFc in PBS overnight at 4°C. Cells were seeded onto the coated plates at $2 x10^4$ cells/well in media. Purified antibody protein, in serial dilutions starting from 2 nM in cell media, was incubated with the cells at 37°C for 24 hrs. Luciferase activity was determined by adding an equal well volume of STEADY-GLO® Substrate (Promega) (Table 7).

TABLE 7

Antibody	IC$_{50}$ (pM)	
	1 nM hDll4-hFc	1.5 nM hDll4-hFc
REGN281	50.5	78.7
REGN421	54.4	87.3
REGN422	88.2	131.1

Example 4. Inhibition of Notch1 Cleavage

[0091] The ability of selected anti-hDll4 antibodies to inhibit Notch1 cleavage was tested by examination of total cleaved Notch1 protein by SDS-Page/Western blotting. Low passage HUVEC cells were cultured as described above. One day prior to analysis 6-well plates were coated with hDll4-hFc in PBS at 4°C overnight (0.2 µg/ml; 1.0 ml PBS/well). Plates were washed 1x with PBS and HUVEC cells were seeded at 7.5 x10^5 cells/well in 2.0 ml total media volume. Immediately following cell seeding, anti-hDll4 antibody was added to each well at 10nM final concentration. Cells were grown for 24 hours at 37°C following which whole cell extracts were prepared and analyzed by SDS-PAGE. Levels of cleaved Notch1 were determined using an anti-cleaved Notch1 (Val1744) antibody (Cell Signaling) and standard western blotting techniques. The anti-hDll4 antibodies were able to entirely block the Notch1 cleavage induced by plate coated hDll4-hFc (data not shown).

Example 5. ADCC and CDC Assays

[0092] Antibody-dependent cell-mediated cytotoxicity (ADCC) induced by two test antibodies (REGN421, REGN422) was assessed using a panel of eight target cell lines with varying hDll4 expression levels. The eight target cell lines were (1) HUVECs; (2) HUVECs stimulated with 10 nM VEGF for 24 hours; (3) Colo205; (4) engineered C6 rat glioma cells expressing eGFP; (5) engineered C6 rat glioma cells expressing hDll4; (6) engineered HT1080 cells expressing eGFP; (7) engineered HT1080 cells expressing hDll4; and (8) HT29. Human Dll4 or eGFP was integrated into the C6 cell or HT1080 genome through retroviral transfection. Briefly, cells from each target cell line (10,000 cells/well in 50 µl) were first mixed with an equal volume of serially diluted REGN421 or REGN422, resulting in a final antibody concentration ranging from 0.169 pM to 10 nM, and incubated for 10 min at room temperature in a 96-well plate format (control = wells without antibody). Separately, human peripheral blood mononuclear cells (PBMCs, effector cells) were prepared following a conventional Ficoll-Hypaque gradient centrifugation enrichment procedure. Approximately 300,000 PBMCs were added to each mixture of antibody and target cells to give a final ratio of effector to target cells of approximately 30:1. The 96-well plates were then incubated for 4 h at 37°C, 5% CO_2 followed by centrifugation at 250 x g. Supernatants were harvested and assayed for lactate dehydrogenase (LDH) activity using the CYTOTOX 96® Non-Radioactive Cytotoxicity Assay system (Promega). Results are shown in Table 8. REGN421-induced dose dependent cell lysis was only observed in C6 cells expressing hDll4 (col. 5), which exhibited the highest hDll4 expression among all cell lines (as determined by immunoprecipitation/Western blot and flow cytometry). The maximum cell cytotoxicity in the C6-hDll4 cell line ranged from 20% to 60%. No REGN421-induced cell lysis was observed in the remaining seven target cell lines. REGN422 did not induce cell lysis in any of the target cell lines.

TABLE 8

Ab	% Maximum Cytotoxicity							
	1	2	3	4	5	6	7	8
REGN421	0	0	0	0	20-60	0	0	0
REGN422	0	0	0	0	0	0	0	0

[0093] Complement-dependent cytotoxicity (CDC) induced by REGN421 was assessed using the same panel of cells lines described above. Briefly, cells from each of the target cell lines (50,000 cells/well in 50 µl) were first mixed with an equal volume of serially diluted REGN421, resulting in a final antibody concentration ranging from 0.169 pM to 10 nM, and incubated for 10 min at room temperature in a 96-well plate format. Normal human serum, with complement components (Quidel Corp., San Diego, CA) was added to each well to give a final serum concentration of 5%. The plates were then incubated at 37°C, 5% CO_2 for 2 hours followed by addition of CELLTITER-BLUE® reagent (Promega) (controls = wells without antibody and wells with antibody but no serum). The plates were incubated overnight and cell survival (CDC levels) assayed. As a positive control, Daudi cells were treated with rituximab. REGN421 exhibited no CDC toward any of the target cell lines tested (data not shown).

Example 6. Epitope Mapping and Specificity

[0094] In order to determine epitope binding specificity, a series of seven chimeric Dll4 proteins were generated in which specific human Dll4 domains were substituted into a mouse Dll4 protein as follows: #1 contained the human N-terminal and DSL domains (S27-Q218); #2 contained human N-terminal, DSL and EGF-1 domains (S27-N252); #3 contained human N-terminal, DSL, EGF-1 and EGF-2 domains (S27-Q283); #4 contained human N-terminal, DSL, EGF-1, EGF-2, EGF-3, EGF-4 and EGF-5; #5 contained human N-terminal domain (S27-R172); #6 contained human DSL domain (V173-Q218); and #7 contained human EGF-2 domain (E252-D282). The chimeric proteins were fused to a mouse IgG2a-Fc fragment and expressed in CHO-K1 cell. The conditioned media were harvested and protein expression confirmed by western blot.

[0095] Binding specificity of test antibodies to hDll4, mDll4, and chimeric proteins #1, #2, #3, and #4 were tested as follows: purified antibodies 22G12, VAW3A7-2, and 15E10 were amine coupled between 5000- 6000 RU on CM5 chip. Conditioned media from CHO K1 cells containing the chimeric Dll4 proteins, hDll4-mFc, and mDll4-mFc were injected sequentially followed by surface regeneration over antibody-coupled surfaces. A blank amine coupled flowcell surface was used as a control for nonspecific binding of the conditioned media. Results are summarized in Table 9. 22G12 bound an epitope between S27-Q218 of hDll4; VAW3A7-2 bound an epitope between Q283-E400 hDll4; and 15E10 bound an epitope between E252-D282 of hDll4.

TABLE 9

Antibody	hDll4-mFc	mDll4-mFc	Chimeric Proteins			
			#1	#2	#3	#4
22G12	+	-	+	+	+	+
VAW3A7-2	+	-	-	-	-	+
15E10	+	-	-	-	+	+

[0096] Binding specificity of purified test mAb to hDll4, mDll4 and the chimeric proteins (described above) was determined (REGN279 = 314266-6F12-B7; REGN287= 318518-1G04-F3; REGN289= 318518-1H08-E9; REGN290=318518-2A07-B3; REGN306= 318518-3F06-A3). Briefly, each Dll4 protein was captured (70-130 RU) on goat anti-mouse IgG antibody surfaces, followed by injection of test mAb at a concentration of 100 µg/ml. An antibody that bound mDll4-mFc was used as a positive control (positive control= 6C10). The results (Table 10) show that REGN279 bound an epitope between S27-Q218 of hDll4; REGN287 bound between Q283-E400 of hDll4; REGN289, REGN290 and REGN306 bound between S27-E400 of hDll4.

TABLE 10

Antibody	hDll4-mFc	mDll4-mFc	Chimeric human-mouse Dll4 Fusion Proteins						
			#1	#2	#3	#4	#5	#6	#7
REGN279	+	-	+	+	+	+	+	-	-
REGN287	+	-	-	-	-	+	-	-	-
REGN289	+	-	+	+	+	+	-	+	-
REGN290	+	-	+	+	+	+	-	+	-
REGN306	+	-	+	+	+	+	-	+	-
Control	+	+	+	+	+	+	+	+	+

[0097] Further epitope binding specificity determinations were conducted as described above with the following purified test antibodies: REGN281=318518-1A10-D8; REGN305=318518-3F04-A6; REGN309=318518-14A07-C4; REGN310=318518-14D08-G1; REGN421, and REGN422. Briefly, each of the Dll4 proteins was captured (240-470 RU) on goat anti-mouse

IgG antibody surfaces, followed by injection of test antibody at a concentration of 100 µg/ml (Table 11).

TABLE 11

Antibody	hDll4-mFc	mDll4-mFc	Chimeric human-mouse Dll4 Fusion Proteins						
			#1	#2	#3	#4	#5	#6	#7
REGN281	+	-	+	+	+	+	+	+	-
REGN305	+	-	-	-	-	+	-	-	-
REGN309	+	-	+	+	+	-	+	+	-
REGN310	+	-	-	-	+	+	-	+	+
REGN421	+	-	+	+	+	+	+	+	-
REGN422	+	-	+	+	+	+	+	+	-

[0100] Western blot analysis. Binding specificity of selected antibodies to chimeric, mouse and human Dll4 was determined by Western blot. Briefly, hDll4-mFc (200 ng per lane), mDll4-mFc (200 ng per lane), and chimeric proteins #1 - #7 (approximate 150 ng per lane) were subjected to electrophoresis on duplicate SDS-PAGE gels using non-reducing sample buffer. Each gel was then transferred to a PVDF membrane. Blots were first exposed to REGN421 at 0.2 µg/ml and then to HRP-conjugated anti-hIgG antibody (Pierce). Control blots were exposed to HRP-conjugated anti-mFc antibody (Pierce). Results: REGN421 recognized hDll4-mFc and chimeric proteins containing the human N-terminal domain (#5), a human DSL domain (#6), or both (#1, #2, #3, and #4). REGN421 did not recognize a chimeric protein containing a human EGF-2 domain (#7).

[0101] Protease digestion analysis. Binding between REGN281 and hDll4 was further assessed by protective protease digestion and liquid chromatography/mass spectrometry (LC/MS) using an HPLC1100 (Agilent) and LCQ Classical Ion Trap Mass Spectrometer (Thermo). Briefly, a mixture of hDll4 and REGN281, in a molar ratio of 1:5, or hDll4 alone, was incubated with protease overnight at either 25°C (for GluC protease) or 37°C (for trypsin). Each of the resulting proteolytic digest mixtures was then subjected to LC/MS. Unique peptide peaks present in proteolytic digests performed in the absence of REGN281, which either diminished or disappeared in proteolytic digests performed in the presence of REGN281, indicate potential REGN281 binding sites on hDll4 that were protected from protease digestion by the binding of REGN281 to hDll4. These unique peptide peaks were analyzed by mass spectrometry. The observed mass, predicted mass, and the N-terminal sequences of the peptides are shown in Table 12.

TABLE 12

Peak	Observed Mass	Predicted Mass	hDll4 Peptide (SEQ ID NO:2)	Protease	Domain
G1	521	521.5	Phe37-Glu40	GluC	N-terminal

G2	1362.8	1363.4	Ala121-Glu132	GluC	N-terminal
T1	758	760.6	Pro49-Arg55	Trypsin	N-terminal
T2	587.1	587.2	Tyr169-Arg172	Trypsin	N-terminal
T3	1607.4	1607.6	Val173-Arg186	Trypsin	DSL
T4	1399	1400.7	Gly42-Arg55	Trypsin	N-terminal
T5	569.2	569.3	Thr56-Arg59	Trypsin	N-terminal
T7	2615	2613.4	Ile143-Arg166	Trypsin	N-terminal
T8	1807.2	1806.9	Ser27-Arg41	Trypsin	N-terminal

Example 7. Binding Affinity of Purified Antibodies to Human and Monkey Dll4.

[0102] The binding affinities of selected purified antibodies to hDll4, *M. facscicularis* Dll4 (mfDll4, SEQ IN NO:956), and *M. mulatta* Dll4 (mmDll4, SEQ ID NO:957) monomers were determined using a BIACORE™ 2000 & 3000. Goat anti-hFc polyclonal antibody reagent immobilized on a BIACORE™ chip was used to present REGN281, REGN421, and REGN422. Varying concentrations of each proteins, hDll4 (from 12.5 nM to 100 nM), mfDll4 (from 3.13. nM to 100 nM), or mmDll4 (from 12.5 nM to 100 nM) were used as analyte, and injected over the antibody surfaces. Antigen-antibody binding and dissociation of bound complex were monitored in real time (Table 13).

TABLE 13

	ka (M-1s-1)			kd (s-1)			K_D (nM)		
	hDll4	mfDll4	mmDll4	hDll4	mfDll4	mmDll4	hDll4	mfDll4	mmDll4
REGN281	1.56×10^5	6.64×10^4	9.27×10^4	2.30×10^{-5}	2.04×10^{-5}	3.05×10^{-5}	0.148	0.307	0.329
REGN421	1.63×10^5	7.28×10^4	9.70×10^4	2.17×10^{-5}	2.02×10^{-5}	3.23×10^{-5}	0.133	0.278	0.333
REGN422	1.64×10^5	8.01×10^4	9.27×10^4	2.36×10^{-5}	2.88×10^{-5}	3.41×10^{-5}	0.144	0.360	0.375

[0103] The binding affinities of anti-hDll4 antibodies toward hDll4 and mmDll4 dimers were also determined using a BIACORE™ 2000 and the method describe above, except that hDll4 was replaced with hDll4-mFc (from 3.13 nM to 100 nM), or mmDll4 with mmDll4-mFc (from 0.78 nM to 25 nM) as analyte (Table 14).

TABLE 14

	ka (M-1s-1)		kd (s-1)		K_D (nM)	
	hDll4-mFc	mmDll4-mFc	hDll4-mFc	mmDll4-mFc	hDll4-mFc	mmDll4-mFc
REGN281	3.02×10^5	3.16×10^5	4.96×10^{-6}	4.64×10^{-6}	0.0163	0.0147
REGN421	3.43×10^5	3.35×10^5	4.70×10^{-6}	3.80×10^{-6}	0.0137	0.013
REGN422	3.46×10^5	4.23×10^5	4.60×10^{-6}	4.15×10^{-6}	0.0133	0.0098

Example 8. Cross-Reactivity of Antibodies With hDll1, hDll3, mDll4, or mfDll4.

[0104] Cross-reactivity of the antibodies to human delta-like ligand1 (SEQ ID NO:953) and human delta-like ligand 3 (SEQ ID NO:954) proteins was determined. REGN281, REGN421 and REGN422 were presented by a goat anti-human kappa (hK) polyclonal antibody reagent (Southern Biotech) immobilized on a BIACORE™ chip, and either hDll4-hFc or hDll1-hFc protein at 100 µg/ml were used as analyte injected over the antibody surfaces. All three anti-hDll4 antibodies only bound to hDll4-hFc, and did not bind hDll1-hFc.

[0105] An alternative BIACORE™ format was used to assess cross-reactivity between anti-hDll4 antibody and either hDll1-hFc or hDll3-hFc. Briefly, ligands hDll4-hFc, hDll1-hFc, and hDll3-hFc were each covalently linked to a CM-5 chip, through amine coupling, to an RU range of about 6,000 to 10,000. REGN421, at 300 µg/ml; was injected over the surface of each chip. REGN421 bound only to hDll4-hFc; no binding was observed to either hDll1-hFc or hDll3-hFc. The same result was observed for REGN422 instead of REGN421.

[0106] OCTET™-based binding assays were employed to determine the binding between selected purified anti-hDll4 antibodies and hDll4-hFc, hDll3-hFc, hDll1-hFc, mfDll4-mmh, or mDll4-mFc. Briefly, strepavidin high binding FA biosensors (ForteBio, Inc., Menlo Park, CA) were first incubated with biotin-anti-hK at 5 µg/ml for 10 min at 30°C, to achieve saturation. Biotin-anti-hK-bound biosensors were then incubated with antibodies REGN281, REGN421 or REGN422, at 20 µg/ml for 10 min at 30°C, to achieve saturation. The antibody-bound biosensors were then incubated with either hDll4-hFc or hDll3-hFc, hDll1-hFc, or mDll4-mFc, at 200 nM, or mfDll4-mmh at 100 nM, for 10 min at 30°C. Changes in the thickness of the biological layer after each incubation were measured. Human Dll4-hFc and mfDll4-mmh bound to anti-hDll4 antibody-bound biosensors, whereas hDll3-hFc, hDll1-hFc, and mDll4-mFc did not bind to anti-hDll4 antibody-bound biosensors.

Example 9. Effect of Anti-hDll4 Antibody on Tumor Growth

[0107] The effect of REGN421 on tumor growth was evaluated on tumors implanted in Severe Combined Immunodeficiency (SCID) mice expressing a humanized Dll4 protein (SCIDxhDll4). Briefly, the humanized Dll4 mouse was made by replacing the entire extracellular domain of the mouse Dll4 gene with the corresponding extracellular region of the human Dll4 gene (7kb) in embryonic stem (ES) cells. Homozygous hDll4 mice were generated and bred into SCID background. Each mouse was then implanted subcutaneously (SC) with 2.5 x 10^6 human HT1080 tumor cells. After the tumors were established in the mice (~ 100-150 mm^3 18 days after implantation), mice were measured and treated with hFc, hDll4-Fc or REGN421. A total of 7 mice were divided into three groups. The first group (n=3) was treated subcutaneously with hFc at 25 mg/kg; the second group (n=1) was treated with hDll4-Fc at 25 mg/kg; and the third group (n=3) was treated with REGN421 at 10 mg/kg. The treatments were repeated every 48 hours starting at day 18. *In vivo* tumor measurements were obtained three days before the initial treatment (day 15), on the same day of each treatment (days 18, 20, and 22), and on day 25. Tumor size was calculated using the formula l x $w^2/2$. Results are shown in Table 15. On day 25, mice were euthanized and each tumor was removed and measured *ex vivo* and calculated (length x width x depth) (Table 16).

[0108] In addition, a group of SCID mice expressing endogenous mDll4 (n=2) was implanted with tumor cells and treated with hDll4-Fc (25 mg/kg) following the same dosing schedule.

TABLE 16

Mouse	Treatment	Tumor Size (mm^3)				
		Day 16	Day 18	Day 20	Day 22	Day 25
SCID	hDll4-hFc	162.0	232.8	320.0	336.0	253.1
SCID	hDll4-hFc	22.5	117.0	117.0	108.0	66.8
SCIDxhDll4	hDll4-hFc	288.0	320.0	352.0	446.0	320.0
SCIDxhDll4	hFc	162.0	288.0	320.0	500.0	550.0
SCIDxhDll4	hFc	162.0	220.5	352.0	662.0	661.5
SCIDxhDll4	hFc	93.8	135.0	179.6	352.0	726.0
SCIDxhDll4	REGN421	144.0	245.0	320.0	162.0	144.0
SCIDxhDll4	REGN421	87.5	162.0	153.0	225.0	135.0
SCIDxhDll4	REGN421	144.0	196.0	272.0	162.0	152.5

TABLE 16

Mouse	Treatment	Tumor Size (mm^3)
SCID	hDll4-hFc	308.0
SCID	hDll4-hFc	105.0
SCIDxhDll4	hDll4-hFc	480.0
SCIDxhDll4	hFc	924.0
SCIDxhDll4	hFc	1020.0
SCIDxhDll4	hFc	792.0
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tccggggtcc ctgacaggtt cagtggcagt ggatcaggca cagattttac actgaagatc 240
agaagagtgg aggctgagga tgttgggatt tattactgca tgcaagctct acacactcct 300
tacacttttg gccaggggac caaggtggag atcaaac 337

<210> 12
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 12
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 Asn
20 25 30

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

<210> 13
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 13
cagagcctcc tgcataatag tggatacaac ttt 33

<210> 14
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 14
Gln Ser Leu Leu His Asn Ser Gly Tyr Asn Phe
1 5 10

<210> 15
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 15
ttgcgttct 9

<210> 16
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 16
Leu Arg Ser
1

<210> 17

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

<220>
<223> Synthetic

<400> 17
atgcaagctc tacacactcc ttacact 27

<210> 18
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 18
Met Gln Ala Leu His Thr Pro Tyr Thr
1 5

<210> 19
<211> 376
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 19
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctggggggtc cctgagactc 60
tcctgtgtag cctctggatt cacctttagt agctattgga tgacctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtggccaac ataaaacaag atggaagtga gaaatactat 180
gtggactctg tgaagggccg attcaccgtc tccagagaca acgccaagaa ctcagtgtat 240
ctgcaaatga gcagcctgag agccgaggac acggctgtgt attactgtgc gagagattgg 300
aactatggcc ccgattacta ctactaccac ggtttggacg tctggggcca agggaccacg 360
gtcaccgtct cctcag 376

<210> 20
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

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

Ala Arg Asp Trp Asn Tyr Gly Pro Asp Tyr Tyr Tyr Tyr His Gly Leu
100 105 110
Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 21
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 21
ggattcacct ttagtagcta ttgg 24

<210> 22
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 22
Gly Phe Thr Phe Ser Ser Tyr Trp
1 5

<210> 23
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 23
ataaaacaag atggaagtga gaaa 24

<210> 24
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 24
Ile Lys Gln Asp Gly Ser Glu Lys
1 5

<210> 25
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 25
gcgagagatt ggaactatgg ccccgattac tactactacc acggtttgga cgtc 54

<210> 26
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 26
Ala Arg Asp Trp Asn Tyr Gly Pro Asp Tyr Tyr Tyr Tyr His Gly Leu
1 5 10 15
Asp Val

<210> 27
<211> 322
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 27
gacctccaga tgacccagtc tccgtcctcc ctgtctgtat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gggcattaga aatgatttag gctggtttca gcagaaacca 120
gggaaagccc ctaagcgcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgctgcct 240
gaagattttg caacttatta ctgtctacag cataatactt acccgtacac ttttggccag 300
gggaccaagc tggagatcaa ac 322

<210> 28
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 28
Asp Leu Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Val Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
20 25 30
Leu Gly Trp Phe Gln Gln Lys Pro Gly Lys 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 Leu Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Thr Tyr Pro Tyr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 29

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

<220>
<223> Synthetic

<400> 29
cagggcatta gaaatgat 18

<210> 30
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 30
Gln Gly Ile Arg Asn Asp
1 5

<210> 31
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 31
gctgcatcc 9

<210> 32
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 32
Ala Ala Ser
1

<210> 33
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 33
ctacagcata atacttaccc gtacact 27

<210> 34
<211> 9
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 34
Leu Gln His Asn Thr Tyr Pro Tyr Thr
1   5

<210> 35
<211> 361
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 35
caggggcagt tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgaag catctggatt cagtttcaga agttatggca tgcactgggt ccgccaggct 120
ccaggcaggg gactggagtg gatggcagtt atttggtacg atggcagtaa gacatactat 180
acagagtccg tgacgggccg attcaccatc tccagagaca attccaagaa cacgctatat 240
ctgcaaatga acagcctgag agccgaggac acggctgttt attactgtgc gagcggtttt 300
tcagtgcctg ccacgatcct tgacaactgg ggccagggaa ccctggtctc cgtctcctca 360
g   361

<210> 36
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 36
Gln Gly Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1   5   10   15
Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Ser Phe Arg Ser Tyr
            20   25   30
Gly Met His Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Met
        35   40   45
Ala Val Ile Trp Tyr Asp Gly Ser Lys Thr Tyr Tyr Thr Glu Ser Val
    50   55   60
Thr Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Ser Gly Phe Ser Val Pro Ala Thr Ile Leu Asp Asn Trp Gly Gln
            100   105   110
Gly Thr Leu Val Ser Val Ser Ser
        115   120

<210> 37
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 37
ggattcagtt tcagaagtta tggc 24

<210> 38
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 38
Gly Phe Ser Phe Arg Ser Tyr Gly
1 5

<210> 39
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 39
atttggtacg atggcagtaa gaca 24

<210> 40
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 40
Ile Trp Tyr Asp Gly Ser Lys Thr
1 5

<210> 41
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 41
gcgagcggtt tttcagtgcc tgccacgatc cttgacaac 39

<210> 42
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 42

Ala Ser Gly Phe Ser Val Pro Ala Thr Ile Leu Asp Asn
1 5 10

<210> 43
<211> 322
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 43
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gggcattaga aatgatttag gctggtttca gcagaaacca 120
gggaaagccc ctaaccgcct gatctatgga gcatccagtt tggaaggtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttcactctca caatcagcag cctgcagcca 240
gaagattttg caacttatta ctgtctacag cataattctt acccgtggac gttcggccaa 300
gggaccaagg tggaaatcaa ac 322

<210> 44
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 44
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
20 25 30
Leu Gly Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Asn Arg Leu Ile
35 40 45
Tyr Gly Ala Ser Ser Leu Glu Gly 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 His Asn Ser Tyr Pro Trp
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 45
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 45
cagggcatta gaaatgat 18

<210> 46
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 46
Gln Gly Ile Arg Asn Asp
1 5

<210> 47
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 47
ggagcatcc 9

<210> 48
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 48
Gly Ala Ser
1

<210> 49
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 49
ctacagcata attcttaccc gtggacg 27

<210> 50
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 50
Leu Gln His Asn Ser Tyr Pro Trp Thr
1 5

<210> 51
<211> 367
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 51
caggtgcagc tggtggagtc tgggggaggc gtagtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtggcagtt atatggtatg atggaaataa taaatactat 180
atagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagaccgt 300
ggatatagtg gctacgaggg atacttcgat ctctggggcc gtggcaccct ggtcactgtc 360
tcctcag 367

<210> 52
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 52
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Val Ile Trp Tyr Asp Gly Asn Asn Lys Tyr Tyr Ile Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Asp Arg Gly Tyr Ser Gly Tyr Glu Gly Tyr Phe Asp Leu Trp
100 105 110
Gly Arg Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 53
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 53
ggattcacct tcagtagcta tggc 24

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

<220>
<223> Synthetic

<400> 54
Gly Phe Thr Phe Ser Ser Tyr Gly
1 5

<210> 55
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 55
atatggtatg atggaaataa taaa 24

<210> 56
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 56
Ile Trp Tyr Asp Gly Asn Asn Lys
1 5

<210> 57
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 57
gcgagagacc gtggatatag tggctacgag ggatacttcg atctc 45

<210> 58
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 58
Ala Arg Asp Arg Gly Tyr Ser Gly Tyr Glu Gly Tyr Phe Asp Leu
1 5 10 15

<210> 59
<211> 337
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 59
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60
ctcaactgta agtccagcca gagtgtttta tacagctcca acaataagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180
gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcaggctga agatgtggca gtttatttct gtcagcaata ttatactact 300
tggacgttcg gccaagggac caaggtggaa atcaaac 337

<210> 60
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 60
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Glu Arg Ala Thr Leu Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
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 Phe Cys Gln Gln
85 90 95
Tyr Tyr Thr Thr Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 61
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 61
cagagtgttt tatacagctc caacaataag aactac 36

<210> 62
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 62
Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr
1 5 10

<210> 63
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 63
tgggcatct 9

<210> 64
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 64
Trp Ala Ser
1

<210> 65
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 65
cagcaatatt atactacttg gacg 24

<210> 66
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 66
Gln Gln Tyr Tyr Thr Thr Trp Thr
1 5

<210> 67
<211> 385
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 67
caggtgcagt tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cctctgcatc caccttcagt aggcatggca tgcactgggt ccgccaggct 120
ccaggcaagg gactggagtg ggtggcagtt atatcatatg atggaaataa taaatactat 180
gtagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga atagcctgag aactgacgac acggctgtgt attattgttc gaaagagtta 300
gtaggtatta ctggaaacct ggtctactac tactactacg gaatggacgt ctggggccaa 360
gggaccacgg tcaccgtctc ctcag 385

<210> 68
<211> 128
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 68
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Ala Ser Thr Phe Ser Arg His
            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 Asn Asn Lys Tyr Tyr Val Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Thr Asp Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ser Lys Glu Leu Val Gly Ile Thr Gly Asn Leu Val Tyr Tyr Tyr Tyr
            100   105   110
Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120   125

<210> 69
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 69
gcatccacct tcagtaggca tggc   24

<210> 70
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 70
Ala Ser Thr Phe Ser Arg His Gly
1   5

<210> 71
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 71
atatcatatg atggaaataa taaa   24

<210> 72
<211> 8

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 72
Ile Ser Tyr Asp Gly Asn Asn Lys
1 5

<210> 73
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 73
tcgaaagagt tagtaggtat tactggaaac ctggtctact actactacta cggaatggac 60
gtc 63

<210> 74
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 74
Ser Lys Glu Leu Val Gly Ile Thr Gly Asn Leu Val Tyr Tyr Tyr Tyr
1 5 10 15
Tyr Gly Met Asp Val
20

<210> 75
<211> 325
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 75
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gactattaac agcagctact taggctggta ccagcagaaa 120
cctggccagg ctcccagact cctcatctat ggtgcatcca acagggccac tggcatccca 180
gacagtttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcaa cattataaca actcacctta cactttggc 300
caggggacca agctggagat caaac 325

<210> 76
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 76
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 Thr Ile Asn Ser Ser
20 25 30
Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Ile Pro Asp Ser 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 His Tyr Asn Asn Ser Pro
85 90 95
Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 77
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 77
cagactatta acagcagcta c 21

<210> 78
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 78
Gln Thr Ile Asn Ser Ser Tyr
1 5

<210> 79
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 79
ggtgcatcc 9

<210> 80
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 80
Gly Ala Ser
1

<210> 81
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 81
caacattata acaactcacc ttacact 27

<210> 82
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 82
Gln His Tyr Asn Asn Ser Pro Tyr Thr
1 5

<210> 83
<211> 361
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 83
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60
acctgcactg tctctggtgg ctccataagc agtggtggtt actactggag ctggatccgc 120
cactacccag ggaagggcct ggagtggatt ggctacgtcc attacagtgg gaacacccac 180
tacaatacgt ccctcaagag gcgacttacc atatcaatag acacgtctaa gagccaattc 240
tccctggatc tgagctctgt gactgccgcg gacacggccg tgtattactg tgcgagagcc 300
ccccgtggat accattactt tgcctactgg ggccagggaa ccctggtcac cgtctcctca 360
g 361

<210> 84
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 84
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30
Gly Tyr Tyr Trp Ser Trp Ile Arg His Tyr Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Val His Tyr Ser Gly Asn Thr His Tyr Asn Thr Ser
50 55 60
Leu Lys Arg Arg Leu Thr Ile Ser Ile Asp Thr Ser Lys Ser Gln Phe
65 70 75 80
Ser Leu Asp Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Ala Arg Ala Pro Arg Gly Tyr His Tyr Phe Ala Tyr Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser
115 120

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<220>
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<210> 86
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<220>
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<400> 86
Gly Gly Ser Ile Ser Ser Gly Gly Tyr Tyr
1 5 10

<210> 87
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<220>
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<400> 87
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<210> 88
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<220>
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<400> 88
Val His Tyr Ser Gly Asn Thr
1 5

<210> 89

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

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<400> 89
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<210> 90
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<220>
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<400> 90
Ala Arg Ala Pro Arg Gly Tyr His Tyr Phe Ala Tyr
1 5 10

<210> 91
<211> 325
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<220>
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<400> 91
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cctggccagg ctcccaggct cctcatcttt ggtgcatcca gcagggccac tggcatacca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccgct cactttcggc 300
ggagggacca aggtggagat caaac 325

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<211> 108
<212> PRT
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<400> 92
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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Ser Arg
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Phe 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> 93
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<220>
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<400> 93
cagagtatta gcagcaggta c 21

<210> 94
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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<400> 94
Gln Ser Ile Ser Ser Arg Tyr
1 5

<210> 95
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<400> 95
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<220>
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<400> 96
Gly Ala Ser
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<210> 97
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 97
cagcagtatg gtagctcacc gctcact 27

<210> 98
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<400> 98
Gln Gln Tyr Gly Ser Ser Pro Leu Thr
1 5

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<212> DNA
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acctgcactg tctctggtgg ctccatcagc agtagtggtt actactggag ttggatccgc 120
cagcacccag ggaagggcct ggagtggatt gggtacgtcc attacagtgg gaacacccac 180
tacagcccgt ccctcaagag tcgacttacc atatcagttg acacgtctaa gaaccagttc 240
tccctgaagc tgagctctgt gactgccgcg gacacggccg tgtattactg tgcgagagcc 300
ccccgtggat accattactt tgcctactgg ggccagggaa ccctggtcac cgtctcctca 360
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<210> 100
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<212> PRT
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<220>
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<400> 100
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Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser
20 25 30
Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45
Trp Ile Gly Tyr Val His Tyr Ser Gly Asn Thr His Tyr Ser Pro Ser
50 55 60
Leu Lys Ser Arg Leu Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80
Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Ala Arg Ala Pro Arg Gly Tyr His Tyr Phe Ala Tyr Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 101
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<400> 101
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<210> 102
<211> 10
<212> PRT
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<220>
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<400> 102
Gly Gly Ser Ile Ser Ser Ser Gly Tyr Tyr
1 5 10

<210> 103
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<220>
<223> Synthetic

<400> 103
gtccattaca gtgggaacac c 21

<210> 104
<211> 7
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<220>
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<400> 104
Val His Tyr Ser Gly Asn Thr
1 5

<210> 105
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<220>
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<400> 105
gcgagagccc cccgtggata ccattacttt gcctac 36

<210> 106
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<220>
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<400> 106
Ala Arg Ala Pro Arg Gly Tyr His Tyr Phe Ala Tyr
1 5 10

<210> 107
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<220>
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<400> 107
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cctggccagg ctcccaggct cctcatcttt ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggcca gacttcactc tcaccattag gagactggag 240
cctgaagatt ttgcggtgta ttactgtcag cagtatggta gttcaccgct cactttcggc 300
ggagggacca aggtggagat caaac 325

<210> 108
<211> 108
<212> PRT
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<220>
<223> Synthetic

<400> 108
Lys 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 Ile Ser Ser Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Phe Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60
Gly Ser Gly Ser Gly Pro Asp Phe Thr Leu Thr Ile Arg 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> 109
<211> 21
<212> DNA
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<220>
<223> Synthetic

<400> 109
cagagtatta gcagcagcta c 21

<210> 110

<211> 7
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<220>
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<400> 110
Gln Ser Ile Ser Ser Ser Tyr
1 5

<210> 111
<211> 9
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<220>
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<400> 111
ggtgcatcc 9

<210> 112
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<220>
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<400> 112
Gly Ala Ser
1

<210> 113
<211> 27
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<220>
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<400> 113
cagcagtatg gtagttcacc gctcact 27

<210> 114
<211> 9
<212> PRT
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<220>
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<400> 114
Gln Gln Tyr Gly Ser Ser Pro Leu Thr
1 5

<210> 115

<211> 358
<212> DNA
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<220>
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<400> 115
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tcctgcaagg cttctggtta caccttttcc acctatggta tcagctgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggatgg atcagcgctt acgacaataa cgcggactat 180
gcacagaact tccaggccag agtcaccatg accacagaca catccacgac cacagcctac 240
atggagctga ggagcctgag atctgacgac acggccgtgt attactgtgc gaggtatagc 300
tggaactttc actggttcga cccctggggc cagggaaccc tggtcaccgt ctcctcag 358

<210> 116
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 116
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser 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 Ala Tyr Asp Asn Asn Ala Asp Tyr Ala Gln Asn Phe
50 55 60
Gln Ala 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 Val Tyr Tyr Cys
85 90 95
Ala Arg Tyr Ser Trp Asn Phe His Trp Phe Asp Pro Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
115

<210> 117
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 117
ggttacacct tttccaccta tggt 24

<210> 118
<211> 8
<212> PRT
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<220>
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<400> 118
Gly Tyr Thr Phe Ser Thr Tyr Gly
1 5

<210> 119
<211> 24
<212> DNA
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<220>
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<400> 119
atcagcgctt acgacaataa cgcg 24

<210> 120
<211> 8
<212> PRT
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<220>
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<400> 120
Ile Ser Ala Tyr Asp Asn Asn Ala
1 5

<210> 121
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
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<400> 121
gcgaggtata gctggaactt tcactggttc gacccc 36

<210> 122
<211> 12
<212> PRT
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<220>
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<400> 122
Ala Arg Tyr Ser Trp Asn Phe His Trp Phe Asp Pro
1 5 10

<210> 123
<211> 325
<212> DNA
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<220>
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<400> 123
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ctctcctgca gggccagtca gagtgttagc agtacctact tagcctggta ccagcagcaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag cagtatggta actcaccgtg gacgttcggc 300
caagggacca aggtggaaat caaac 325

<210> 124
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 124
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Thr
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Gln 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 Asn Ser Pro
85 90 95
Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 125
<211> 21
<212> DNA
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<220>
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<400> 125
cagagtgtta gcagtaccta c 21

<210> 126
<211> 7
<212> PRT
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<220>
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<400> 126
Gln Ser Val Ser Ser Thr Tyr
1 5

<210> 127
<211> 9
<212> DNA
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<220>
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<400> 127
ggtgcatcc 9

<210> 128
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
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<400> 128
Gly Ala Ser
1

<210> 129
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<400> 129
cagcagtatg gtaactcacc gtggacg 27

<210> 130
<211> 9
<212> PRT
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<220>
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<400> 130
Gln Gln Tyr Gly Asn Ser Pro Trp Thr
1 5

<210> 131
<211> 358
<212> DNA
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<220>
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<400> 131
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tcctgcaggg cttctggtta cacctttacc aactatggta tcacctgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggatgg atcagcgctt acagtggtaa cacagactat 180
gcacagaagt tccaggccag aatcaccatg accacagaca catccacgac cacagcctac 240
atggaactga ggagcctgac atctgacgac acggccgtgt attactgtgc gaggtatagc 300
tggaactttc actggttcga cccctggggc cagggaaccc tggtcaccgt ctcctcag 358

<210> 132

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

<220>
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<400> 132
Gln Val His Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Arg Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30
Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Trp Ile Ser Ala Tyr Ser Gly Asn Thr Asp Tyr Ala Gln Lys Phe
50 55 60
Gln Ala Arg Ile Thr Met Thr Thr Asp Thr Ser Thr Thr Thr Ala Tyr
65 70 75 80
Met Glu Leu Arg Ser Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Tyr Ser Trp Asn Phe His Trp Phe Asp Pro Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
115

<210> 133
<211> 24
<212> DNA
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<220>
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<400> 133
ggttacacct ttaccaacta tggt 24

<210> 134
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<212> PRT
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<220>
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<400> 134
Gly Tyr Thr Phe Thr Asn Tyr Gly
1 5

<210> 135
<211> 24
<212> DNA
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<400> 135
atcagcgctt acaggggtaa caca 24

<210> 136
<211> 8
<212> PRT
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<220>
<223> Synthetic

<400> 136
Ile Ser Ala Tyr Ser Gly Asn Thr
1 5

<210> 137
<211> 36
<212> DNA
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<220>
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<400> 137
gcgaggtata gctggaactt tcactggttc gacccc 36

<210> 138
<211> 12
<212> PRT
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<220>
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<400> 138
Ala Arg Tyr Ser Trp Asn Phe His Trp Phe Asp Pro
1 5 10

<210> 139
<211> 325
<212> DNA
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<220>
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<400> 139
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ctctcctgca gggccagtca gagtgttagt agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagtctggag 240
cctgaagatt ttgcagtgta ttactgtcag cagtgtggtg gctcaccgtg gacgttcggc 300
caagggacca gggtggagat caaac 325

<210> 140
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
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<400> 140
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1 5 10 15
Asp Arg Val Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Cys Gly Gly Ser Pro
85 90 95
Trp Thr Phe Gly Gln Gly Thr Arg Val Glu Ile Lys
100 105

<210> 141
<211> 21
<212> DNA
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<220>
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<400> 141
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<210> 142
<211> 7
<212> PRT
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<220>
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<400> 142
Gln Ser Val Ser Ser Ser Tyr
1 5

<210> 143
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
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<400> 143
ggtgcatcc 9

<210> 144
<211> 3
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Gly Ala Ser
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<210> 145
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<212> DNA
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<220>
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<400> 145
cagcagtgtg gtggctcacc gtggacg 27

<210> 146
<211> 9
<212> PRT
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<220>
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<400> 146
Gln Gln Cys Gly Gly Ser Pro Trp Thr
1 5

<210> 147
<211> 358
<212> DNA
<213> Artificial Sequence

<220>
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<400> 147
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gcctgcaagg cttctggtta cacctttacc cactatggtt tcacctgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggatgg atcagcgctt acagtggtca tacagactat 180
gcacggaagt tccaggccag agtcaccatg accacagaca cattcacgac cacagcctac 240
atggaactga ggagcctgag atctgacgac acggccgttt attactgtgc gagttatagc 300
tggaactttc actggttcga cccctggggc cagggaaccc tggtcaccgt ctcctcag 358

<210> 148
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
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<400> 148
Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ala Cys Lys Ala Ser Gly Tyr Thr Phe Thr His Tyr
20 25 30
Gly Phe Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Trp Ile Ser Ala Tyr Ser Gly His Thr Asp Tyr Ala Arg Lys Phe
50 55 60

Gln Ala Arg Val Thr Met Thr Thr Asp Thr Phe Thr 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
Ala Ser Tyr Ser Trp Asn Phe His Trp Phe Asp Pro Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
115

<210> 149
<211> 24
<212> DNA
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<220>
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<400> 149
ggttacacct ttacccacta tggt 24

<210> 150
<211> 8
<212> PRT
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<220>
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<400> 150
Gly Tyr Thr Phe Thr His Tyr Gly
1 5

<210> 151
<211> 24
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<220>
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<400> 151
atcagcgctt acagtggtca taca 24

<210> 152
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
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<400> 152
Ile Ser Ala Tyr Ser Gly His Thr
1 5

<210> 153
<211> 36
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 153
gcgagttata gctggaactt tcactggttc gacccc 36

<210> 154
<211> 12
<212> PRT
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<220>
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<400> 154
Ala Ser Tyr Ser Trp Asn Phe His Trp Phe Asp Pro
1 5 10

<210> 155
<211> 325
<212> DNA
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<220>
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<400> 155
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ctctcctgca gggccagtca gagtgttagt accacctact tagcctggta ccagcagaaa 120
cctggccagg ctcccagtct cctcatctat ggtacatcca ccagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggact gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag cagtgtggtg gctcaccgtg gacgttcggc 300
caagggacca aggtgaaaat caaac 325

<210> 156
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
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<400> 156
Gln 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 Thr Thr
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Ser Leu Leu
35 40 45
Ile Tyr Gly Thr Ser Thr 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 Cys Gly Gly Ser Pro
85 90 95
Trp Thr Phe Gly Gln Gly Thr Lys Val Lys Ile Lys
100 105

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<210> 157
<211> 21
<212> DNA
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<220>
<223> Synthetic

<400> 157
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<210> 158
<211> 7
<212> PRT
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<220>
<223> Synthetic

<400> 158
Gln Ser Val Ser Thr Thr Tyr
1               5


<210> 159
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 159
ggtacatcc                                                9

<210> 160
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 160
Gly Thr Ser
1


<210> 161
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 161
cagcagtgtg gtggctcacc gtggacg                            27

<210> 162
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<211> 9
<212> PRT
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<220>
<223> Synthetic

<400> 162
Gln Gln Cys Gly Gly Ser Pro Trp Thr
1 5

<210> 163
<211> 367
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 163
caggtgcagt tggtgcagtc tggggctgag gtgaagaagc ctggggccgc tgtgaaggtc 60
tcctgcaagg cttctggata cacgttcacc agttatgata tcaactgggt gcgacaggcc 120
actggacaag ggcttgagtg gatgggatgg ataaacccta acagtggtaa cacaggctat 180
gcacagaagt ttcagggcag agtcaccttg accaggaaca cctccataag cacagcctac 240
atggaactga gcagcctgag atctgaggac acggccgttt attactgtgc gagagaggga 300
tattgtggtg gtgattgcta tgcttttgat atctggggcc aagggacaat ggtcaccgtc 360
tcttcag 367

<210> 164
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 164
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ala Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30
Asp Ile Asn Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Trp Ile Asn Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe
50 55 60
Gln Gly Arg Val Thr Leu Thr Arg Asn Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Glu Gly Tyr Cys Gly Gly Asp Cys Tyr Ala Phe Asp Ile Trp
100 105 110
Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 165
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 165
ggatacacgt tcaccagtta tgat 24

<210> 166
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 166
Gly Tyr Thr Phe Thr Ser Tyr Asp
1 5

<210> 167
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 167
ataaacccta acagtggtaa caca 24

<210> 168
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 168
Ile Asn Pro Asn Ser Gly Asn Thr
1 5

<210> 169
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 169
gcgagagagg gatattgtgg tggtgattgc tatgcttttg atatc 45

<210> 170
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 170
Ala Arg Glu Gly Tyr Cys Gly Gly Asp Cys Tyr Ala Phe Asp Ile
1   5   10   15

<210> 171
<211> 325
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 171
gaaattgtgt tgacacaatc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatcttt ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccgct cactttcggc 300
ggagggacca aggtggagat caaac 325

<210> 172
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 172
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1   5   10   15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
            20   25   30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35   40   45
Ile Phe 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> 173
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 173
cagagtgtta gcagcagcta c 21

<210> 174
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 174
Gln Ser Val Ser Ser Ser Tyr
1 5

<210> 175
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 175
ggtgcatcc 9

<210> 176
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 176
Gly Ala Ser
1

<210> 177
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 177
cagcagtatg gtagctcacc gctcact 27

<210> 178
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 178
Gln Gln Tyr Gly Ser Ser Pro Leu Thr
1 5

<210> 179
<211> 361
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 179
cagctgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
acctgcactg tctctggtgg ctccatcagc agtagtagtt actactgggg ctggatccgc 120
cagcccccag ggaaggggct ggagtggatt gggagtatct attatagtgg gagcacctac 180
tacaacccgt ccctcaagag tcgagtcacc atatccgtag acacgtccaa gaaccagttc 240
tccctgaagc tgagctctgt gaccgccgca gacacggctg tgtattactg tgcggcaaac 300
tgggacgacg ccttcttctt tgactactgg ggccagggaa ccctggtcac cgtctcctca 360
g 361

<210> 180
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 180
Gln Leu 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 Gly Ser Ile Ser Ser Ser
20 25 30
Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45
Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60
Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80
Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Ala Ala Asn Trp Asp Asp Ala Phe Phe Phe Asp Tyr Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 181
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 181
ggtggctcca tcagcagtag tagttactac 30

<210> 182
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 182

Gly Gly Ser Ile Ser Ser Ser Ser Tyr Tyr
1 5 10

<210> 183
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 183
atctattata gtgggagcac c 21

<210> 184
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 184
Ile Tyr Tyr Ser Gly Ser Thr
1 5

<210> 185
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 185
gcggcaaact gggacgacgc cttcttcttt gactac 36

<210> 186
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 186
Ala Ala Asn Trp Asp Asp Ala Phe Phe Phe Asp Tyr
1 5 10

<210> 187
<211> 322
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 187

gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctataag gcgtctagtt tagaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240
gatgattttg caacttatta ctgccaacag tataatagtt attcgtacac ttttggccag 300
gggaccaagc tggagatcaa ac 322

<210> 188
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 188
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 Ser Tyr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 189
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 189
cagagtatta gtagctgg 18

<210> 190
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 190
Gln Ser Ile Ser Ser Trp
1 5

<210> 191
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 191
aaggcgtct 9

<210> 192
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 192
Lys Ala Ser
1

<210> 193
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 193
caacagtata atagttattc gtacact 27

<210> 194
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 194
Gln Gln Tyr Asn Ser Tyr Ser Tyr Thr
1 5

<210> 195
<211> 352
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 195
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgcaagg cttctggata caccttcacc ggctactata ttcactgggt acgacaggcc 120
cctggacaag gccttgagtg gatgggatgg atcaacccta acagtggtgg cacaaactat 180
gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcac cacagcctac 240
atggagctga gcaggctgat atctgacgac acggccgtgt attactgtgc gagaggaccc 300
tgggatttct ttgactactg gggccaggga accctggtca ccgtctcctc ag 352

<210> 196
<211> 117

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 196
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 Gly Tyr
            20   25   30
Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45
Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
    50   55   60
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Thr Thr Ala Tyr
65   70   75   80
Met Glu Leu Ser Arg Leu Ile Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Gly Pro Trp Asp Phe Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100   105   110
Val Thr Val Ser Ser
        115

<210> 197
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 197
ggatacacct tcaccggcta ctat 24

<210> 198
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 198
Gly Tyr Thr Phe Thr Gly Tyr Tyr
1   5

<210> 199
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 199
atcaacccta acagtggtgg caca 24

<210> 200

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

<220>
<223> Synthetic

<400> 200
Ile Asn Pro Asn Ser Gly Gly Thr
1 5

<210> 201
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 201
gcgagaggac cctgggattt ctttgactac 30

<210> 202
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 202
Ala Arg Gly Pro Trp Asp Phe Phe Asp Tyr
1 5 10

<210> 203
<211> 340
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 203
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60
atcaactgca agtccagcca gagtgtttta tacagctcca acaataagaa ctacttagct 120
tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180
gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcaata ttatagtact 300
ccgtacactt ttggccaggg gaccaagctg gagatcaaac 340

<210> 204
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 204

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

<210> 205
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 205
cagagtgttt tatacagctc caacaataag aactac 36

<210> 206
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 206
Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr
1 5 10

<210> 207
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 207
tgggcatct 9

<210> 208
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 208
Trp Ala Ser
1

<210> 209
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 209
cagcaatatt atagtactcc gtacact 27

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

<220>
<223> Synthetic

<400> 210
Gln Gln Tyr Tyr Ser Thr Pro Tyr Thr
1 5

<210> 211
<211> 352
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 211
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgcaagg cttctggata caccttcacc ggctactata ttcactgggt acgacaggcc 120
cctggacaag gccttgagtg gatgggatgg atcaacccta acagtggtgg cacaaactat 180
gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240
atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gagaggaccc 300
tgggatttct ttgactactg gggccaggga accctggtca ccgtctcctc ag 352

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

<220>
<223> Synthetic

<400> 212
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 Gly Tyr
20 25 30
Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe

50 55 60
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Gly Pro Trp Asp Phe Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110
Val Thr Val Ser Ser
115

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

<220>
<223> Synthetic

<400> 213
ggatacacct tcaccggcta ctat 24

<210> 214
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 214
Gly Tyr Thr Phe Thr Gly Tyr Tyr
1 5

<210> 215
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 215
atcaacccta acagtggtgg caca 24

<210> 216
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 216
Ile Asn Pro Asn Ser Gly Gly Thr
1 5

<210> 217
<211> 30

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 217
gcgagaggac cctgggattt ctttgactac 30

<210> 218
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 218
Ala Arg Gly Pro Trp Asp Phe Phe Asp Tyr
1 5 10

<210> 219
<211> 340
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 219
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60
atcaactgca agtccagcca gagtgtttta tacagctcca acaataagaa ctacttagct 120
tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180
gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcaata ttatagtact 300
ccgtacactt ttggccaggg gaccaagctg gagatcaaac 340

<210> 220
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 220
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 Ser
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 Gln Gln
85 90 95
Tyr Tyr Ser Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
100 105 110

Lys

<210> 221
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 221
cagagtgttt tatacagctc caacaataag aactac 36

<210> 222
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 222
Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr
1 5 10

<210> 223
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 223
tgggcatct 9

<210> 224
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 224
Trp Ala Ser
1

<210> 225
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 225

cagcaatatt atagtactcc gtacact 27

<210> 226
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 226
Gln Gln Tyr Tyr Ser Thr Pro Tyr Thr
1 5

<210> 227
<211> 361
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 227
caggtgcagt tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60
acctgcactg tctctggtgg ctccatcggc agtggtggtt actactggag ctggatccgc 120
cagcacccag ggaagggcct ggagtggatt gggtacgtcc attacagtgg gaacacccac 180
tacaacccgt ccctcaagag tcgactttcc atatcaatag acacgtctaa gatccagttc 240
tccctgaagc tgagctctgt gactgccgcg gacacggccg tgtattactg tgcgagagcc 300
ccccgtggat accattactt tgcctactgg ggccagggaa ccctggtcac cgtctcctca 360
g 361

<210> 228
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 228
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Gly Ser Gly
20 25 30
Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45
Trp Ile Gly Tyr Val His Tyr Ser Gly Asn Thr His Tyr Asn Pro Ser
50 55 60
Leu Lys Ser Arg Leu Ser Ile Ser Ile Asp Thr Ser Lys Ile Gln Phe
65 70 75 80
Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Ala Arg Ala Pro Arg Gly Tyr His Tyr Phe Ala Tyr Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 229
<211> 30

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 229
ggtggctcca tcggcagtgg tggttactac 30

<210> 230
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 230
Gly Gly Ser Ile Gly Ser Gly Gly Tyr Tyr
1 5 10

<210> 231
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 231
gtccattaca gtgggaacac c 21

<210> 232
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 232
Val His Tyr Ser Gly Asn Thr
1 5

<210> 233
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 233
gcgagagccc cccgtggata ccattacttt gcctac 36

<210> 234
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 234
Ala Arg Ala Pro Arg Gly Tyr His Tyr Phe Ala Tyr
1 5 10

<210> 235
<211> 325
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 235
gaaattgtgt tgacacaatc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatcttt ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccgct cactttcggc 300
ggagggacca aggtggagat caaac 325

<210> 236
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 236
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Phe 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> 237
<211> 21
<212> DNA
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<220>
<223> Synthetic

<400> 237
cagagtgtta gcagcagcta c 21

<210> 238
<211> 7
<212> PRT
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<220>
<223> Synthetic

<400> 238
Gln Ser Val Ser Ser Ser Tyr
1   5

<210> 239
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 239
ggtgcatcc 9

<210> 240
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 240
Gly Ala Ser
1

<210> 241
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 241
cagcagtatg gtagctcacc gctcact 27

<210> 242
<211> 9
<212> PRT
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<220>
<223> Synthetic

<400> 242
Gln Gln Tyr Gly Ser Ser Pro Leu Thr
1   5

<210> 243
<211> 361
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 243
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60
acctgcactg tctctggtgg ctccatcagc agtggtggtt actactggag ctggatccgc 120
cagtacccag ggaagggcct ggagtggatt ggttacgtcc attacagtgg gagcacccac 180
tacaacccgt ccctcaagag tcgacttacc atatcaatag acacgtctaa gagccagttc 240
tccctgaagc tgagctctgt gactgccgcg gacacggccg tgtattactg tgcgagagcc 300
ccccgtggat accattactt tgcctactgg ggccagggaa ccctggtcac cgtctcctca 360
g 361

<210> 244
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 244
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30
Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Tyr Pro Gly Lys Gly Leu Glu
35 40 45
Trp Ile Gly Tyr Val His Tyr Ser Gly Ser Thr His Tyr Asn Pro Ser
50 55 60
Leu Lys Ser Arg Leu Thr Ile Ser Ile Asp Thr Ser Lys Ser Gln Phe
65 70 75 80
Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Ala Arg Ala Pro Arg Gly Tyr His Tyr Phe Ala Tyr Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 245
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 245
ggtggctcca tcagcagtgg tggttactac 30

<210> 246
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 246
Gly Gly Ser Ile Ser Ser Gly Gly Tyr Tyr
1 5 10

<210> 247
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 247
gtccattaca gtgggagcac c 21

<210> 248
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 248
Val His Tyr Ser Gly Ser Thr
1 5

<210> 249
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
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<400> 249
gcgagagccc cccgtggata ccattacttt gcctac 36

<210> 250
<211> 12
<212> PRT
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<220>
<223> Synthetic

<400> 250
Ala Arg Ala Pro Arg Gly Tyr His Tyr Phe Ala Tyr
1 5 10

<210> 251
<211> 325
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 251
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ctctcctgca gggccagtca gagtgttagc agcaggtact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatcttt ggtgcatcca gcagggccac tggcatacca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccgct cactttcggc 300
ggagggacca aggtggagat caaac 325

<210> 252
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 252
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Arg
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Phe 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> 253
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 253
cagagtgtta gcagcaggta c 21

<210> 254
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 254
Gln Ser Val Ser Ser Arg Tyr
1 5

<210> 255
<211> 9

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 255
ggtgcatcc 9

<210> 256
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 256
Gly Ala Ser
1

<210> 257
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 257
cagcagtatg gtagctcacc gctcact 27

<210> 258
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 258
Gln Gln Tyr Gly Ser Ser Pro Leu Thr
1 5

<210> 259
<211> 355
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 259
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acctgcactg tctctggtgg ctccatcagc agtggtggtt actactggag ctggatccgc 120
cagcacccag ggaagggcct ggagtggatt gggtacatct attacagtgg gagcacctac 180
tacaacccgt ccctcaagag tcgaattatc atatcagtag acacgtctaa gaaccagttc 240
tccctgaagc tgagctctgt gactgccgcg gacacggccg tgtattactg tgcgagagaa 300
ggggctatgg tttttgacta ctggggccag ggaaccctgg tcaccgtctc ctcag 355

<210> 260
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 260
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30
Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45
Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60
Leu Lys Ser Arg Ile Ile Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80
Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Ala Arg Glu Gly Ala Met Val Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110
Leu Val Thr Val Ser Ser
115

<210> 261
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 261
ggtggctcca tcagcagtgg tggttactac 30

<210> 262
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 262
Gly Gly Ser Ile Ser Ser Gly Gly Tyr Tyr
1 5 10

<210> 263
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 263

atctattaca gtgggagcac c 21

<210> 264
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 264
Ile Tyr Tyr Ser Gly Ser Thr
1 5

<210> 265
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 265
gcgagagaag gggctatggt ttttgactac 30

<210> 266
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 266
Ala Arg Glu Gly Ala Met Val Phe Asp Tyr
1 5 10

<210> 267
<211> 322
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 267
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atcacttgct gggccagtca gggcattagc agttatttag cctggtatca gcaaaaacca 120
gggaaagccc ctaaactcct gatttatgct gcatccgctt tgcaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtcaacag cttaatagtt acccgttcac ttttggccag 300
gggaccaagc tggagatcaa ac 322

<210> 268
<211> 107
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 268
Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Trp Ala Ser Gln Gly Ile Ser Ser Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Ala Ala Ser Ala 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 Phe
85 90 95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 269
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 269
cagggcatta gcagttat 18

<210> 270
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 270
Gln Gly Ile Ser Ser Tyr
1 5

<210> 271
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 271
gctgcatcc 9

<210> 272
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 272
Ala Ala Ser
1

<210> 273
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 273
caacagctta atagttaccc gttcact 27

<210> 274
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 274
Gln Gln Leu Asn Ser Tyr Pro Phe Thr
1 5

<210> 275
<211> 355
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 275
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acctgcactg tctctggtgg ctccatcagc agtggtggtt actactggag ctggatccgc 120
cagcacccag ggaagggcct ggagtggatt gggtacatct attacagtgg gagcacctac 180
tacaacccgt ccctcaagag tcgaattatc atatcagtag acacgtctaa gaaccagttc 240
tccctgaagc tgagctctgt gactgccgcg gacacggccg tgtattactg tgcgagagaa 300
ggggctatgg tttttgacta ctggggccag ggaaccctgg tcaccgtctc ctcag 355

<210> 276
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 276
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30
Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

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

<210> 277
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 277
ggtggctcca tcagcagtgg tggttactac 30

<210> 278
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 278
Gly Gly Ser Ile Ser Ser Gly Gly Tyr Tyr
1 5 10

<210> 279
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 279
atctattaca gtgggagcac c 21

<210> 280
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 280
Ile Tyr Tyr Ser Gly Ser Thr
1 5

<210> 281

<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 281
gcgagagaag gggctatggt ttttgactac 30

<210> 282
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 282
Ala Arg Glu Gly Ala Met Val Phe Asp Tyr
1 5 10

<210> 283
<211> 322
<212> DNA
<213> Artificial Sequence

<220>
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<400> 283
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atcacttgct gggccagtca gggcattagc agttatttag cctggtatca gcaaaaacca 120
gggaaagccc ctaaactcct gatttatgct gcatccgctt tgcaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtcaacag cttaatagtt acccgttcac ttttggccag 300
gggaccaagc tggagatcaa ac 322

<210> 284
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 284
Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Trp Ala Ser Gln Gly Ile Ser Ser Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Ala Ala Ser Ala 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 Phe
85 90 95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys

100 105

<210> 285
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 285
cagggcatta gcagttat 18

<210> 286
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 286
Gln Gly Ile Ser Ser Tyr
1 5

<210> 287
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 287
gctgcatcc 9

<210> 288
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 288
Ala Ala Ser
1

<210> 289
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 289
caacagctta atagttaccc gttcact 27

<210> 290
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 290
Gln Gln Leu Asn Ser Tyr Pro Phe Thr
1   5

<210> 291
<211> 355
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 291
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acctgcactg tctctggtgg ctccatcagc agtggtggtt actactggac ctggatccgc 120
cagcacccag ggaagggcct ggagtggatt gggtacatct attacagtgg gagcacctac 180
tacaacccgt ccctcaagag tcgagttatc atatcagtag acacgtctaa gaaccagttc 240
tccctgaagc tgagctctgt gactgccgcg gacacggccg tgtattactg tgcgagagaa 300
ggggctatgg tttttgacta ctggggccag ggaaccctgg tcaccgtctc ctcag 355

<210> 292
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 292
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1   5   10   15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20   25   30
Gly Tyr Tyr Trp Thr Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
        35   40   45
Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50   55   60
Leu Lys Ser Arg Val Ile Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65   70   75   80
Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85   90   95
Cys Ala Arg Glu Gly Ala Met Val Phe Asp Tyr Trp Gly Gln Gly Thr
            100   105   110
Leu Val Thr Val Ser Ser
        115

<210> 293
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 293
ggtggctcca tcagcagtgg tggttactac 30

<210> 294
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 294
Gly Gly Ser Ile Ser Ser Gly Gly Tyr Tyr
1 5 10

<210> 295
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 295
atctattaca gtgggagcac c 21

<210> 296
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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<400> 296
Ile Tyr Tyr Ser Gly Ser Thr
1 5

<210> 297
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 297
gcgagagaag gggctatggt ttttgactac 30

<210> 298
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 298
Ala Arg Glu Gly Ala Met Val Phe Asp Tyr
1 5 10

<210> 299
<211> 322
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 299
gacatccagt tgacccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgct gggccagtca gggcattagc agttatttag cctggtatca gcaaaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccgctt tgcaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtcaacag cttaatagtt acccgttcac ttttggccag 300
gggaccaagc tggagatcaa ac 322

<210> 300
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 300
Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Trp Ala Ser Gln Gly Ile Ser Ser Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Ala Ala Ser Ala 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 Phe
85 90 95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 301
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 301
cagggcatta gcagttat 18

<210> 302
<211> 6

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 302
Gln Gly Ile Ser Ser Tyr
1 5

<210> 303
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 303
gctgcatcc 9

<210> 304
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 304
Ala Ala Ser
1

<210> 305
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 305
caacagctta atagttaccc gttcact 27

<210> 306
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 306
Gln Gln Leu Asn Ser Tyr Pro Phe Thr
1 5

<210> 307
<211> 355

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 307
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60
acctgcactg tctctggtgg ctccatcagc agtggtggtt actactggac ctggatccgc 120
cagtacccag ggaagggcct ggagtggatt gggtacatct attacagtgg gagcacctac 180
tacaacccgt ccctcaagag tcgagttatc atatcagtag acacgtctaa gaaccagttc 240
tccctgaggc tgagctctgt gactgccgcg gacacggccg tgtattactg tgcgagagaa 300
ggggctatgg tttttgacta ctggggccag ggaaccctgg tcaccgtctc ctcag 355

<210> 308
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 308
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30
Gly Tyr Tyr Trp Thr Trp Ile Arg Gln Tyr Pro Gly Lys Gly Leu Glu
35 40 45
Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60
Leu Lys Ser Arg Val Ile Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80
Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Ala Arg Glu Gly Ala Met Val Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110
Leu Val Thr Val Ser Ser
115

<210> 309
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 309
ggtggctcca tcagcagtgg tggttactac 30

<210> 310
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 310

Gly Gly Ser Ile Ser Ser Gly Gly Tyr Tyr
1 5 10

<210> 311
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 311
atctattaca gtgggagcac c 21

<210> 312
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 312
Ile Tyr Tyr Ser Gly Ser Thr
1 5

<210> 313
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 313
gcgagagaag gggctatggt ttttgactac 30

<210> 314
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 314
Ala Arg Glu Gly Ala Met Val Phe Asp Tyr
1 5 10

<210> 315
<211> 322
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 315

gacatccagt tgacccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgct gggccagtca gggcattagc agttatttag cctggtatca gcaaaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccgctt tgcaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtcaacag cttaatagtt acccgttcac ttttggccag 300
gggaccaagc tggagatcaa ac 322

<210> 316
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 316
Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Trp Ala Ser Gln Gly Ile Ser Ser Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Ala Ala Ser Ala 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 Phe
85 90 95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 317
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 317
cagggcatta gcagttat 18

<210> 318
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 318
Gln Gly Ile Ser Ser Tyr
1 5

<210> 319
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 319
gctgcatcc 9

<210> 320
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 320
Ala Ala Ser
1

<210> 321
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 321
caacagctta atagttaccc gttcact 27

<210> 322
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 322
Gln Gln Leu Asn Ser Tyr Pro Phe Thr
1 5

<210> 323
<211> 358
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 323
caggttcacc tggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgcaggg cttctggtta cacctttacc aactatggta tcacctgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggatgg atcagcgcta acagtggtaa cacagactct 180
gcacagaagt tccaggccag agtcaccatg accacagaca catccacgac cacagcctac 240
atggaactga ggagcctgag atctgacgac acggccgtgt attattgtgc gacgtatagt 300
tggaactttc actggttcga cccctggggc cagggaaccc tggtcaccgt ctcctcag 358

<210> 324
<211> 119

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 324
Gln Val His Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Arg Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30
Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Trp Ile Ser Ala Asn Ser Gly Asn Thr Asp Ser Ala Gln Lys Phe
50 55 60
Gln Ala 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 Val Tyr Tyr Cys
85 90 95
Ala Thr Tyr Ser Trp Asn Phe His Trp Phe Asp Pro Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
115

<210> 325
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 325
ggttacacct ttaccaacta tggt 24

<210> 326
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 326
Gly Tyr Thr Phe Thr Asn Tyr Gly
1 5

<210> 327
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 327
atcagcgcta acagtggtaa caca 24

<210> 328

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

<220>
<223> Synthetic

<400> 328
Ile Ser Ala Asn Ser Gly Asn Thr
1 5

<210> 329
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 329
gcgacgtata gttggaactt tcactggttc gacccc 36

<210> 330
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 330
Ala Thr Tyr Ser Trp Asn Phe His Trp Phe Asp Pro
1 5 10

<210> 331
<211> 325
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 331
gaaattgtgt tgacgcagtc tccaggcact ctgtctttgt ctccagggga aagagtcacc 60
ctctcctgca gggccagtca gagtgtcagt accaactact taacctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcattc tcaccatcag aagtctggag 240
cctgaagatt ttgcagtgta ttactgtcag cagtgtggtg gctcaccgtg gacgttcggc 300
caagggacca gggtggaaat caaac 325

<210> 332
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 332

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

<210> 333
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 333
cagagtgtca gtaccaacta c   21

<210> 334
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 334
Gln Ser Val Ser Thr Asn Tyr
1   5

<210> 335
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 335
ggtgcatcc   9

<210> 336
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 336
Gly Ala Ser

1

<210> 337
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 337
cagcagtgtg gtggctcacc gtggacg 27

<210> 338
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 338
Gln Gln Cys Gly Gly Ser Pro Trp Thr
1 5

<210> 339
<211> 355
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 339
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc tctgagactc 60
tcctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120
ccaggcaagg gactggagtg ggtggcagtt atatggtatg atggaagtaa taaatattat 180
ggagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agccgaggac acggctgtat attactgtgc gagagatgga 300
gtagacggtg cttttgatat ttggggccaa gggacaacgg tcaccgtctc ttcag 355

<210> 340
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 340
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Gly Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

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

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

<220>
<223> Synthetic

<400> 341
ggattcacct tcagtagcta tggc 24

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

<220>
<223> Synthetic

<400> 342
Gly Phe Thr Phe Ser Ser Tyr Gly
1 5

<210> 343
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 343
atatggtatg atggaagtaa taaa 24

<210> 344
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 344
Ile Trp Tyr Asp Gly Ser Asn Lys
1 5

<210> 345
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 345
gcgagagatg gagtagacgg tgcttttgat att 33

<210> 346
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 346
Ala Arg Asp Gly Val Asp Gly Ala Phe Asp Ile
1 5 10

<210> 347
<211> 322
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 347
gccatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca ggacattaga aatgatttag gctggtatca gcagaaacca 120
gggaaagccc ctaaactcct gatctatgct gcatccagtt tacaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tggcacagat ttcactctca ccatcagcag actgcagcct 240
gaagattttg caacttatta ctgtcaacaa gattacaatt acctgtatac ttttggccag 300
gggaccaacc tggagatcaa ac 322

<210> 348
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 348
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 Arg Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Tyr Asn Tyr Leu Tyr
85 90 95
Thr Phe Gly Gln Gly Thr Asn Leu Glu Ile Lys
100 105

<210> 349
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 349
caggacatta gaaatgat 18

<210> 350
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 350
Gln Asp Ile Arg Asn Asp
1 5

<210> 351
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 351
gctgcatcc 9

<210> 352
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 352
Ala Ala Ser
1

<210> 353
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 353
caacaagatt acaattacct gtatact 27

<210> 354
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 354
Gln Gln Asp Tyr Asn Tyr Leu Tyr Thr
1 5

<210> 355
<211> 364
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 355
gaggtgcagt tggtggagtc gggggaggc ttggtccagc ctggggggtc cctgagactc 60
tcctgtgaag cctctggatt cacctttgat aactattata tgacctgggt ccgccagact 120
ccagggaagg ggctggagtg ggtggccaac ataaaggaag atggaaatga tagatactat 180
gtggactctg tgaagggccg cttcaccatc tccagagaca acgccaagca gtcactgttt 240
ctacaaatga acagtctgag agccgaggac acggctgttt attactgtgc gagagaattt 300
tggagtggcc ctcactacgg tttggacgtc tggggccaag ggaccacggt caccgtctcc 360
tcag 364

<210> 356
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 356
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 Glu Ala Ser Gly Phe Thr Phe Asp Asn Tyr
20 25 30
Tyr Met Thr Trp Val Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Asn Ile Lys Glu Asp Gly Asn Asp Arg Tyr Tyr Val Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Gln Ser Leu Phe
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
65 90 95
Ala Arg Glu Phe Trp Ser Gly Pro His Tyr Gly Leu Asp Val Trp Gly
100 105 110
Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 357
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 357
ggattcacct ttgataacta ttat   24

<210> 358
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 358
Gly Phe Thr Phe Asp Asn Tyr Tyr
1   5

<210> 359
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 359
ataaaggaag atggaaatga taga   24

<210> 360
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 360
Ile Lys Glu Asp Gly Asn Asp Arg
1   5

<210> 361
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 361
gcgagagaat tttggagtgg ccctcactac ggtttggacg tc   42

<210> 362
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 362
Ala Arg Glu Phe Trp Ser Gly Pro His Tyr Gly Leu Asp Val
1 5 10

<210> 363
<211> 322
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 363
gccctccaga tgacccagtc tccatcctcc ctgtctgcac ctgtaggcga cagagtcacc 60
atcacttgcc gggcaagtca ggacgttaga aataatttag gctggtatca gcagaaacca 120
gggaatgccc ctaaattcct gatctatgct gcatccagtt tacaaagtgg aatcccatca 180
aggttcagcg gcagtggatc tggctcagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtctacaa gattacaatt accctccgac gttcggccag 300
gggaccaagg tggaaatcaa gc 322

<210> 364
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 364
Ala Leu Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Pro Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Arg Asn Asn
20 25 30
Leu Gly Trp Tyr Gln Gln Lys Pro Gly Asn Ala Pro Lys Phe Leu Ile
35 40 45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Ser 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 Pro
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 365
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 365
caggacgtta gaaataat 18

<210> 366
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 366
Gln Asp Val Arg Asn Asn
1 5

<210> 367
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 367
gctgcatcc 9

<210> 368
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 368
Ala Ala Ser
1

<210> 369
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 369
ctacaagatt acaattaccc tccgacg 27

<210> 370
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 370
Leu Gln Asp Tyr Asn Tyr Pro Pro Thr
1 5

<210> 371
<211> 370
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 371
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cgtctggatt caccttcagt agttatggca tgcactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtggcagtt ttatggtatg atggaagtaa taaaaactat 180
gtagactccg tgaagggccg attcaccatc tcaagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagatcac 300
gattttagga gtggttatga ggggtggttc gacccctggg gccagggaac cctggtcacc 360
gtctcctcag 370

<210> 372
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 372
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Val Leu Trp Tyr Asp Gly Ser Asn Lys Asn Tyr Val Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Asp His Asp Phe Arg Ser Gly Tyr Glu Gly Trp Phe Asp Pro
100 105 110
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 373
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 373
ggattcacct tcagtagtta tggc 24

<210> 374
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 374
Gly Phe Thr Phe Ser Ser Tyr Gly

1 5

<210> 375
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 375
ttatggtatg atggaagtaa taaa 24

<210> 376
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 376
Leu Trp Tyr Asp Gly Ser Asn Lys
1 5

<210> 377
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 377
gcgagagatc acgattttag gagtggttat gaggggtggt tcgacccc 48

<210> 378
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 378
Ala Arg Asp His Asp Phe Arg Ser Gly Tyr Glu Gly Trp Phe Asp Pro
1 5 10 15

<210> 379
<211> 322
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 379
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttcgc agctacttag cctggtacca acagaaacct 120
ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 240
gaagattttg cagtttatta ctgtcagcac cgtagcaact ggcctcccac tttcggcgga 300
gggaccgagg tggaggtcag ac 322

<210> 380
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 380
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Arg Ser Asn Trp Pro Pro
85 90 95
Thr Phe Gly Gly Gly Thr Glu Val Glu Val Arg
100 105

<210> 381
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 381
cagagtgttc gcagctac 18

<210> 382
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 382
Gln Ser Val Arg Ser Tyr
1 5

<210> 383
<211> 9
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 383
gatgcatcc 9

<210> 384
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 384
Asp Ala Ser
1

<210> 385
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 385
cagcaccgta gcaactggcc tcccact 27

<210> 386
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 386
Gln His Arg Ser Asn Trp Pro Pro Thr
1 5

<210> 387
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 387
taccggctcc cgatgg 16

<210> 388
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 388
ggcggctaag gtgtttgga 19

<210> 389
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 389
ttgggaatga ggaaagcaaa ct 22

<210> 390
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 390
ctgaagtacc ggaggaga 18

<210> 391
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 391
atcacgctgg tggtcctctt 20

<210> 392
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 392
gctgcggcga gtgctt 16

<210> 393
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 393
tggcaaatgc tggacccaac aca 23

<210> 394
<211> 19
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 394
gggtcctggc atcttgtcc 19

<210> 395
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 395
gcagatgaaa aactgggaac ca 22

<210> 396
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 396
caggtgcagc tggtgcagtc aggtccagga ctggtgaagc cctcgcagaa cctctcactc 60
acctgtgcca tctccggaga cagtgtctct agtgatagtg ctgcttggaa ctggatcagg 120
cagtccccat cgagaggcct tgagtggctg ggaaggacat actacaggtc caagtggtat 180
aatgattatg cagtatctgt gaaaagtcga ataaccttca acccagatac atccaagaac 240
cacatctccc tgcagctgaa ctctgtgact cccgaggaca cggctatcta ttactgtgca 300
agagaggggg ataattggaa ttacggctgg ctcgacccct ggggccaggg aaccacggtc 360
accgtctcct ca 372

<210> 397
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 397
Gln Val Gln Leu Val Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Asn Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asp
20 25 30
Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
35 40 45
Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50 55 60
Val Ser Val Lys Ser Arg Ile Thr Phe Asn Pro Asp Thr Ser Lys Asn
65 70 75 80
His Ile Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Ile
85 90 95
Tyr Tyr Cys Ala Arg Glu Gly Asp Asn Trp Asn Tyr Gly Trp Leu Asp
100 105 110
Pro Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 398
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 398
ggagacagtg tctctagtga tagtgctgct 30

<210> 399
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 399
Gly Asp Ser Val Ser Ser Asp Ser Ala Ala
1 5 10

<210> 400
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 400
acatactaca ggtccaagtg gtataat 27

<210> 401
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 401
Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn
1 5

<210> 402
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 402
gcaagagagg gggataattg gaattacggc tggctcgacc cc 42

<210> 403
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 403
Ala Arg Glu Gly Asp Asn Trp Asn Tyr Gly Trp Leu Asp Pro
1 5 10

<210> 404
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 404
gacatccagt tgacccagtc tccactctcc ctgcccgtca cccctggaga gccggcctcc 60
atctcctgca ggtctagtca gagcctcctt cttagtaatg gatacaacta tttggattgg 120
tacctgcaga agccagggca gtctccacaa ctcctgatct atttggtttc tagtcgggcc 180
tccggggtcc ctgacaggtt cagtggcagt ggatccggca cagattttac actgaaaatc 240
agcagagtgg aggctgagga ttttggaatt tattattgta tgcaagctct acaaactccg 300
tacacttttg gccgggggac caaggtggaa atcaaa 336

<210> 405
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 405
Asp Ile Gln Leu 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 Leu 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 Val Ser Ser 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 Phe Gly Ile Tyr Tyr Cys Met Gln Ala
85 90 95
Leu Gln Thr Pro Tyr Thr Phe Gly Arg Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 406
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 406
cagagcctcc ttcttagtaa tggatacaac tat 33

<210> 407
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 407
Gln Ser Leu Leu Leu Ser Asn Gly Tyr Asn Tyr
1 5 10

<210> 408
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 408
ttggtttct 9

<210> 409
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 409
Leu Val Ser
1

<210> 410
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 410
atgcaagctc tacaaactcc gtacact 27

<210> 411
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 411

Met Gln Ala Leu Gln Thr Pro Tyr Thr
1 5

<210> 412
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 412
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60
acctgcactg tctctggtgg ctccgtcagc agtggtaatt actactggag ctgggtccgc 120
caacacccag ggaagggcct ggagtggttt ggttacatca aaaacagtgg gggcacctac 180
tacaacccgt ccctcaagag tcgaattacc atatcagtag acacgtctaa gaaccacttc 240
tccctgaggc tgagctctat gacggccgcg gacacggccg tgtattactg tgcgagagct 300
ggttcgggga gtcactactt tgactactgg ggccagggaa ccctggtcac cgtctcctca 360

<210> 413
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 413
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Ser Gly
20 25 30
Asn Tyr Tyr Trp Ser Trp Val Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45
Trp Phe Gly Tyr Ile Lys Asn Ser Gly Gly Thr Tyr Tyr Asn Pro Ser
50 55 60
Leu Lys Ser Arg Ile Thr Ile Ser Val Asp Thr Ser Lys Asn His Phe
65 70 75 80
Ser Leu Arg Leu Ser Ser Met Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Ala Arg Ala Gly Ser Gly Ser His Tyr Phe Asp Tyr Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 414
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 414
ggtggctccg tcagcagtgg taattactac 30

<210> 415
<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 415
Gly Gly Ser Val Ser Ser Gly Asn Tyr Tyr
1 5 10

<210> 416
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 416
atcaaaaaca gtgggggcac c 21

<210> 417
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 417
Ile Lys Asn Ser Gly Gly Thr
1 5

<210> 418
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 418
gcgagagcgg gttcggggag tcactacttt gactac 36

<210> 419
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 419
Ala Arg Ala Gly Ser Gly Ser His Tyr Phe Asp Tyr
1 5 10

<210> 420
<211> 324

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 420
gacatccagt tgacccagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttagc agcaactact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt gtgcagtgta ttactgtcag cagtacggtt actcaccgat caccttcggc 300
caagggacca agctggagat caaa 324

<210> 421
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 421
Asp Ile Gln Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
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 Cys Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Tyr Ser Pro
85 90 95
Ile Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 422
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 422
cagagtgtta gcagcaacta c 21

<210> 423
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 423
Gln Ser Val Ser Ser Asn Tyr
1 5

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

<220>
<223> Synthetic

<400> 424
ggtgcatcc 9

<210> 425
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 425
Gly Ala Ser
1

<210> 426
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 426
cagcagtacg gttactcacc gatcacc 27

<210> 427
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 427
Gln Gln Tyr Gly Tyr Ser Pro Ile Thr
1 5

<210> 428
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 428
gaggtgcagc tggtgcagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cgtctggatt caccttcagt agttatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtgtcattt ttatggtatg atggaactaa taaaaactat 180
gtagagtccg tgaagggccg attcaccatc tcaagagaca attccaagaa tatgctgtat 240
ctggaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagatcac 300
gattttagga gtggttatga ggggtggttc gacccctggg gccagggaac cctggtcacc 360
gtctcctca 369

<210> 429
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 429
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys 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
Ser Phe Leu Trp Tyr Asp Gly Thr Asn Lys Asn Tyr Val Glu Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met 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 Asp His Asp Phe Arg Ser Gly Tyr Glu Gly Trp Phe Asp Pro
100 105 110
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 430
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 430
ggattcacct tcagtagtta tggc 24

<210> 431
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 431
Gly Phe Thr Phe Ser Ser Tyr Gly
1 5

<210> 432
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 432
ttatggtatg atggaactaa taaa 24

<210> 433
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 433
Leu Trp Tyr Asp Gly Thr Asn Lys
1 5

<210> 434
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 434
gcgagagatc acgattttag gagtggttat gaggggtggt tcgacccc 48

<210> 435
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 435
Ala Arg Asp His Asp Phe Arg Ser Gly Tyr Glu Gly Trp Phe Asp Pro
1 5 10 15

<210> 436
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 436
gaaatagtga tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttagc agctacttag cctggtacca acagaaacct 120
ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 240
gaagattttg cagtttatta ctgtcaacac cgtagcaact ggcctcccac tttcggcgga 300
gggaccaagg tggaaatcaa a 321

<210> 437

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

<220>
<223> Synthetic

<400> 437
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Arg Ser Asn Trp Pro Pro
85 90 95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 438
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 438
cagagtgtta gcagctac 18

<210> 439
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 439
Gln Ser Val Ser Ser Tyr
1 5

<210> 440
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 440
gatgcatcc 9

<210> 441
<211> 3

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 441
Asp Ala Ser
1

<210> 442
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 442
caacaccgta gcaactggcc tcccact 27

<210> 443
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 443
Gln His Arg Ser Asn Trp Pro Pro Thr
1 5

<210> 444
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 444
caggtacagc tgcagcagtc gggtccagga ctgctgaaac cttcacagac cctgtccctc 60
acctgctctg tctctggtgg ctccatcagc agtggtaatt actactggac ctggatccgc 120
cagcacccag ggaagggcct ggagtggatt gggtacatca agaacagtgg aagcgcctac 180
tacaatccgt ccctcaagag tcgacttacc atgtcaatag acacgtctca gaaccacttc 240
tccttgattt tgacttctgt gactgccgcg gacacggcct tatattactg tgcgagagat 300
gaaaatatag cagttcgtca tgcttttgat atctggggcc aagggacatc ggtcaccgtc 360
tcctca 366

<210> 445
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 445

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

<210> 446
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 446
ggtggctcca tcagcagtgg taattactac 30

<210> 447
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 447
Gly Gly Ser Ile Ser Ser Gly Asn Tyr Tyr
1 5 10

<210> 448
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 448
atcaagaaca gtggaagcgc c 21

<210> 449
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 449
Ile Lys Asn Ser Gly Ser Ala
1 5

<210> 450
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 450
gcgagagatg aaaatatagc agttcgtcat gcttttgata tc 42

<210> 451
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 451
Ala Arg Asp Glu Asn Ile Ala Val Arg His Ala Phe Asp Ile
1 5 10

<210> 452
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 452
gaaatagtgt tgacacagtc tccaggcgcc ctgtctttgt ctccaggaga aagagccacc 60
ctctcctgta gggccagtcg gactgttagc agcagctact tagcctggta ccaacagaaa 120
cctggccagg ctcccaggct cctcatctat ggtacatcca gccgggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcac cagactggag 240
cctgaagatt ttgcaatata ttactgtcag cagtctggtt actcacctct cactttcggc 300
ggagggacca aggtggaaat caaa 324

<210> 453
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 453
Glu Ile Val Leu Thr Gln Ser Pro Gly Ala Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Arg Thr Val Ser Ser Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Gly Thr 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 Thr Arg Leu Glu
65 70 75 80
Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Gln Ser Gly Tyr Ser Pro
85 90 95
Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 454
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 454
cggactgtta gcagcagcta c 21

<210> 455
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 455
Arg Thr Val Ser Ser Ser Tyr
1 5

<210> 456
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 456
ggtacatcc 9

<210> 457
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 457
Gly Thr Ser
1

<210> 458
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 458
cagcagtctg gttactcacc tctcact 27

<210> 459
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 459
Gln Gln Ser Gly Tyr Ser Pro Leu Thr
1 5

<210> 460
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 460
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60
acctgcactg tctctgatga ctccatcaac aatgttgaat cctactggac ctggatccgc 120
caacacccag ggaagggcct ggagtggatt ggatacatca aatacactgg gggcatccac 180
tataacccgt ccctcaagag tcgactcgcc atatcagtgg acacgtcaaa gaaccagttc 240
tccctgaaaa tgaactctgt gactgccgcg gacacggcca aatattactg tgcgagagca 300
cgtggaagtc atacttttga tgtctggggc caggggacaa cggtcaccgt ctcctca 357

<210> 461
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 461
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Asp Asp Ser Ile Asn Asn Val
20 25 30
Glu Ser Tyr Trp Thr Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45
Trp Ile Gly Tyr Ile Lys Tyr Thr Gly Gly Ile His Tyr Asn Pro Ser
50 55 60
Leu Lys Ser Arg Leu Ala Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80
Ser Leu Lys Met Asn Ser Val Thr Ala Ala Asp Thr Ala Lys Tyr Tyr
85 90 95
Cys Ala Arg Ala Arg Gly Ser His Thr Phe Asp Val Trp Gly Gln Gly
100 105 110
Thr Thr Val Thr Val Ser Ser
115

<210> 462
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 462
gatgactcca tcaacaatgt tgaatcctac 30

<210> 463
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 463
Asp Asp Ser Ile Asn Asn Val Glu Ser Tyr
1 5 10

<210> 464
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 464
atcaaataca ctgggggcat c 21

<210> 465
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 465
Ile Lys Tyr Thr Gly Gly Ile
1 5

<210> 466
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 466
gcgagagcac gtggaagtca tacttttgat gtc 33

<210> 467
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 467
Ala Arg Ala Arg Gly Ser His Thr Phe Asp Val
1 5 10

<210> 468
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 468
gccatccggt tgacccagtc tccaggcacc ctgtcttggt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttagc agtaactact tagcctggta ccagcagaaa 120
cctggccagg ctccccgact cctcatttat ggtgcatcca gcagggtcgc tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcactgta ttattgtcag caatatagta ggtcaccgat caccttcggc 300
caagggacca agctggagat caaa 324

<210> 469
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 469
Ala Ile Arg Leu Thr Gln Ser Pro Gly Thr Leu Ser Trp 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
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 Val Ala 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 Leu Tyr Tyr Cys Gln Gln Tyr Ser Arg Ser Pro
85 90 95
Ile Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 470
<211> 21
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<220>
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<400> 470
cagagtgtta gcagtaacta c 21

<210> 471
<211> 7
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<220>
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<400> 471
Gln Ser Val Ser Ser Asn Tyr
1 5

<210> 472
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 472
ggtgcatcc 9

<210> 473
<211> 3
<212> PRT
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<220>
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<400> 473
Gly Ala Ser
1

<210> 474
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 474
cagcaatata gtaggtcacc gatcacc 27

<210> 475
<211> 9
<212> PRT
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<220>
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<400> 475

Gln Gln Tyr Ser Arg Ser Pro Ile Thr
1 5

<210> 476
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
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<400> 476
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60
acctgcactg tctctggtgg ctccatcaac agtgttactt actactggac ctggatccgc 120
cagcacccag ggaggggcct agagtggatt gggtacatca aattcagtgg gagcacctac 180
tacaacccgt ccctcaaggg tcgagtcacc atatcagtgg acacgtctaa gaaccaattc 240
tccctaaaaa ttaactctgt gactgccgcg gacacggccg tgttttactg tgcgagagct 300
tctggaagtc atacttttga tatctggggc caagggacaa tggtcaccgt ctcctca 357

<210> 477
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 477
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Asn Ser Val
20 25 30
Thr Tyr Tyr Trp Thr Trp Ile Arg Gln His Pro Gly Arg Gly Leu Glu
35 40 45
Trp Ile Gly Tyr Ile Lys Phe Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60
Leu Lys Gly Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80
Ser Leu Lys Ile Asn Ser Val Thr Ala Ala Asp Thr Ala Val Phe Tyr
85 90 95
Cys Ala Arg Ala Ser Gly Ser His Thr Phe Asp Ile Trp Gly Gln Gly
100 105 110
Thr Met Val Thr Val Ser Ser
115

<210> 478
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 478
ggtggctcca tcaacagtgt tacttactac 30

<210> 479
<211> 10
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 479
Gly Gly Ser Ile Asn Ser Val Thr Tyr Tyr
1 5 10

<210> 480
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 480
atcaaattca gtgggagcac c 21

<210> 481
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 481
Ile Lys Phe Ser Gly Ser Thr
1 5

<210> 482
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 482
gcgagagctt ctggaagtca tacttttgat atc 33

<210> 483
<211> 11
<212> PRT
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<220>
<223> Synthetic

<400> 483
Ala Arg Ala Ser Gly Ser His Thr Phe Asp Ile
1 5 10

<210> 484
<211> 321
<212> DNA

<213> Artificial Sequence

<220>
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<400> 484
gccatccgga tgacccagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgct gggccagtca gagtattagc ggctattttg cctggtatca acagaaacct 120
ggccaggctc ccaggctcct catctatgat acatcctaca gggccactga cgtcccagcc 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcaacaa cctagagcct 240
gaagattttg cagtttatta ctgtcagcag cgtagcgact ggccgctcag cttcggcgga 300
gggaccaaac tggagatcaa a 321

<210> 485
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 485
Ala Ile Arg Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Trp Ala Ser Gln Ser Ile Ser Gly Tyr
20 25 30
Phe Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Asp Thr Ser Tyr Arg Ala Thr Asp Val Pro Ala Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Asn Leu Glu Pro
65 70 75 80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asp Trp Pro Leu
85 90 95
Ser Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 486
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 486
cagagtatta gcggctat 18

<210> 487
<211> 6
<212> PRT
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<220>
<223> Synthetic

<400> 487
Gln Ser Ile Ser Gly Tyr
1 5

<210> 488
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 488
gatacatcc   9

<210> 489
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 489
Asp Thr Ser
1

<210> 490
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 490
cagcagcgta gcgactggcc gctcagc   27

<210> 491
<211> 9
<212> PRT
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<220>
<223> Synthetic

<400> 491
Gln Gln Arg Ser Asp Trp Pro Leu Ser
1   5

<210> 492
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 492
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60
acctgcactg tctctggtgg ctccatcaac agtgttactt actactggac ctggatccgc 120
cagcacccag ggaggggcct agagtggatt gggtacatca aattcagtgg gagcacctac 180

tacaacccgt ccctcaaggg tcgagtcacc atatcagtgg acacgtctaa gaaccaattc 240
tcccttaaaa ttaactctgt gactgccgcg gacacggccg tgttttactg tgcgagagct 300
tctggaagtc atacttttga tatctggggc caagggacaa tggtcaccgt ctcctca 357

<210> 493
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 493
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Asn Ser Val
20 25 30
Thr Tyr Tyr Trp Thr Trp Ile Arg Gln His Pro Gly Arg Gly Leu Glu
35 40 45
Trp Ile Gly Tyr Ile Lys Phe Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60
Leu Lys Gly Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80
Ser Leu Lys Ile Asn Ser Val Thr Ala Ala Asp Thr Ala Val Phe Tyr
85 90 95
Cys Ala Arg Ala Ser Gly Ser His Thr Phe Asp Ile Trp Gly Gln Gly
100 105 110
Thr Met Val Thr Val Ser Ser
115

<210> 494
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 494
ggtggctcca tcaacagtgt tacttactac 30

<210> 495
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 495
Gly Gly Ser Ile Asn Ser Val Thr Tyr Tyr
1 5 10

<210> 496
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 496
atcaaattca gtgggagcac c   21

<210> 497
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 497
Ile Lys Phe Ser Gly Ser Thr
1   5

<210> 498
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 498
gcgagagctt ctggaagtca tacttttgat atc   33

<210> 499
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 499
Ala Arg Ala Ser Gly Ser His Thr Phe Asp Ile
1   5   10

<210> 500
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 500
gatattgtga tgacccagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttagc aacagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctct ggtgcgtcca gcagggtcac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttggaatgta ttactgtcag cagtatagta ggtcaccgat caccttcggc 300
caagggacca aggtggaaat caaa   324

<210> 501
<211> 108
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 501
Asp Ile Val Met 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 Asn Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Ser Gly Ala Ser Ser Arg Val 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 Gly Met Tyr Tyr Cys Gln Gln Tyr Ser Arg Ser Pro
85 90 95
Ile Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 502
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 502
cagagtgtta gcaacagcta c 21

<210> 503
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 503
Gln Ser Val Ser Asn Ser Tyr
1 5

<210> 504
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 504
ggtgcgtcc 9

<210> 505
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 505
Gly Ala Ser
1

<210> 506
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 506
cagcagtata gtaggtcacc gatcacc 27

<210> 507
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 507
Gln Gln Tyr Ser Arg Ser Pro Ile Thr
1 5

<210> 508
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 508
gaggtgcagc tggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgcaagg cttctggtta ctcctttacc agctttggtt tcagctgggt gcgacaggcc 120
cctggacaag gacttgagtg gctgggatgg atcagcgctt acagtggtga cacagactat 180
gcacagaagt tccagggcag agtcaccctg accactgaca catccacgac cactgcctac 240
atggagctga ggagcctgag atctgacgac acggccgtct attactgtgc gcgatataac 300
tggaacctcc actggttcga cccctggggc cagggaaccc tggtcaccgt ctcctca 357

<210> 509
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 509
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Phe

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

<210> 510
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 510
ggttactcct ttaccagctt tggt 24

<210> 511
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 511
Gly Tyr Ser Phe Thr Ser Phe Gly
1 5

<210> 512
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 512
atcagcgctt acagtggtga caca 24

<210> 513
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 513
Ile Ser Ala Tyr Ser Gly Asp Thr
1 5

<210> 514
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 514
gcgcgatata actggaacct ccactggttc gacccc 36

<210> 515
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 515
Ala Arg Tyr Asn Trp Asn Leu His Trp Phe Asp Pro
1 5 10

<210> 516
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 516
gacatccgga tgacccagtc tccaggcatc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gaatattaaa agcaactact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatcttt ggtacatcca acagggccac tgccatttca 180
gacaggttca gtggcagtgg gtctgggaca gacttccttt tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag cagtatggta actcaccgtg gacgttcggc 300
caagggacca aagtggatat caaa 324

<210> 517
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 517
Asp Ile Arg Met Thr Gln Ser Pro Gly Ile Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asn Ile Lys Ser Asn
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Phe Gly Thr Ser Asn Arg Ala Thr Ala Ile Ser Asp Arg Phe Ser
50 55 60
Gly Ser Gly Ser Gly Thr Asp Phe Leu Phe Thr Ile Ser Arg Leu Glu
65 70 75 80

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

<210> 518
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 518
cagaatatta aaagcaacta c 21

<210> 519
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 519
Gln Asn Ile Lys Ser Asn Tyr
1 5

<210> 520
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 520
ggtacatcc 9

<210> 521
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 521
Gly Thr Ser
1

<210> 522
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 522
cagcagtatg gtaactcacc gtggacg 27

<210> 523
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 523
Gln Gln Tyr Gly Asn Ser Pro Trp Thr
1 5

<210> 524
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 524
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60
acctgcactg tctctgatgg ctccatcaac agtgttgaat cctactggac ctggatccgc 120
cagcacccag ggaagggcct ggagtggatt ggatacatca aatacactgg gggcatccac 180
tataacccgt ccctcaagag tcgacttgcc atatcagtgg acacgtcaaa gaaccagttc 240
tccctgaaaa tgagctctgt gactgccgcg gacacggccg tgtattactg tgcgagagca 300
cgtggaagtc atacttttga tgtctggggc caggggacaa tggtcaccgt ctcttca 357

<210> 525
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 525
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Asp Gly Ser Ile Asn Ser Val
20 25 30
Glu Ser Tyr Trp Thr Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45
Trp Ile Gly Tyr Ile Lys Tyr Thr Gly Gly Ile His Tyr Asn Pro Ser
50 55 60
Leu Lys Ser Arg Leu Ala Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80
Ser Leu Lys Met Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Ala Arg Ala Arg Gly Ser His Thr Phe Asp Val Trp Gly Gln Gly
100 105 110
Thr Met Val Thr Val Ser Ser
115

<210> 526

<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 526
gatggctcca tcaacagtgt tgaatcctac 30

<210> 527
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 527
Asp Gly Ser Ile Asn Ser Val Glu Ser Tyr
1 5 10

<210> 528
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 528
atcaaataca ctgggggcat c 21

<210> 529
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 529
Ile Lys Tyr Thr Gly Gly Ile
1 5

<210> 530
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 530
gcgagagcac gtggaagtca tacttttgat gtc 33

<210> 531
<211> 11
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 531
Ala Arg Ala Arg Gly Ser His Thr Phe Asp Val
1   5   10

<210> 532
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 532
gaaattgtgc tgactcagtc tccaggcacc ctgtcttggt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtattagc agtaactact tagcctggta ccagcagaaa 120
cctggccagg ctcccagact cctcatttat ggtgcatcca gcagggtcac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcactgta ttattgtcag cagtatagta ggtcaccgat caccttcggc 300
caagggacca aggtggatat caaa 324

<210> 533
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 533
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Trp Ser Pro Gly
1   5   10   15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Ser Asn
            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 Val 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 Leu Tyr Tyr Cys Gln Gln Tyr Ser Arg Ser Pro
                85   90   95
Ile Thr Phe Gly Gln Gly Thr Lys Val Asp Ile Lys
            100   105

<210> 534
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 534
cagagtatta gcagtaacta c 21

<210> 535
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 535
Gln Ser Ile Ser Ser Asn Tyr
1   5

<210> 536
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 536
ggtgcatcc   9

<210> 537
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 537
Gly Ala Ser
1

<210> 538
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 538
cagcagtata gtaggtcacc gatcacc   27

<210> 539
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 539
Gln Gln Tyr Ser Arg Ser Pro Ile Thr
1   5

<210> 540
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 540
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60
acctgcactg tctctggtgg ctccgtcagc agtggtaatt actactggag ctggatccgc 120
cagcacccag ggaagggcct ggagtggttt gggtacatca aaaacagtgg gggcacctac 180
tacaacccgt ccctcaagag tcgaattacc atatcagtag acacgtctaa gaaccacttc 240
tccctgaggc tgagctctat gacggccgcg gacacggccg tgtattactg tgcgagagct 300
ggttcgggga gtcactactt tgactactgg ggccagggaa ccctggtcac cgtctcctca 360

<210> 541
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 541
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Ser Gly
20 25 30
Asn Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45
Trp Phe Gly Tyr Ile Lys Asn Ser Gly Gly Thr Tyr Tyr Asn Pro Ser
50 55 60
Leu Lys Ser Arg Ile Thr Ile Ser Val Asp Thr Ser Lys Asn His Phe
65 70 75 80
Ser Leu Arg Leu Ser Ser Met Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Ala Arg Ala Gly Ser Gly Ser His Tyr Phe Asp Tyr Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 542
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 542
ggtggctccg tcagcagtgg taattactac 30

<210> 543
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 543
Gly Gly Ser Val Ser Ser Gly Asn Tyr Tyr
1 5 10

<210> 544
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 544
atcaaaaaca gtgggggcac c 21

<210> 545
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 545
Ile Lys Asn Ser Gly Gly Thr
1 5

<210> 546
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 546
gcgagagctg gttcggggag tcactacttt gactac 36

<210> 547
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 547
Ala Arg Ala Gly Ser Gly Ser His Tyr Phe Asp Tyr
1 5 10

<210> 548
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 548
gaaacgacac tcacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggctca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt gtgcagtgta ttactgtcag cagtatggtt actcaccgat caccttcggc 300
caagggacca aggtggaaat caaa 324

<210> 549
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 549
Glu Thr Thr Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Leu 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 Cys Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Tyr Ser Pro
85 90 95
Ile Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 550
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 550
cagagtgtta gcagcagcta c 21

<210> 551
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 551
Gln Ser Val Ser Ser Ser Tyr
1 5

<210> 552

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

<220>
<223> Synthetic

<400> 552
ggtgcatcc 9

<210> 553
<211> 3
<212> PRT
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<220>
<223> Synthetic

<400> 553
Gly Ala Ser
1

<210> 554
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 554
cagcagtatg gttactcacc gatcacc 27

<210> 555
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 555
Gln Gln Tyr Gly Tyr Ser Pro Ile Thr
1 5

<210> 556
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 556
gaagtgcagc tggtgcagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtacag cgtctggatt caccttcagt agctatgcca tgtactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtggcagtt atatggtatg atggaagtaa taaaaactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacactgtat 240
ctgcaagtga acagcctgag agccgaggac acggctgtgt attactgtgc gagagatcac 300

gatttttga gtggttatga ggggtggttc gacccctggg gccagggaac cctggtcacc 360
gtctcctca 369

<210> 557
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 557
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30
Ala Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Asn 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 Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Asp His Asp Phe Leu Ser Gly Tyr Glu Gly Trp Phe Asp Pro
100 105 110
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 558
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 558
ggattcacct tcagtagcta tgcc 24

<210> 559
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 559
Gly Phe Thr Phe Ser Ser Tyr Ala
1 5

<210> 560
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 560
atatggtatg atggaagtaa taaa 24

<210> 561
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 561
Ile Trp Tyr Asp Gly Ser Asn Lys
1 5

<210> 562
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 562
gcgagagatc acgatttttt gagtggttat gaggggtggt tcgacccc 48

<210> 563
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 563
Ala Arg Asp His Asp Phe Leu Ser Gly Tyr Glu Gly Trp Phe Asp Pro
1 5 10 15

<210> 564
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 564
gaaattgtgc tgactcagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttagt agctacttag cctggtacca acagaaacct 120
ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagtag cctagagcct 240
gaagattttg cagtttatta ctgtcagcaa cgtagcaact ggcctcccac tttcggcgga 300
gggaccaaag tggatatcaa a 321

<210> 565
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 565
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
85 90 95
Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys
100 105

<210> 566
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 566
cagagtgtta gtagctac 18

<210> 567
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 567
Gln Ser Val Ser Ser Tyr
1 5

<210> 568
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 568
gatgcatcc 9

<210> 569
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 569
Asp Ala Ser
1

<210> 570
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 570
cagcaacgta gcaactggcc tcccact 27

<210> 571
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 571
Gln Gln Arg Ser Asn Trp Pro Pro Thr
1 5

<210> 572
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 572
gaggtgcagc tggtgcagtc tggagctgaa gtgaagaacc ctggggcctc agttagggtc 60
tcctgcaagg cttctggtta cacctttacc acctatggta tcacctgggt gcgacagggc 120
cctggacaag ggcttgagtg gatgggatgg atcagcgctt tcaatggtga cacaaacttt 180
gcacagaacc tccagaacag agtcaccctg accacagaca catccactag cacagcctat 240
atggaactga ggagcctgag atctgacgac acggccgttt attactgtgc gagaggggga 300
ggagctcgtc cggggaactt cttcttctac ggtatggacg tctggggcca ggggaccacg 360
gtcaccgtct cctca 375

<210> 573
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 573
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Asn Pro Gly Ala
1 5 10 15
Ser Val Arg Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr

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

<210> 574
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 574
ggttacacct ttaccaccta tggt 24

<210> 575
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 575
Gly Tyr Thr Phe Thr Thr Tyr Gly
1 5

<210> 576
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 576
atcagcgctt tcaatggtga caca 24

<210> 577
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 577
Ile Ser Ala Phe Asn Gly Asp Thr
1 5

<210> 578
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 578
gcgagagggg gaggagctcg tccggggaac ttcttcttct acggtatgga cgtc 54

<210> 579
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 579
Ala Arg Gly Gly Gly Ala Arg Pro Gly Asn Phe Phe Phe Tyr Gly Met
1 5 10 15
Asp Val

<210> 580
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 580
gatgttgtga tgactcagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgta gggccagtca gagttttgcc agctacttag cctggtacca acagaaacct 120
ggccaggctc ccaggctcct catctatgat acctcctaca gggccactgg cgtcccagcc 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca acatcagcaa cctggagcct 240
gaagattttg cagtttatta ctgtcagcaa cgtggcaact ggccgctcac tttcggcgga 300
gggaccaagg tggaaatcaa a 321

<210> 581
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 581
Asp Val Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Phe Ala Ser Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Asp Thr Ser Tyr Arg Ala Thr Gly Val Pro Ala Arg Phe Ser Gly
50 55 60

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

<210> 582
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 582
cagagtttg ccagctac 18

<210> 583
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 583
Gln Ser Phe Ala Ser Tyr
1 5

<210> 584
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 584
gatacctcc 9

<210> 585
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 585
Asp Thr Ser
1

<210> 586
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 586
cagcaacgtg gcaactggcc gctcact 27

<210> 587
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 587
Gln Gln Arg Gly Asn Trp Pro Leu Thr
1 5

<210> 588
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 588
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tcctgcaagg cttctggtta cacctttagc tacaatggtg tcacttgggt acgacaggcc 120
cctggacaag ggcttgagtg gatgggatgg atcagcgctt acgatggtaa cacagactat 180
gcacagaagt tccaagacag aatcaccatg accacagaca catccacgag tacagcctac 240
atggaactga ggagccttag atctgacgac acggccgtct attactgtgc gaggtatagt 300
tggaacaacc actggttcga cccctggggc cagggaaccc tggtcaccgt ctcctca 357

<210> 589
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 589
Gln Val Gln Leu Val Gln Ser Gly Thr Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Tyr Asn
20 25 30
Gly Val Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Trp Ile Ser Ala Tyr Asp Gly Asn Thr Asp Tyr Ala Gln Lys Phe
50 55 60
Gln Asp Arg Ile 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 Tyr Ser Trp Asn Asn His Trp Phe Asp Pro Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
115

<210> 590
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 590
ggttacacct ttagctacaa tggt 24

<210> 591
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 591
Gly Tyr Thr Phe Ser Tyr Asn Gly
1 5

<210> 592
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 592
atcagcgctt acgatggtaa caca 24

<210> 593
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 593
Ile Ser Ala Tyr Asp Gly Asn Thr
1 5

<210> 594
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 594
gcgaggtata gttggaacaa ccactggttc gacccc 36

<210> 595

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

<220>
<223> Synthetic

<400> 595
Ala Arg Tyr Ser Trp Asn Asn His Trp Phe Asp Pro
1 5 10

<210> 596
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 596
gatattgtga tgactcagtc tccaggcacc ctgtctttgt ctccaggaga cggggccacc 60
ctctcctgca gggccagtca gagtgtttcc ggcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatttat ggtgcatcca acagggccac tggcatccca 180
gacaggttca ctggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta tttctgtcag cagagtgctt tctcaccgtg gacgttcggc 300
caagggacca agctggagat caaa 324

<210> 597
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 597
Asp Ile Val Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Asp Gly Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Gly Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Ile Pro Asp Arg Phe Thr
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 Phe Cys Gln Gln Ser Ala Phe Ser Pro
85 90 95
Trp Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 598
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
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<400> 598
cagagtgttt ccggcagcta c 21

<210> 599
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 599
Gln Ser Val Ser Gly Ser Tyr
1 5

<210> 600
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 600
ggtgcatcc 9

<210> 601
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 601
Gly Ala Ser
1

<210> 602
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 602
cagcagagtg ctttctcacc gtggacg 27

<210> 603
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 603
Gln Gln Ser Ala Phe Ser Pro Trp Thr

1 5

<210> 604
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 604
gaagtgcagc tggtgcagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt atgtacgaca tgcactgggt ccgccaaact 120
ataggaaaag gtctggagtg ggtctcagca attggtactg ctggtgacac atactatcca 180
ggctccgtga agggccgatt caccatctcc agagaaaatg ccaagaactc cttgtttctt 240
caaatgaaca gcctgagagc cggggacacg gctgtttatt actgtgtaag atccgggact 300
acagagtggt tcgacccctg gggccaggga accccggtca ctgtctcctc a 351

<210> 605
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 605
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Met Tyr
20 25 30
Asp Met His Trp Val Arg Gln Thr Ile Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Ala Ile Gly Thr 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 Phe 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 Ser Gly Thr Thr Glu Trp Phe Asp Pro Trp Gly Gln Gly Thr Pro
100 105 110
Val Thr Val Ser Ser
115

<210> 606
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 606
ggattcacct tcagtatgta cgac 24

<210> 607
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 607
Gly Phe Thr Phe Ser Met Tyr Asp
1 5

<210> 608
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 608
attggtactg ctggtgacac a 21

<210> 609
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 609
Ile Gly Thr Ala Gly Asp Thr
1 5

<210> 610
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 610
gtaagatccg ggactacaga gtggttcgac ccc 33

<210> 611
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 611
Val Arg Ser Gly Thr Thr Glu Trp Phe Asp Pro
1 5 10

<210> 612
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 612
gacatccggt tgacccagtc tccatcttcc gtgtctgcat ctgtgggaga cagagtcacc 60
atcacttgtc ggacgagtca gggtattagt agctggttag cctggtatca gcagaaacca 120
ggaaaagccc ctaacctcct gatctatgct gcatccagtt tacaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttacta ttgtctacag gctaacagtt tcccgtacac ttttggccag 300
gggaccaagg tggagatcaa a 321

<210> 613
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 613
Asp Ile Arg Leu Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Gly Ile Ser Ser Trp
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn 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 Ala Asn Ser Phe Pro Tyr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 614
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 614
cagggtatta gtagctgg 18

<210> 615
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 615
Gln Gly Ile Ser Ser Trp
1 5

<210> 616
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 616
gctgcatcc 9

<210> 617
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 617
Ala Ala Ser
1

<210> 618
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 618
ctacaggcta acagtttccc gtacact 27

<210> 619
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 619
Leu Gln Ala Asn Ser Phe Pro Tyr Thr
1 5

<210> 620
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 620
caggtccagc tggtgcagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cgtctggatt caccttcagt agttatggca tgcactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtggcagtt ttatggtatg atggaagtaa taaaaactat 180
gtagactccg tgaagggccg attcaccatc tcaagagaca attccaagaa cacgctttat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attattgtgc gagagatcat 300
gattttagga gtggttatga ggggtggttc gacccctggg gccagggaac cctggtcacc 360
gtctcctca 369

<210> 621
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 621
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys 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 Leu Trp Tyr Asp Gly Ser Asn Lys Asn Tyr Val Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Asp His Asp Phe Arg Ser Gly Tyr Glu Gly Trp Phe Asp Pro
100 105 110
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 622
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
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<400> 622
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<210> 623
<211> 8
<212> PRT
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<220>
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<400> 623
Gly Phe Thr Phe Ser Ser Tyr Gly
1 5

<210> 624
<211> 24
<212> DNA
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<220>

<223> Synthetic

<400> 624
ttatggtatg atggaagtaa taaa 24

<210> 625
<211> 8
<212> PRT
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<220>
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<400> 625
Leu Trp Tyr Asp Gly Ser Asn Lys
1 5

<210> 626
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 626
gcgagagatc atgattttag gagtggttat gaggggtggt tcgacccc 48

<210> 627
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
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<400> 627
Ala Arg Asp His Asp Phe Arg Ser Gly Tyr Glu Gly Trp Phe Asp Pro
1 5 10 15

<210> 628
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 628
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ctctcctgca gggccagtca gagtgttcgc agctacttag cctggtacca acagaaacct 120
ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 240
gaagattttg cagtttatta ctgtcaacac cgtagcaact ggcctcccac tttcggcgga 300
gggaccaagg tggaaatcaa a 321

<210> 629
<211> 107
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 629
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1   5   10   15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Tyr
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35   40   45
Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65   70   75   80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Arg Ser Asn Trp Pro Pro
                85   90   95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 630
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 630
cagagtgttc gcagctac 18

<210> 631
<211> 6
<212> PRT
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<220>
<223> Synthetic

<400> 631
Gln Ser Val Arg Ser Tyr
1   5

<210> 632
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 632
gatgcatcc 9

<210> 633
<211> 3
<212> PRT
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<220>
<223> Synthetic

<400> 633
Asp Ala Ser
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<210> 634
<211> 27
<212> DNA
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<220>
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<400> 634
caacaccgta gcaactggcc tcccact 27

<210> 635
<211> 9
<212> PRT
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<220>
<223> Synthetic

<400> 635
Gln His Arg Ser Asn Trp Pro Pro Thr
1 5

<210> 636
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
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<400> 636
caggtcacct tgaaggagtc gggcccagga ctggtgaagt cttcggagac cctgtccctc 60
acttgcactg tctctactgg ctccatcagc agtagtagtt actactgggc ctggatccgc 120
cagcccccag ggaagggact ggagtggatt gggagtatct attatagtgg gagtaaattc 180
tacagcccgt ccctcaagag tcgagtcacc atatacgttg acacgtccaa gaatcagttc 240
tccctgcaac tgagctcggt gaccgccgca gacacggctg tatattactg tgcgagacag 300
gtcggtgcaa tctttgacta ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> 637
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
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<400> 637
Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Leu Val Lys Ser Ser Glu
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Thr Gly Ser Ile Ser Ser Ser

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

<210> 638
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 638
actggctcca tcagcagtag tagttactac 30

<210> 639
<211> 10
<212> PRT
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<220>
<223> Synthetic

<400> 639
Thr Gly Ser Ile Ser Ser Ser Ser Tyr Tyr
1 5 10

<210> 640
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 640
atctattata gtgggagtaa a 21

<210> 641
<211> 7
<212> PRT
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<220>
<223> Synthetic

<400> 641
Ile Tyr Tyr Ser Gly Ser Lys
1 5

<210> 642
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 642
gcgagacagg tcggtgcaat ctttgactac 30

<210> 643
<211> 10
<212> PRT
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<220>
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<400> 643
Ala Arg Gln Val Gly Ala Ile Phe Asp Tyr
1 5 10

<210> 644
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
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<400> 644
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atctcttgcc gggccagtca gagtattagt agttggttgg cctggtatca gcacaaacca 120
gggaaagccc ctaaactcct gctctataag gcgtctagtt tagaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagag ttcactctca ccatcagcag cctgcagcct 240
gatgattttg caacttatta ctgccaacag tataatagtt attctcggac gttcggccaa 300
gggaccaagg tggagatcaa a 321

<210> 645
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 645
Ala Ile Arg Leu Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
20 25 30
Leu Ala Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Leu
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 Ser Arg
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 646
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 646
cagagtatta gtagttgg 18

<210> 647
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 647
Gln Ser Ile Ser Ser Trp
1 5

<210> 648
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 648
aaggcgtct 9

<210> 649
<211> 3
<212> PRT
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<220>
<223> Synthetic

<400> 649
Lys Ala Ser
1

<210> 650
<211> 27
<212> DNA
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<220>
<223> Synthetic

<400> 650
caacagtata atagttattc tcggacg 27

<210> 651
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 651
Gln Gln Tyr Asn Ser Tyr Ser Arg Thr
1 5

<210> 652
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 652
gaggtgcagc tggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgcaagg cctctggtta cacctttaac atctatggta tcagctgggt acgacaggcc 120
cctggacaag ggcttgagtg gatgggatgg atcagcgctt acaatggtaa cacaaactat 180
gcacagaaac tccagggcag agtcaccatg accacagaaa catccacgac cacagcctac 240
atggagttga ggagcctgag atctgacgac acggccgtgt attactgtgc gagagattct 300
gattggggaa ctccctacca ctactacggt atggacgtct ggggccaagg gaccacggtc 360
accgtctcct ca 372

<210> 653
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 653
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Asn Ile Tyr
20 25 30
Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu
50 55 60
Gln Gly Arg Val Thr Met Thr Thr Glu Thr Ser Thr 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
Ala Arg Asp Ser Asp Trp Gly Thr Pro Tyr His Tyr Tyr Gly Met Asp
100 105 110
Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 654
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 654
ggttacacct ttaacatcta tggt 24

<210> 655
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 655
Gly Tyr Thr Phe Asn Ile Tyr Gly
1 5

<210> 656
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 656
atcagcgctt acaatggtaa caca 24

<210> 657
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 657
Ile Ser Ala Tyr Asn Gly Asn Thr
1 5

<210> 658
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 658
gcgagagatt ctgattgggg aactccctac cactactacg gtatggacgt c 51

<210> 659
<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 659
Ala Arg Asp Ser Asp Trp Gly Thr Pro Tyr His Tyr Tyr Gly Met Asp
1 5 10 15
Val

<210> 660
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 660
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atcaactgca agtccagcca gaatatttta tacacctcca acaataagaa ctacttagct 120
tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atttacccgg 180
aaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcaata ttataatact 300
cctcggacgt tcggccaagg gaccaaggtg gatatcaaa 339

<210> 661
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 661
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Asn Ile Leu Tyr 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 Phe Thr Arg Lys 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 Asn Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Asp Ile
100 105 110
Lys

<210> 662
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 662
cagaatattt tatacacctc caacaataag aactac 36

<210> 663
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 663
Gln Asn Ile Leu Tyr Thr Ser Asn Asn Lys Asn Tyr
1 5 10

<210> 664
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 664
tgggcattt 9

<210> 665
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 665
Trp Ala Phe
1

<210> 666
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 666
cagcaatatt ataatactcc tcggacg 27

<210> 667
<211> 9
<212> PRT
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<220>
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<400> 667
Gln Gln Tyr Tyr Asn Thr Pro Arg Thr
1 5

<210> 668
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 668
cagatcacct tgaaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60
acctgcactg tctctgatgg ctccatcaac agtggtggtt cctactggag ctggatccgc 120
cagcacccgg ggaagggcct ggagtggatt gggtacatca aatacagtgg gggcgtccac 180
tataacccgt ccctcaagag tcgaatcacc atatcagtgg acacgtctaa gaaccatttc 240
tccctgaaaa tgacctctgt gactgccgcg gacacggccg tgtatttctg tgcgagagca 300
cctggaagtc acacttttga tatctggggc caggggacaa tggtcaccgt ctcttca 357

<210> 669
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
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<400> 669
Gln Ile Thr Leu Lys Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Asp Gly Ser Ile Asn Ser Gly
20 25 30
Gly Ser Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45
Trp Ile Gly Tyr Ile Lys Tyr Ser Gly Gly Val His Tyr Asn Pro Ser
50 55 60
Leu Lys Ser Arg Ile Thr Ile Ser Val Asp Thr Ser Lys Asn His Phe
65 70 75 80
Ser Leu Lys Met Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe
85 90 95
Cys Ala Arg Ala Pro Gly Ser His Thr Phe Asp Ile Trp Gly Gln Gly
100 105 110
Thr Met Val Thr Val Ser Ser
115

<210> 670
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
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<400> 670
gatggctcca tcaacagtgg tggttcctac 30

<210> 671

<211> 10
<212> PRT
<213> Artificial Sequence

<220>
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<400> 671
Asp Gly Ser Ile Asn Ser Gly Gly Ser Tyr
1   5   10

<210> 672
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 672
atcaaataca gtgggggcgt c   21

<210> 673
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 673
Ile Lys Tyr Ser Gly Gly Val
1   5

<210> 674
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 674
gcgagagcac ctggaagtca cacttttgat atc   33

<210> 675
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 675
Ala Arg Ala Pro Gly Ser His Thr Phe Asp Ile
1   5   10

<210> 676

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

<220>
<223> Synthetic

<400> 676
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ctctcctgca gggccagtca gagtgttagc aacaactact tagcctggta ccagcagaaa 120
cctggccagg ctcccagact cctcatctat ggtacatcca atagggtcag tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgaactata ttattgtcag cagtatagta ggtcaccgat caccttcggc 300
caagggacac gactggagat taaa 324

<210> 677
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 677
Asp Ile Val Met 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 Asn Asn
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 Thr Ser Asn Arg Val Ser 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 Glu Leu Tyr Tyr Cys Gln Gln Tyr Ser Arg Ser Pro
85 90 95
Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 678
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
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<400> 678
cagagtgtta gcaacaacta c 21

<210> 679
<211> 7
<212> PRT
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<220>
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<400> 679
Gln Ser Val Ser Asn Asn Tyr

1 5

<210> 680
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
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<400> 680
ggtacatcc 9

<210> 681
<211> 3
<212> PRT
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<220>
<223> Synthetic

<400> 681
Gly Thr Ser
1

<210> 682
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 682
cagcagtata gtaggtcacc gatcacc 27

<210> 683
<211> 9
<212> PRT
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<220>
<223> Synthetic

<400> 683
Gln Gln Tyr Ser Arg Ser Pro Ile Thr
1 5

<210> 684
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 684
gaggtgcagc tggtgcagtc tgggggaggc ttggtacaac ctggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttaac aactttgcca tgacctgggt ccgccaggct 120
ccagggaagg gcctggagtg ggtctcaact attagtggta gtggcgttga cacatactgc 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacactgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagatggc 300
gccttctata gtggctacga acactactgg ggccagggaa caatggtcac cgtctcctca 360

<210> 685
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
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<400> 685
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Asn Phe
20 25 30
Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Thr Ile Ser Gly Ser Gly Val Asp Thr Tyr Cys 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 Gly Ala Phe Tyr Ser Gly Tyr Glu His Tyr Trp Gly Gln
100 105 110
Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 686
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 686
ggattcacct ttaacaactt tgcc 24

<210> 687
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 687
Gly Phe Thr Phe Asn Asn Phe Ala
1 5

<210> 688
<211> 24
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 688
attagtggta gtggcgttga caca 24

<210> 689
<211> 8
<212> PRT
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<220>
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<400> 689
Ile Ser Gly Ser Gly Val Asp Thr
1 5

<210> 690
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
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<400> 690
gcgaaagatg gcgccttcta tagtggctac gaacactac 39

<210> 691
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 691
Ala Lys Asp Gly Ala Phe Tyr Ser Gly Tyr Glu His Tyr
1 5 10

<210> 692
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
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<400> 692
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ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtacatcca acagggcctc tggcatccca 180
gacaggctca ttggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
tctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctcg gacgttcggc 300
caagggacca aagtggatat caaa 324

<210> 693
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 693
Glu Thr Thr Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Gly Thr Ser Asn Arg Ala Ser Gly Ile Pro Asp Arg Leu Ile
50 55 60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80
Ser Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95
Arg Thr Phe Gly Gln Gly Thr Lys Val Asp Ile Lys
100 105

<210> 694
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 694
cagagtgtta gcagcagcta c 21

<210> 695
<211> 7
<212> PRT
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<220>
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<400> 695
Gln Ser Val Ser Ser Ser Tyr
1 5

<210> 696
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 696
ggtacatcc 9

<210> 697

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

<220>
<223> Synthetic

<400> 697
Gly Thr Ser
1

<210> 698
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 698
cagcagtatg gtagctcacc tcggacg 27

<210> 699
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 699
Gln Gln Tyr Gly Ser Ser Pro Arg Thr
1 5

<210> 700
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
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<400> 700
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tcctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtggcagtt atatggtatg atggaagtaa taaatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa catgctgtat 240
ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc ggcttacgat 300
atttgattg gttattcccc ggttgactac tggggccagg gaaccctggt caccgtctcc 360
tca 363

<210> 701
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 701
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met 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 Ala Tyr Asp Ile Leu Ile Gly Tyr Ser Pro Val Asp Tyr Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 702
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 702
ggattcacct tcagtagcta tggc 24

<210> 703
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 703
Gly Phe Thr Phe Ser Ser Tyr Gly
1 5

<210> 704
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 704
atatggtatg atggaagtaa taaa 24

<210> 705
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
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<400> 705
Ile Trp Tyr Asp Gly Ser Asn Lys
1 5

<210> 706
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 706
gcggcttacg atattttgat tggttattcc ccggttgact ac 42

<210> 707
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 707
Ala Ala Tyr Asp Ile Leu Ile Gly Tyr Ser Pro Val Asp Tyr
1 5 10

<210> 708
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 708
gatattgtga tgacccagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gactgttagt agcaacttag cctggttcca gcagaaacct 120
ggccaggctc ccagactcct catctatgat gcatccacca gggccactgg tatcccagcc 180
aggttcagtg gcagtgggtc tgggacagaa ttcactctca ccatcagcag cctgcagtct 240
gaagattttg cagtttatta ctgtcagcag tataataact ggtacacttt tggccagggg 300
accaagctgg agatcaaa 318

<210> 709
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 709
Asp 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 Thr Val Ser Ser Asn
20 25 30
Leu Ala Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

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

<210> 710
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 710
cagactgtta gtagcaac 18

<210> 711
<211> 6
<212> PRT
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<220>
<223> Synthetic

<400> 711
Gln Thr Val Ser Ser Asn
1 5

<210> 712
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 712
gatgcatcc 9

<210> 713
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 713
Asp Ala Ser
1

<210> 714
<211> 24
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 714
cagcagtata ataactggta cact 24

<210> 715
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 715
Gln Gln Tyr Asn Asn Trp Tyr Thr
1 5

<210> 716
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 716
gaggtgcagc tggtgcagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60
acctgcactg tctctggtgg ctccattacc agtggtggtt actactggac ctggatccgc 120
cagcacccag ggaagggcct ggaatggatt ggatacatca aatttagtgg gaacacctac 180
tacaacccgt ccctcaggag tcgagtcacc atatcacttg acacgtctaa gaatcagttc 240
tccctgaata tgacctctgt gactgccgcg gacacggccg tgtattattg tgcgagagca 300
cctggaagtc ataactttga catctggggc caagggacaa tggtcaccgt ctcttca 357

<210> 717
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 717
Glu Val Gln Leu Val Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Thr Ser Gly
20 25 30
Gly Tyr Tyr Trp Thr Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45
Trp Ile Gly Tyr Ile Lys Phe Ser Gly Asn Thr Tyr Tyr Asn Pro Ser
50 55 60
Leu Arg Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe
65 70 75 80
Ser Leu Asn Met Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Ala Arg Ala Pro Gly Ser His Asn Phe Asp Ile Trp Gly Gln Gly
100 105 110
Thr Met Val Thr Val Ser Ser

115

<210> 718
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 718
ggtggctcca ttaccagtgg tggttactac 30

<210> 719
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 719
Gly Gly Ser Ile Thr Ser Gly Gly Tyr Tyr
1 5 10

<210> 720
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 720
atcaaattta gtgggaacac c 21

<210> 721
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 721
Ile Lys Phe Ser Gly Asn Thr
1 5

<210> 722
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 722
gcgagagcac ctggaagtca taactttgac atc 33

<210> 723
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 723
Ala Arg Ala Pro Gly Ser His Asn Phe Asp Ile
1 5 10

<210> 724
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 724
gccatccggt tgacccagtc tccagacacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtgt gagtattagt aataactatt tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag aagactggag 240
tctgcagatt ttgcaccgta ttactgtcag caatatagta ggtcaccgat caccttcggc 300
caagggacac gactggagat taaa 324

<210> 725
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 725
Ala Ile Arg Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Val Ser Ile Ser Asn Asn
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 Arg Arg Leu Glu
65 70 75 80
Ser Ala Asp Phe Ala Pro Tyr Tyr Cys Gln Gln Tyr Ser Arg Ser Pro
85 90 95
Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 726
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 726
gtgagtatta gtaataacta t 21

<210> 727
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 727
Val Ser Ile Ser Asn Asn Tyr
1 5

<210> 728
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 728
ggtgcatcc 9

<210> 729
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 729
Gly Ala Ser
1

<210> 730
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 730
cagcaatata gtaggtcacc gatcacc 27

<210> 731
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 731
Gln Gln Tyr Ser Arg Ser Pro Ile Thr
1 5

<210> 732
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 732
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60
acctgcactg tctctggtgg ctccatcaac agtgttactt actactggac ctggatccgc 120
cagcacccag ggaggggcct agagtggatt gggtacatca aattcagtgg gagcacctac 180
tacaacccgt ccctcaaggg tcgagtcacc atatcagtgg acacgtctaa gaaccaattc 240
tcccttaaaa ttaactctgt gactgccgcg gacacggccg tgttttactg tgcgagagct 300
tctggaagtc atacttttga tatctggggc caagggacaa tggtcaccgt ctcctca 357

<210> 733
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 733
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Asn Ser Val
20 25 30
Thr Tyr Tyr Trp Thr Trp Ile Arg Gln His Pro Gly Arg Gly Leu Glu
35 40 45
Trp Ile Gly Tyr Ile Lys Phe Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60
Leu Lys Gly Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80
Ser Leu Lys Ile Asn Ser Val Thr Ala Ala Asp Thr Ala Val Phe Tyr
85 90 95
Cys Ala Arg Ala Ser Gly Ser His Thr Phe Asp Ile Trp Gly Gln Gly
100 105 110
Thr Met Val Thr Val Ser Ser
115

<210> 734
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 734
ggtggctcca tcaacagtgt tacttactac 30

<210> 735
<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 735
Gly Gly Ser Ile Asn Ser Val Thr Tyr Tyr
1   5   10

<210> 736
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 736
atcaaattca gtgggagcac c   21

<210> 737
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 737
Ile Lys Phe Ser Gly Ser Thr
1   5

<210> 738
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 738
gcgagagctt ctggaagtca tactttgat atc   33

<210> 739
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 739
Ala Arg Ala Ser Gly Ser His Thr Phe Asp Ile
1   5   10

<210> 740
<211> 324

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 740
gaaacgacac tcacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttagc aacagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctct ggtgcgtcca gcagggtcac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttggaatgta ttactgtcag cagtatagta ggtcaccgat caccttcggc 300
caagggacca agctggagat caaa 324

<210> 741
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 741
Glu Thr Thr 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 Asn Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Ser Gly Ala Ser Ser Arg Val 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 Gly Met Tyr Tyr Cys Gln Gln Tyr Ser Arg Ser Pro
85 90 95
Ile Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 742
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 742
cagagtgtta gcaacagcta c 21

<210> 743
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 743
Gln Ser Val Ser Asn Ser Tyr
1 5

<210> 744
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 744
ggtgcgtcc 9

<210> 745
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 745
Gly Ala Ser
1

<210> 746
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 746
cagcagtata gtaggtcacc gatcacc 27

<210> 747
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 747
Gln Gln Tyr Ser Arg Ser Pro Ile Thr
1 5

<210> 748
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 748
gaggtgcagc tggtgcagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60
tcctgtgcag cctctggagt caccttggat gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaagt attagttgga atagtggtag tataggctat 180
gcggactctg tgaagggccg cttcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgc aaaagatggg 300
tggaacccgt actactttga ctattggggc cagggaataa cggtcaccgt ctcctca 357

<210> 749
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 749
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Leu 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 Ser Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95
Ala Lys Asp Gly Trp Asn Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110
Ile Thr Val Thr Val Ser Ser
115

<210> 750
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 750
ggagtcacct tggatgatta tgcc 24

<210> 751
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 751
Gly Val Thr Leu Asp Asp Tyr Ala
1 5

<210> 752
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 752
attagttgga atagtggtag tata 24

<210> 753
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 753
Ile Ser Trp Asn Ser Gly Ser Ile
1 5

<210> 754
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 754
gcaaaagatg ggtggaaccc gtactacttt gactat 36

<210> 755
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 755
Ala Lys Asp Gly Trp Asn Pro Tyr Tyr Phe Asp Tyr
1 5 10

<210> 756
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 756
gacatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gggcattaga agtgatttag gctggtatca gcagaaacca 120
gggaaagccc ctaagcgcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtctacag cataatagtt accctctcac tttcggcgga 300
gggaccaagg tggaaatcaa a 321

<210> 757
<211> 107

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 757
Asp 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 Gly Ile Arg Ser Asp
20 25 30
Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
35 40 45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu
85 90 95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 758
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 758
cagggcatta gaagtgat 18

<210> 759
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 759
Gln Gly Ile Arg Ser Asp
1 5

<210> 760
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 760
gctgcatcc 9

<210> 761
<211> 3
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 761
Ala Ala Ser
1

<210> 762
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 762
ctacagcata atagttaccc tctcact 27

<210> 763
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 763
Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 764
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 764
cagatcacct tgaaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60
acctgcgccg tctctggtga ctccttcagc agtggtaatt actactggag ctggatccgc 120
caacacccag ggaagggcct ggagtggatt gggtacatca agtacactgg gagcacctac 180
tacaacccgt ccctcaagag tcgagttatt atattagtag acacgtctaa gacccagttc 240
tccctgaagc tgagctctgt gaatgccgcg gacacggccg tgtattactg tgcgagagca 300
cctggaactc atgcttttga tgtttggggc caagggacaa tggtcaccgt ctcctca 357

<210> 765
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 765
Gln Ile Thr Leu Lys Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

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

<210> 766
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 766
ggtgactcct tcagcagtgg taattactac 30

<210> 767
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 767
Gly Asp Ser Phe Ser Ser Gly Asn Tyr Tyr
1 5 10

<210> 768
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 768
atcaagtaca ctgggagcac c 21

<210> 769
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 769
Ile Lys Tyr Thr Gly Ser Thr

1 5

<210> 770
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 770
gcgagagcac ctggaactca tgcttttgat gtt 33

<210> 771
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 771
Ala Arg Ala Pro Gly Thr His Ala Phe Asp Val
1 5 10

<210> 772
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 772
gaaacgacac tcacgcagtc tccaggcacc ctgtctttgt ttccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttagc agtagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgtgaca gactccactc tcaccatcag cagcctggag 240
cctgaagatt ttgcagtgta ttactgtcag cagtatagta ggtcaccgat caccttcggc 300
caagggacca agctggagat caaa 324

<210> 773
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 773
Glu Thr Thr Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Phe Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60
Gly Ser Gly Ser Val Thr Asp Ser Thr Leu Thr Ile Ser Ser Leu Glu

65 70 75 80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ser Arg Ser Pro
85 90 95
Ile Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 774
<211> 21
<212> DNA
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<220>
<223> Synthetic

<400> 774
cagagtgtta gcagtagcta c 21

<210> 775
<211> 7
<212> PRT
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<220>
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<400> 775
Gln Ser Val Ser Ser Ser Tyr
1 5

<210> 776
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
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<400> 776
ggtgcatcc 9

<210> 777
<211> 3
<212> PRT
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<220>
<223> Synthetic

<400> 777
Gly Ala Ser
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<210> 778
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 778
cagcagtata gtaggtcacc gatcacc 27

<210> 779
<211> 9
<212> PRT
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<220>
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<400> 779
Gln Gln Tyr Ser Arg Ser Pro Ile Thr
1 5

<210> 780
<211> 360
<212> DNA
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<220>
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<400> 780
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tcctgtgcag cctctggatt cacctttaac aactttgcca tgacctgggt ccgccaggct 120
ccagggaagg gcctggagtg ggtctcaact attagtggta gtggcgttga cacatactgc 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacactgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgttc gaaagatggc 300
gccttctata gtggctacga acactactgg ggccagggaa ccacggtcac cgtctcctca 360

<210> 781
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 781
Glu Val Gln Leu Val Gln Ser Gly Gly Ala 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 Phe
20 25 30
Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Thr Ile Ser Gly Ser Gly Val Asp Thr Tyr Cys 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
Ser Lys Asp Gly Ala Phe Tyr Ser Gly Tyr Glu His Tyr Trp Gly Gln
100 105 110
Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 782
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 782
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<210> 783
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 783
Gly Phe Thr Phe Asn Asn Phe Ala
1   5

<210> 784
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 784
attagtggta gtggcgttga caca   24

<210> 785
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 785
Ile Ser Gly Ser Gly Val Asp Thr
1   5

<210> 786
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 786
tcgaaagatg gcgccttcta tagtggctac gaacactac   39

<210> 787

<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 787
Ser Lys Asp Gly Ala Phe Tyr Ser Gly Tyr Glu His Tyr
1 5 10

<210> 788
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 788
gaaacgacac tcacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtacatcca acagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
tctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctcg gacgttcggc 300
caagggacca aggtggagat caaa 324

<210> 789
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 789
Glu Thr Thr Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Gly Thr Ser Asn 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
Ser Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95
Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 790
<211> 21
<212> DNA
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<220>
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<400> 790
cagagtgtta gcagcagcta c 21

<210> 791
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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<400> 791
Gln Ser Val Ser Ser Ser Tyr
1 5

<210> 792
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 792
ggtacatcc 9

<210> 793
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 793
Gly Thr Ser
1

<210> 794
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 794
cagcagtatg gtagctcacc tcggacg 27

<210> 795
<211> 9
<212> PRT
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<220>
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<400> 795
Gln Gln Tyr Gly Ser Ser Pro Arg Thr

1 5

<210> 796
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 796
gaagtgcagc tggtgcagtc tggacctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgcaagg cttctggtta cacctttacc tactatggta tcagttggat acgacagacc 120
cctggacaag ggcttgagtg gatgggatgg atcagcgctt acgatggtaa cacagactat 180
gcacagaagt tccaagacag aatcaccatg accacagaca catcctcgac cacagcctac 240
atggaactga ggagcctgag atctgacgac acggccgtct attactgtgc gaggtatagt 300
tggaacaagc actggttcga cccctggggc cagggaacca tggtcaccgt ctcttca 357

<210> 797
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 797
Glu Val Gln Leu Val Gln Ser Gly Pro 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 Tyr Tyr
20 25 30
Gly Ile Ser Trp Ile Arg Gln Thr Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Trp Ile Ser Ala Tyr Asp Gly Asn Thr Asp Tyr Ala Gln Lys Phe
50 55 60
Gln Asp Arg Ile Thr Met Thr Thr Asp Thr Ser 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
Ala Arg Tyr Ser Trp Asn Lys His Trp Phe Asp Pro Trp Gly Gln Gly
100 105 110
Thr Met Val Thr Val Ser Ser
115

<210> 798
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 798
ggttacacct ttacctacta tggt 24

<210> 799
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 799
Gly Tyr Thr Phe Thr Tyr Tyr Gly
1 5

<210> 800
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 800
atcagcgctt acgatggtaa caca 24

<210> 801
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 801
Ile Ser Ala Tyr Asp Gly Asn Thr
1 5

<210> 802
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 802
gcgaggtata gttggaacaa gcactggttc gacccc 36

<210> 803
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 803
Ala Arg Tyr Ser Trp Asn Lys His Trp Phe Asp Pro
1 5 10

<210> 804
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 804
gaaattgtga tgacacagtc tccaggcacc ctgtctttgt ctccagggga cagagccacc 60
ctctcctgca gggccagtca gagtgttacc ggcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccagact cctcatctat ggtgcatcca acagggccac tggcatccca 180
gacaggttca ctggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta tttctgtcaa cagtctgctt tctcaccgtg gacgttcggc 300
caggggacca aggtggaaat caaa 324

<210> 805
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 805
Glu Ile Val Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Asp Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Gly Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Ile Pro Asp Arg Phe Thr
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 Phe Cys Gln Gln Ser Ala Phe Ser Pro
85 90 95
Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 806
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 806
cagagtgtta ccggcagcta c 21

<210> 807
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 807
Gln Ser Val Thr Gly Ser Tyr
1 5

<210> 808
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 808
ggtgcatcc 9

<210> 809
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 809
Gly Ala Ser
1

<210> 810
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 810
caacagtctg ctttctcacc gtggacg 27

<210> 811
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 811
Gln Gln Ser Ala Phe Ser Pro Trp Thr
1 5

<210> 812
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 812
gaggtgcagc tggtgcagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60
tcctgtgcag cctctggagt caccttggat gattatgcca tgcactgggt ccggcaagct 120
ccagggaagg gcctggagtg ggtctcaagt attagttgga atagtggtag tataggctat 180
gcggactctg tgaagggccg cttcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgc aaaagatggg 300
tggaacccgt actactttga ctattggggc cagggaatac cggtcaccgt ctcctca 357

<210> 813
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 813
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Leu 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 Ser Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95
Ala Lys Asp Gly Trp Asn Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110
Ile Pro Val Thr Val Ser Ser
115

<210> 814
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 814
ggagtcacct tggatgatta tgcc 24

<210> 815
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 815
Gly Val Thr Leu Asp Asp Tyr Ala
1 5

<210> 816
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 816
attagttgga atagtggtag tata 24

<210> 817
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 817
Ile Ser Trp Asn Ser Gly Ser Ile
1 5

<210> 818
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 818
gcaaaagatg ggtggaaccc gtactacttt gactat 36

<210> 819
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 819
Ala Lys Asp Gly Trp Asn Pro Tyr Tyr Phe Asp Tyr
1 5 10

<210> 820
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 820
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gggcattaga agtgatttag gctggtatca gcagaaacca 120
gggaaagccc ctaagcgcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240
gaagattttg caacctatta ctgtctacag cataatagtt accctctcac tttcggcgga 300
gggaccaagc tggagatcaa a 321

<210> 821
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 821
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Ser Asp
20 25 30
Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
35 40 45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu
85 90 95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 822
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 822
cagggcatta gaagtgat 18

<210> 823
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 823
Gln Gly Ile Arg Ser Asp
1 5

<210> 824
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 824
gctgcatcc 9

<210> 825
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 825
Ala Ala Ser
1

<210> 826
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 826
ctacagcata atagttaccc tctcact 27

<210> 827
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 827
Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 828
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 828
caggtacagc tgcagcagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60
acctgcgctg tctctggtga ctccttcagc agtggtaatt actactggag ctggatccgc 120
caacacccag ggaagggcct ggagtggatt gggtacatca agtacactgg gagcacctac 180
tacaacccgt ccctcaagag tcgagttacc atattagtag acacgtctaa gacccagttc 240
tccctgaagc tgagctctgt gactgccgcg gacacggccg tgtattactg tgcgagagca 300
cctggaactc atgttttgga tgtctggggc caagggacaa tggtcaccgt ctcttca 357

<210> 829
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 829
Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Asp Ser Phe Ser Ser Gly
20 25 30

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

<210> 830
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 830
ggtgactcct tcagcagtgg taattactac 30

<210> 831
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 831
Gly Asp Ser Phe Ser Ser Gly Asn Tyr Tyr
1 5 10

<210> 832
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 832
atcaagtaca ctgggagcac c 21

<210> 833
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 833
Lys Tyr Thr Gly Ser Thr
1 5

<210> 834
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 834
gcgagagcac ctggaactca tgtttttgat gtc 33

<210> 835
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 835
Ala Arg Ala Pro Gly Thr His Val Phe Asp Val
1 5 10

<210> 836
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 836
gacatccagt tgacccagtc tccaggcacc ctgtctttgc ttccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttagc agtagctatt tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgtgaca gacttcactc tcaccatcag cagcctggag 240
cctgaagatt ttgcagtgta ttactgtcag cagtatagta ggtcaccgat caccttcggc 300
caagggacca aggtggagat caaa 324

<210> 837
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 837
Asp Ile Gln Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Leu Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60
Gly Ser Gly Ser Val Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ser Arg Ser Pro

85 90 95
Ile Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 838
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 838
cagagtgtta gcagtagcta t 21

<210> 839
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 839
Gln Ser Val Ser Ser Ser Tyr
1 5

<210> 840
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 840
ggtgcatcc 9

<210> 841
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 841
Gly Ala Ser
1

<210> 842
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 842
cagcagtata gtaggtcacc gatcacc   27

<210> 843
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 843
Gln Gln Tyr Ser Arg Ser Pro Ile Thr
1   5

<210> 844
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 844
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60
acctgcactg tctctggtgg ctccatcagc agtggtggtt actactggag ttggatccgc 120
cagcacccag ggaagggcct ggagtggatt gggtacatcc attatagtgg gaacacccac 180
tacaatccga ccctcaagag tcgaattacc atatcagtag acacgtctaa gaaccagttc 240
tcccttgagg tgaactctgt gactgccgcg gacacggccg tatactactg tgcgaggaat 300
atggttcggg gagttcactg gttcgacccc tggggccagg gaaccacggt caccgtctcc 360
tca   363

<210> 845
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 845
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1   5   10   15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20   25   30
Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
        35   40   45
Trp Ile Gly Tyr Ile His Tyr Ser Gly Asn Thr His Tyr Asn Pro Thr
    50   55   60
Leu Lys Ser Arg Ile Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65   70   75   80
Ser Leu Glu Val Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85   90   95
Cys Ala Arg Asn Met Val Arg Gly Val His Trp Phe Asp Pro Trp Gly
            100   105   110
Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 846

<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 846
ggtggctcca tcagcagtgg tggttactac 30

<210> 847
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 847
Gly Gly Ser Ile Ser Ser Gly Gly Tyr Tyr
1 5 10

<210> 848
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 848
atccattata gtgggaacac c 21

<210> 849
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 849
Ile His Tyr Ser Gly Asn Thr
1 5

<210> 850
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 850
gcgaggaata tggttcgggg agttcactgg ttcgacccc 39

<210> 851
<211> 13
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 851
Ala Arg Asn Met Val Arg Gly Val His Trp Phe Asp Pro
1 5 10

<210> 852
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 852
gaaatagtgt tgacacagtc tccaggcacc ctgtctttgt ctccagggga gagagccacc 60
ctcttctgtt gggccagtcg gagtgttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctct ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtata tttctgtcaa cagtatagta gttcaccgct cactttcggc 300
ggagggacca agctggagat caaa 324

<210> 853
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 853
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 Phe Cys Trp Ala Ser Arg Ser Val Ser Ser Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Ser 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 Phe Cys Gln Gln Tyr Ser Ser Ser Pro
85 90 95
Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 854
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 854
cggagtgtta gcagcagcta c 21

<210> 855
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 855
Arg Ser Val Ser Ser Ser Tyr
1 5

<210> 856
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 856
ggtgcatcc 9

<210> 857
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 857
Gly Ala Ser
1

<210> 858
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 858
caacagtata gtagttcacc gctcact 27

<210> 859
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 859
Gln Gln Tyr Ser Ser Ser Pro Leu Thr
1 5

<210> 860
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 860
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60
acctgcactg tctctagtga ctccatcagc agtggtaata actactggac ctggatccgc 120
cagcacccag ggaggggcct ggagtggatt gggtacatca aatacactgg gagcgcccac 180
tacaacccgt ccctcaagag tcgagtcacc atgtcagtag acacgtctaa gaatcagttc 240
tccctgaaaa tgacctctgt gactgacgcg gacacggccg tgtattattg tgcgagggca 300
cctggaagcc attcttttga tatatggggc cgagggacaa tggtcaccgt ctcctca 357

<210> 861
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 861
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Ser Asp Ser Ile Ser Ser Gly
20 25 30
Asn Asn Tyr Trp Thr Trp Ile Arg Gln His Pro Gly Arg Gly Leu Glu
35 40 45
Trp Ile Gly Tyr Ile Lys Tyr Thr Gly Ser Ala His Tyr Asn Pro Ser
50 55 60
Leu Lys Ser Arg Val Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80
Ser Leu Lys Met Thr Ser Val Thr Asp Ala Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Ala Arg Ala Pro Gly Ser His Ser Phe Asp Ile Trp Gly Arg Gly
100 105 110
Thr Met Val Thr Val Ser Ser
115

<210> 862
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 862
agtgactcca tcagcagtgg taataactac 30

<210> 863
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 863
Ser Asp Ser Ile Ser Ser Gly Asn Asn Tyr
1 5 10

<210> 864
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 864
atcaaataca ctgggagcgc c 21

<210> 865
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 865
Ile Lys Tyr Thr Gly Ser Ala
1 5

<210> 866
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 866
gcgagggcac ctggaagcca ttctttgat ata 33

<210> 867
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 867
Ala Arg Ala Pro Gly Ser His Ser Phe Asp Ile
1 5 10

<210> 868
<211> 324
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 868
gatgttgtga tgacccagtc tccaggcacc ctgtttttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaacatcag cagactggag 240
cctgaagatt ttgcactgta ttactgtcag cagtatagta ggtcaccgat caccttcggc 300
caagggacac gactggagat taaa 324

<210> 869
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 869
Asp Val Val Met Thr Gln Ser Pro Gly Thr Leu Phe Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile Ser Arg Leu Glu
65 70 75 80
Pro Glu Asp Phe Ala Leu Tyr Tyr Cys Gln Gln Tyr Ser Arg Ser Pro
85 90 95
Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 870
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 870
cagagtgtta gcagcagcta c 21

<210> 871
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 871
Gln Ser Val Ser Ser Ser Tyr
1 5

<210> 872
<211> 9

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 872
ggtgcatcc 9

<210> 873
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 873
Gly Ala Ser
1

<210> 874
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 874
cagcagtata gtaggtcacc gatcacc 27

<210> 875
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 875
Gln Gln Tyr Ser Arg Ser Pro Ile Thr
1 5

<210> 876
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 876
caggtgcagc tggtgcagtc tgggggaggc ttggtacaac ctggggggtc cctaagactc 60
tcctgtgcag cctctggatt cacctctaac aactttgcca tgacctgggt ccgccaggct 120
ccagggaagg gcctggagtg ggtctcaact attagtggta gtggcgttga cacatactgc 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacactgtat 240
ctgcaaatga acagcctgag agtcgaggac acggccgtat attactgtgc taaagatggc 300
gccttctata gtggctacga acactactgg ggccagggaa ccctggtcac cgtctcctca 360

<210> 877
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 877
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Ser Asn Asn Phe
20 25 30
Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Thr Ile Ser Gly Ser Gly Val Asp Thr Tyr Cys 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 Val Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Lys Asp Gly Ala Phe Tyr Ser Gly Tyr Glu His Tyr Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 878
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 878
ggattcacct ctaacaactt tgcc 24

<210> 879
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 879
Gly Phe Thr Ser Asn Asn Phe Ala
1 5

<210> 880
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 880
attagtggta gtggcgttga caca 24

<210> 881
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 881
Ile Ser Gly Ser Gly Val Asp Thr
1 5

<210> 882
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 882
gctaaagatg gcgccttcta tagtggctac gaacactac 39

<210> 883
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 883
Ala Lys Asp Gly Ala Phe Tyr Ser Gly Tyr Glu His Tyr
1 5 10

<210> 884
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 884
gatgttgtga tgacccagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtacatcca acagggcctc tggcatccca 180
gacaagttca ttggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
tctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctcg gacgttcggc 300
caagggacca aagtggatat caaa 324

<210> 885
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 885
Asp Val Val Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Gly Thr Ser Asn Arg Ala Ser Gly Ile Pro Asp Lys Phe Ile
50 55 60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80
Ser Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95
Arg Thr Phe Gly Gln Gly Thr Lys Val Asp Ile Lys
100 105

<210> 886
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 886
cagagtgtta gcagcagcta c 21

<210> 887
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 887
Gln Ser Val Ser Ser Ser Tyr
1 5

<210> 888
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 888
ggtacatcc 9

<210> 889
<211> 3
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 889
Gly Thr Ser
1

<210> 890
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 890
cagcagtatg gtagctcacc tcggacg 27

<210> 891
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 891
Gln Gln Tyr Gly Ser Ser Pro Arg Thr
1 5

<210> 892
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 892
caggtgcagc tgcaggagtc cggccccggc ctggtgaagc cctcccagac cctgtccctg 60
acctgcaccg tgtccggcgg ctccatcggc tccggcggct actactggtc ctggatccgg 120
cagcaccccg gcaagggcct ggagtggatc ggctacgtgc actactccgg caacacctac 180
tacaacccct ccctgaagtc ccgggtgacc atctccgtgg acacctccaa gaaccagttc 240
tccctgaagc tgtcctccgt gaccgccgcc gacaccgccg tgtactactg cgcccgggcc 300
ccccggggct accactactt cgcctactgg ggccagggca ccctggtgac cgtgtcctcc 360

<210> 893
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 893
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Gly Ser Gly
20 25 30

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

<210> 894
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 894
gagatcgtgc tgacccagtc ccccggcacc ctgtccctgt cccccggcga gcgggccacc 60
ctgtcctgcc gggcctccca gtccgtgtcc tcctcctacc tggcctggta ccagcagaag 120
cccggccagg ccccccggct gctgatctac ggcgcctcct cccgggccac cggcatcccc 180
gaccggttct ccggctccgg ctccggcacc gacttcaccc tgaccatctc ccggctggag 240
cccgaggact tcgccgtgta ctactgccag cagtacggct cctcccccct gaccttcggc 300
ggcggcacca aggtggagat caag 324

<210> 895
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 895
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95
Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 896
<211> 369
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 896
caggtgcagc tggtggagtc cggcggcggc gtggtgcagc ccggccggtc cctgcggctg 60
tcctgcgccg cctccggctt caccttctcc tcctacggca tgcactgggt gcggcaggcc 120
cccggcaagg gcctggagtg ggtggccgtg ctgtggtacg acggcaccaa caagtactac 180
gccgactccg tgaagggccg gttcaccatc tcccgggaca actccaagaa caccctgtac 240
ctgcagatga actccctgcg ggccgaggac accgccgtgt actactgcgc ccgggaccac 300
gacttccggt ccggctacga gggctggttc gacccctggg gccagggcac cctggtgacc 360
gtgtcctcc 369

<210> 897
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 897
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Val Leu Trp Tyr Asp Gly Thr Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Asp His Asp Phe Arg Ser Gly Tyr Glu Gly Trp Phe Asp Pro
100 105 110
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 898
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 898
gagatcgtgc tgacccagtc ccccgccacc ctgtccctgt cccccggcga gcgggccacc 60
ctgtcctgcc gggcctccca gtccgtgtcc tcctacctgg cctggtacca gcagaagccc 120
ggccaggccc cccggctgct gatctacgac gcctccaacc gggccaccgg catccccgcc 180
cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctggagccc 240
gaggacttcg ccgtgtacta ctgccagcac cggtccaact ggccccccac cttcggcggc 300
ggcaccaagg tggagatcaa g 321

<210> 899
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 899
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1   5   10   15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35   40   45
Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65   70   75   80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Arg Ser Asn Trp Pro Pro
                85   90   95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 900
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 900
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cgtctggatt caccttcagt agttatggca tgcactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtgtcattt ttatggtatg atggaactaa taaaaactat 180
gtagagtccg tgaagggccg attcaccatc tccagagaca attccaagaa tatgctgtat 240
ctggaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagatcac 300
gattttagga gtggttatga ggggtggttc gacccctggg gccagggaac cctggtcacc 360
gtctcctca 369

<210> 901
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 901
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Phe Leu Trp Tyr Asp Gly Thr Asn Lys Asn Tyr Val Glu Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met 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 Asp His Asp Phe Arg Ser Gly Tyr Glu Gly Trp Phe Asp Pro
            100   105   110
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 902
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 902
gaaatagtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttagc agctacttag cctggtacca acagaaacct 120
ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 240
gaagattttg cagtttatta ctgtcaacac cgtagcaact ggcctcccac tttcggcgga 300
gggaccaagg tggaaatcaa a 321

<210> 903
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 903
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Arg Ser Asn Trp Pro Pro
85 90 95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 904
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 904
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60
acctgcactg tctctggtgg ctccatcagc agtggtggtt actactggag ttggatccgc 120
cagcacccag ggaagggcct ggagtggatt gggtacatcc attatagtgg gaacacccac 180
tacaatccga ccctcaagag tcgaattacc atatcagtag acacgtctaa gaaccagttc 240
tcccttgagg tgaactctgt gactgccgcg gacacggccg tatactactg tgcgaggaat 300
atggttcggg gagttcactg gttcgacccc tggggccagg gaaccacggt caccgtctcc 360
tca 363

<210> 905
<211> 121

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 905
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30
Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45
Trp Ile Gly Tyr Ile His Tyr Ser Gly Asn Thr His Tyr Asn Pro Thr
50 55 60
Leu Lys Ser Arg Ile Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80
Ser Leu Glu Val Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Ala Arg Asn Met Val Arg Gly Val His Trp Phe Asp Pro Trp Gly
100 105 110
Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 906
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 906
gaaatagtgt tgacacagtc tccaggcacc ctgtctttgt ctccagggga gagagccacc 60
ctcttctgtt gggccagtcg gagtgttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctct ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtata tttctgtcaa cagtatagta gttcaccgct cactttcggc 300
ggagggacca agctggagat caaa 324

<210> 907
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 907
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 Phe Cys Trp Ala Ser Arg Ser Val Ser Ser Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Ser 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 Phe Cys Gln Gln Tyr Ser Ser Ser Pro

85 90 95
Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 908
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 908
caggtgcagc tgcaggagtc cggccccggc ctggtgaagc cctcccagac cctgtccctg 60
acctgcaccg tgtccggcgg ctccatctcc tccggcggct actactggtc ctggatccgg 120
cagcaccccg gcaagggcct ggagtggatc ggctacatcc actactccgg caacacctac 180
tacaacccct ccctgaagtc ccgggtgacc atctccgtgg acacctccaa gaaccagttc 240
tccctgaagc tgtcctccgt gaccgccgcc gacaccgccg tgtactactg cgcccggaac 300
atggtgcggg gcgtgcactg gttcgacccc tggggccagg gcaccctggt gaccgtgtcc 360
tcc 363

<210> 909
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 909
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30
Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45
Trp Ile Gly Tyr Ile His Tyr Ser Gly Asn Thr Tyr Tyr Asn Pro Ser
50 55 60
Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80
Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Ala Arg Asn Met Val Arg Gly Val His Trp Phe Asp Pro Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 910
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 910
gagatcgtgc tgacccagtc ccccggcacc ctgtccctgt cccccggcga gcgggccacc 60
ctgtcctgcc gggcctcccg gtccgtgtcc tcctcctacc tggcctggta ccagcagaag 120
cccggccagg ccccccggct gctgatctac ggcgcctcct cccgggccac cggcatcccc 180

gaccggttct ccggctccgg ctccggcacc gacttcaccc tgaccatctc ccggctggag 240
cccgaggact tcgccgtgta ctactgccag cagtactcct cctcccccct gaccttcggc 300
ggcggcacca aggtggagat caag 324

<210> 911
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 911
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 Arg Ser Val Ser Ser Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ser Ser Ser Pro
85 90 95
Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 912
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 912
caggtgcagc tgcaggagtc gggcctagga ctggtgaagc cttcacagac cctgtccctc 60
acctgcactg tctctggtgg ctccatcagc agtggtggtt actactggag ttggatccgc 120
cagcacccag ggaagggcct ggagtggatt gggtacatcc attatagtgg gaacacccac 180
tacaatccga ccctcaagag tcgaattacc atatcagtag acacgtctaa gaaccagttc 240
tcccttgagg tgaactctgt gactgccgcg gacacggccg tatactactg tgcgaggaat 300
atggttcggg gagttcactg gttcgacccc tggggccagg gaaccctggt caccgtctcc 360
tca 363

<210> 913
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 913
Gln Val Gln Leu Gln Glu Ser Gly Leu Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30
Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile His Tyr Ser Gly Asn Thr His Tyr Asn Pro Thr
50 55 60
Leu Lys Ser Arg Ile Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80
Ser Leu Glu Val Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Ala Arg Asn Met Val Arg Gly Val His Trp Phe Asp Pro Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 914
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 914
gaaatagtgt tgacacagtc tccaggcacc ctgtctttgt ctccagggga gagagccacc 60
ctcttctgtt gggccagtcg gagtgttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctct ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtata tttctgtcaa cagtatagta gttcaccgct cactttcggc 300
ggagggacca aggtggaaat caaa 324

<210> 915
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 915
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 Phe Cys Trp Ala Ser Arg Ser Val Ser Ser Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Ser 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 Phe Cys Gln Gln Tyr Ser Ser Ser Pro
85 90 95
Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 916
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 916
caggtgcagc tgcaggagtc cggccccggc ctggtgaagc cctcccagac cctgtccctg 60
acctgcaccg tgtccggcgg ctccatcacc tccggcggct actactggtc ctggatccgg 120
cagcaccccg gcaagggcct ggagtggatc ggctacatca agttctccgg caacacctac 180
tacaacccct ccctgaagtc ccgggtgacc atctccgtgg acacctccaa gaaccagttc 240
tccctgaagc tgtcctccgt gaccgccgcc gacaccgccg tgtactactg cgcccgggcc 300
cccggctccc acaacttcga catctggggc cagggcacca tggtgaccgt gtcctcc 357

<210> 917
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 917
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Thr Ser Gly
20 25 30
Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45
Trp Ile Gly Tyr Ile Lys Phe Ser Gly Asn Thr Tyr Tyr Asn Pro Ser
50 55 60
Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80
Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Ala Arg Ala Pro Gly Ser His Asn Phe Asp Ile Trp Gly Gln Gly
100 105 110
Thr Met Val Thr Val Ser Ser
115

<210> 918
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 918
gagatcgtgc tgacccagtc ccccggcacc ctgtccctgt cccccggcga gcgggccacc 60
ctgtcctgcc gggcctccgt gtccatctcc aacaactacc tggcctggta ccagcagaag 120
cccggccagg ccccccggct gctgatctac ggcgcctcct cccgggccac cggcatcccc 180
gaccggttct ccggctccgg ctccggcacc gacttcaccc tgaccatccg gcggctggag 240
cccgaggact tcgcccccta ctactgccag cagtactccc ggtcccccat caccttcggc 300
cagggcaccc ggctggagat caag 324

<210> 919
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 919
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 Val Ser Ile Ser Asn Asn
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 Arg Arg Leu Glu
65 70 75 80
Pro Glu Asp Phe Ala Pro Tyr Tyr Cys Gln Gln Tyr Ser Arg Ser Pro
85 90 95
Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 920
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 920
gaggtgcagc tggtggagtc cggcggcggc ctggtgcagc ccggcggctc cctgcggctg 60
tcctgcgccg cctccggctt caccttcaac aacttcgcca tgtcctgggt gcggcaggcc 120
cccggcaagg gcctggagtg ggtgtccgcc atctccggct ccggcgtgga cacctactac 180
gccgactccg tgaagggccg gttcaccatc tcccgggaca actccaagaa caccctgtac 240
ctgcagatga actccctgcg ggccgaggac accgccgtgt actactgctc caaggacggc 300
gccttctact ccggctacga gcactactgg ggccagggca ccctggtgac cgtgtcctcc 360

<210> 921
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 921
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Asn Phe
20 25 30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Ala Ile Ser Gly Ser Gly Val Asp 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
Ser Lys Asp Gly Ala Phe Tyr Ser Gly Tyr Glu His Tyr Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 922
<211> 324

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 922
gagatcgtgc tgacccagtc ccccggcacc ctgtccctgt cccccggcga gcgggccacc 60
ctgtcctgcc gggcctccca gtccgtgtcc tcctcctacc tggcctggta ccagcagaag 120
cccggccagg ccccccggct gctgatctac ggcacctcct cccgggccac cggcatcccc 180
gaccggttct ccggctccgg ctccggcacc gacttcaccc tgaccatctc ccggctggag 240
cccgaggact tcgccgtgta ctactgccag cagtacggct cctccccccg gaccttcggc 300
cagggcacca aggtggagat caag 324

<210> 923
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 923
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Gly Thr 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
Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 924
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 924
caggtgcagc tggtgcagtc cggcgccgag gtgaagaagc ccggcgcctc cgtgaaggtg 60
tcctgcaagg cctccggcta caccttcacc tactacggca tctcctgggt gcggcaggcc 120
cccggccagg gcctggagtg gatgggctgg atctccgcct acgacggcaa caccaactac 180
gcccagaagc tgcagggccg ggtgaccatg accaccgaca cctccacctc caccgcctac 240
atggagctgc ggtccctgcg gtccgacgac accgccgtgt actactgcgc ccggtactcc 300
tggaacaagc actggttcga cccctggggc cagggcaccc tggtgaccgt gtcctcc 357

<210> 925
<211> 119
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 925
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 Tyr Tyr
            20   25   30
Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45
Gly Trp Ile Ser Ala Tyr Asp 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 Tyr Ser Trp Asn Lys His Trp Phe Asp Pro Trp Gly Gln Gly
            100   105   110
Thr Leu Val Thr Val Ser Ser
        115

<210> 926
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 926
gagatcgtgc tgacccagtc ccccggcacc ctgtccctgt cccccggcga gcgggccacc 60
ctgtcctgcc gggcctccca gtccgtgacc ggctcctacc tggcctggta ccagcagaag 120
cccggccagg ccccccggct gctgatctac ggcgcctcct cccgggccac cggcatcccc 180
gaccggttct ccggctccgg ctccggcacc gacttcaccc tgaccatctc ccggctggag 240
cccgaggact tcgccgtgta ctactgccag cagtccgcct tctccccctg gaccttcggc 300
cagggcacca aggtggagat caag   324

<210> 927
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 927
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 Thr Gly Ser
            20   25   30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35   40   45
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50   55   60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65   70   75   80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Ala Phe Ser Pro
                85   90   95
Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 928
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> VARIANT
<222> (1)...(8)
<223> Xaa = Any amino acid or absent

<400> 928
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 929
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> VARIANT
<222> (1)...(8)
<223> Xaa = Any amino acid or absent

<400> 929
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 930
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> VARIANT
<222> (1)...(16)
<223> Xaa = Any amino acid or absent

<400> 930
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

<210> 931
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<220>
<221> VARIANT
<222> (1)...(7)
<223> Xaa = Any amino acid or absent

<400> 931
Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 932
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> VARIANT
<222> (1)...(3)
<223> Xaa = Any amino acid or absent

<400> 932
Xaa Xaa Xaa
1

<210> 933
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> VARIANT
<222> (1)...(9)
<223> Xaa = Any amino acid or absent

<400> 933
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 934
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 934
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60
acctgcactg tctctggtgg ctccattacc agtggtggtt actactggac ctggatccgc 120
cagcacccag ggaagggcct ggaatggatt ggatacatca aatttagtgg gaacacctac 180
tacaacccgt ccctcaggag tcgagtcacc atatcacttg acacgtctaa gaatcagttc 240

tccctgaata tgacctctgt gactgccgcg gacacggccg tgtattattg tgcgagagca 300
cctggaagtc ataactttga catctggggc caagggacaa tggtcaccgt ctcttca 357

<210> 935
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 935
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Thr Ser Gly
20 25 30
Gly Tyr Tyr Trp Thr Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45
Trp Ile Gly Tyr Ile Lys Phe Ser Gly Asn Thr Tyr Tyr Asn Pro Ser
50 55 60
Leu Arg Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe
65 70 75 80
Ser Leu Asn Met Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Ala Arg Ala Pro Gly Ser His Asn Phe Asp Ile Trp Gly Gln Gly
100 105 110
Thr Met Val Thr Val Ser Ser
115

<210> 936
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 936
gaaatcgtgt tgacccagtc tccagacacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtgt gagtattagt aataactatt tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag aagactggag 240
tctgcagatt ttgcaccgta ttactgtcag caatatagta ggtcaccgat caccttcggc 300
caagggacac gactggagat taaa 324

<210> 937
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 937
Glu Ile Val Leu Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Val Ser Ile Ser Asn Asn
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 Arg Arg Leu Glu
65 70 75 80
Ser Ala Asp Phe Ala Pro Tyr Tyr Cys Gln Gln Tyr Ser Arg Ser Pro
85 90 95
Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 938
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 938
gaagtgcagc tggtggagtc tgggggagcc ttggtacaac ctggggggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttaac aactttgcca tgacctgggt ccgccaggct 120
ccagggaagg gcctggagtg ggtctcaact attagtggta gtggcgttga cacatactgc 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacactgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgttc gaaagatggc 300
gccttctata gtggctacga acactactgg ggccagggaa ccctggtcac cgtctcctca 360

<210> 939
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 939
Glu Val Gln Leu Val Glu Ser Gly Gly Ala 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 Phe
20 25 30
Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Thr Ile Ser Gly Ser Gly Val Asp Thr Tyr Cys 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
Ser Lys Asp Gly Ala Phe Tyr Ser Gly Tyr Glu His Tyr Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 940
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 940
gaaattgtgc tcacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtacatcca acagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
tctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctcg gacgttcggc 300
caagggacca aggtggagat caaa 324

<210> 941
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 941
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Gly Thr Ser Asn 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
Ser Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95
Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 942
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 942
caggtgcagc tggtgcagtc tggacctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgcaagg cttctggtta cacctttacc tactatggta tcagttggat acgacagacc 120
cctggacaag ggcttgagtg gatgggatgg atcagcgctt acgatggtaa cacagactat 180
gcacagaagt tccaagacag aatcaccatg accacagaca catcctcgac cacagcctac 240
atggaactga ggagcctgag atctgacgac acggccgtct attactgtgc gaggtatagt 300
tggaacaagc actggttcga cccctggggc cagggaaccc tggtcaccgt ctcttca 357

<210> 943
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 943
Gln Val Gln Leu Val Gln Ser Gly Pro 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 Tyr Tyr
20 25 30
Gly Ile Ser Trp Ile Arg Gln Thr Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Trp Ile Ser Ala Tyr Asp Gly Asn Thr Asp Tyr Ala Gln Lys Phe
50 55 60
Gln Asp Arg Ile Thr Met Thr Thr Asp Thr Ser 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
Ala Arg Tyr Ser Trp Asn Lys His Trp Phe Asp Pro Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
115

<210> 944
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 944
gaaattgtgt tgacacagtc tccaggcacc ctgtctttgt ctccagggga cagagccacc 60
ctctcctgca gggccagtca gagtgttacc ggcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccagact cctcatctat ggtgcatcca acagggccac tggcatccca 180
gacaggttca ctggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta tttctgtcaa cagtctgctt tctcaccgtg gacgttcggc 300
caggggacca aggtggaaat caaa 324

<210> 945
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 945
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Asp Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Gly Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Ile Pro Asp Arg Phe Thr
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 Phe Cys Gln Gln Ser Ala Phe Ser Pro
85 90 95
Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 946
<211> 361
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 946
caggtgcagt tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60
acctgcactg tctctggtgg ctccatcggc agtggtggtt actactggag ctggatccgc 120
cagcacccag ggaagggcct ggagtggatt gggtacgtcc attacagtgg gaacacccac 180
tacaacccgt ccctcaagag tcgactttcc atatcaatag acacgtctaa gatccagttc 240
tccctgaagc tgagctctgt gactgccgcg gacacggccg tgtattactg tgcgagagcc 300
ccccgtggat accattactt tgcctactgg ggccagggaa ccctggtcac cgtctcctca 360
g 361

<210> 947
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 947
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Gly Ser Gly
20 25 30
Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45
Trp Ile Gly Tyr Val His Tyr Ser Gly Asn Thr His Tyr Asn Pro Ser
50 55 60
Leu Lys Ser Arg Leu Ser Ile Ser Ile Asp Thr Ser Lys Ile Gln Phe
65 70 75 80
Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Ala Arg Ala Pro Arg Gly Tyr His Tyr Phe Ala Tyr Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 948
<211> 325
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 948
gaaattgtgt tgacacaatc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatcttt ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccgct cactttcggc 300
ggagggacca aggtggagat caaac 325

<210> 949
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 949
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Phe 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> 950
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 950
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95
Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 951
<211> 327
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 951
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

<210> 952
<211> 327
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 952
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1 5 10 15
Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65 70 75 80
Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95
Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
100 105 110
Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
115 120 125
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
130 135 140
Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145 150 155 160
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
165 170 175
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
180 185 190
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
195 200 205
Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
210 215 220
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225 230 235 240
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
245 250 255
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
260 265 270
Thr Thr Pro 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> 953
<211> 544
<212> PRT
<213> Homo sapiens

<400> 953
Met Gly Ser Arg Cys Ala Leu Ala Leu Ala Val Leu Ser Ala Leu Leu
1 5 10 15
Cys Gln Val Trp Ser Ser Gly Val Phe Glu Leu Lys Leu Gln Glu Phe
20 25 30
Val Asn Lys Lys Gly Leu Leu Gly Asn Arg Asn Cys Cys Arg Gly Gly
35 40 45
Ala Gly Pro Pro Pro Cys Ala Cys Arg Thr Phe Phe Arg Val Cys Leu
50 55 60
Lys His Tyr Gln Ala Ser Val Ser Pro Glu Pro Pro Cys Thr Tyr Gly
65 70 75 80
Ser Ala Val Thr Pro Val Leu Gly Val Asp Ser Phe Ser Leu Pro Asp
85 90 95
Gly Gly Gly Ala Asp Ser Ala Phe Ser Asn Pro Ile Arg Phe Pro Phe
100 105 110
Gly Phe Thr Trp Pro Gly Thr Phe Ser Leu Ile Ile Glu Ala Leu His
115 120 125
Thr Asp Ser Pro Asp Asp Leu Ala Thr Glu Asn Pro Glu Arg Leu Ile
130 135 140
Ser Arg Leu Ala Thr Gln Arg His Leu Thr Val Gly Glu Glu Trp Ser
145 150 155 160
Gln Asp Leu His Ser Ser Gly Arg Thr Asp Leu Lys Tyr Ser Tyr Arg
165 170 175
Phe Val Cys Asp Glu His Tyr Tyr Gly Glu Gly Cys Ser Val Phe Cys
180 185 190
Arg Pro Arg Asp Asp Ala Phe Gly His Phe Thr Cys Gly Glu Arg Gly
195 200 205
Glu Lys Val Cys Asn Pro Gly Trp Lys Gly Pro Tyr Cys Thr Glu Pro
210 215 220
Ile Cys Leu Pro Gly Cys Asp Glu Gln His Gly Phe Cys Asp Lys Pro
225 230 235 240
Gly Glu Cys Lys Cys Arg Val Gly Trp Gln Gly Arg Tyr Cys Asp Glu
245 250 255
Cys Ile Arg Tyr Pro Gly Cys Leu His Gly Thr Cys Gln Gln Pro Trp
260 265 270
Gln Cys Asn Cys Gln Glu Gly Trp Gly Gly Leu Phe Cys Asn Gln Asp
275 280 285
Leu Asn Tyr Cys Thr His His Lys Pro Cys Lys Asn Gly Ala Thr Cys
290 295 300
Thr Asn Thr Gly Gln Gly Ser Tyr Thr Cys Ser Cys Arg Pro Gly Tyr
305 310 315 320
Thr Gly Ala Thr Cys Glu Leu Gly Ile Asp Glu Cys Asp Pro Ser Pro
325 330 335
Cys Lys Asn Gly Gly Ser Cys Thr Asp Leu Glu Asn Ser Tyr Ser Cys
340 345 350
Thr Cys Pro Pro Gly Phe Tyr Gly Lys Ile Cys Glu Leu Ser Ala Met
355 360 365
Thr Cys Ala Asp Gly Pro Cys Phe Asn Gly Gly Arg Cys Ser Asp Ser
370 375 380
Pro Asp Gly Gly Tyr Ser Cys Arg Cys Pro Val Gly Tyr Ser Gly Phe
385 390 395 400
Asn Cys Glu Lys Lys Ile Asp Tyr Cys Ser Ser Ser Pro Cys Ser Asn
405 410 415
Gly Ala Lys Cys Val Asp Leu Gly Asp Ala Tyr Leu Cys Arg Cys Gln
420 425 430
Ala Gly Phe Ser Gly Arg His Cys Asp Asp Asn Val Asp Asp Cys Ala
435 440 445
Ser Ser Pro Cys Ala Asn Gly Gly Thr Cys Arg Asp Gly Val Asn Asp
450 455 460
Phe Ser Cys Thr Cys Pro Pro Gly Tyr Thr Gly Arg Asn Cys Ser Ala

465 470 475 480
Pro Val Ser Arg Cys Glu His Ala Pro Cys His Asn Gly Ala Thr Cys
485 490 495
His Glu Arg Gly His Arg Tyr Val Cys Glu Cys Ala Arg Gly Tyr Gly
500 505 510
Gly Pro Asn Cys Gln Phe Leu Leu Pro Glu Leu Pro Pro Gly Pro Ala
515 520 525
Val Val Asp Leu Thr Glu Lys Leu Glu Gly Gln Gly Gly Pro Phe Pro
530 535 540

<210> 954
<211> 490
<212> PRT
<213> Homo sapiens

<400> 954
Met Val Ser Pro Arg Met Ser Gly Leu Leu Ser Gln Thr Val Ile Leu
1 5 10 15
Ala Leu Ile Phe Leu Pro Gln Thr Arg Pro Ala Gly Val Phe Glu Leu
20 25 30
Gln Ile His Ser Phe Gly Pro Gly Pro Gly Pro Gly Ala Pro Arg Ser
35 40 45
Pro Cys Ser Ala Arg Leu Pro Cys Arg Leu Phe Phe Arg Val Cys Leu
50 55 60
Lys Pro Gly Leu Ser Glu Glu Ala Ala Glu Ser Pro Cys Ala Leu Gly
65 70 75 80
Ala Ala Leu Ser Ala Arg Gly Pro Val Tyr Thr Glu Gln Pro Gly Ala
85 90 95
Pro Ala Pro Asp Leu Pro Leu Pro Asp Gly Leu Leu Gln Val Pro Phe
100 105 110
Arg Asp Ala Trp Pro Gly Thr Phe Ser Phe Ile Ile Glu Thr Trp Arg
115 120 125
Glu Glu Leu Gly Asp Gln Ile Gly Gly Pro Ala Trp Ser Leu Leu Ala
130 135 140
Arg Val Ala Gly Arg Arg Arg Leu Ala Ala Gly Gly Pro Trp Ala Arg
145 150 155 160
Asp Ile Gln Arg Ala Gly Ala Trp Glu Leu Arg Phe Ser Tyr Arg Ala
165 170 175
Arg Cys Glu Pro Pro Ala Val Gly Thr Ala Cys Thr Arg Leu Cys Arg
180 185 190
Pro Arg Ser Ala Pro Ser Arg Cys Gly Pro Gly Leu Arg Pro Cys Ala
195 200 205
Pro Leu Glu Asp Glu Cys Glu Ala Pro Pro Val Cys Arg Ala Gly Cys
210 215 220
Ser Pro Glu His Gly Phe Cys Glu Gln Pro Gly Glu Cys Arg Cys Leu
225 230 235 240
Glu Gly Trp Thr Gly Pro Leu Cys Thr Val Pro Val Ser Thr Ser Ser
245 250 255
Cys Leu Ser Pro Arg Gly Pro Ser Ser Ala Thr Thr Gly Cys Leu Val
260 265 270
Pro Gly Pro Gly Pro Cys Asp Gly Asn Pro Cys Ala Asn Gly Gly Ser
275 280 285
Cys Ser Glu Thr Pro Arg Ser Phe Glu Cys Thr Cys Pro Arg Gly Phe
290 295 300
Tyr Gly Leu Arg Cys Glu Val Ser Gly Val Thr Cys Ala Asp Gly Pro
305 310 315 320
Cys Phe Asn Gly Gly Leu Cys Val Gly Gly Ala Asp Pro Asp Ser Ala
325 330 335
Tyr Ile Cys His Cys Pro Pro Gly Phe Gln Gly Ser Asn Cys Glu Lys
340 345 350

Arg Val Asp Arg Cys Ser Leu Gln Pro Cys Arg Asn Gly Gly Leu Cys
355 360 365
Leu Asp Leu Gly His Ala Leu Arg Cys Arg Cys Arg Ala Gly Phe Ala
370 375 380
Gly Pro Arg Cys Glu His Asp Leu Asp Asp Cys Ala Gly Arg Ala Cys
385 390 395 400
Ala Asn Gly Gly Thr Cys Val Glu Gly Gly Gly Ala His Arg Cys Ser
405 410 415
Cys Ala Leu Gly Phe Gly Gly Arg Asp Cys Arg Glu Arg Ala Asp Pro
420 425 430
Cys Ala Ala Arg Pro Cys Ala His Gly Gly Arg Cys Tyr Ala His Phe
435 440 445
Ser Gly Leu Val Cys Ala Cys Ala Pro Gly Tyr Met Gly Ala Arg Cys
450 455 460
Glu Phe Pro Val His Pro Asp Gly Ala Ser Ala Leu Pro Ala Ala Pro
465 470 475 480
Pro Gly Leu Arg Pro Gly Asp Pro Gln Arg
485 490

<210> 955
<211> 527
<212> PRT
<213> Mus musculus

<400> 955
Met Thr Pro Ala Ser Arg Ser Ala Cys Arg Trp Ala Leu Leu Leu Leu
1 5 10 15
Ala Val Leu Trp Pro Gln Gln Arg Ala Ala Gly Ser Gly Ile Phe Gln
20 25 30
Leu Arg Leu Gln Glu Phe Val Asn Gln Arg Gly Met Leu Ala Asn Gly
35 40 45
Gln Ser Cys Glu Pro Gly Cys Arg Thr Phe Phe Arg Ile Cys Leu Lys
50 55 60
His Phe Gln Ala Thr Phe Ser Glu Gly Pro Cys Thr Phe Gly Asn Val
65 70 75 80
Ser Thr Pro Val Leu Gly Thr Asn Ser Phe Val Val Arg Asp Lys Asn
85 90 95
Ser Gly Ser Gly Arg Asn Pro Leu Gln Leu Pro Phe Asn Phe Thr Trp
100 105 110
Pro Gly Thr Phe Ser Leu Asn Ile Gln Ala Trp His Thr Pro Gly Asp
115 120 125
Asp Leu Arg Pro Glu Thr Ser Pro Gly Asn Ser Leu Ile Ser Gln Ile
130 135 140
Ile Ile Gln Gly Ser Leu Ala Val Gly Lys Ile Trp Arg Thr Asp Glu
145 150 155 160
Gln Asn Asp Thr Leu Thr Arg Leu Ser Tyr Ser Tyr Arg Val Ile Cys
165 170 175
Ser Asp Asn Tyr Tyr Gly Glu Ser Cys Ser Arg Leu Cys Lys Lys Arg
180 185 190
Asp Asp His Phe Gly His Tyr Glu Cys Gln Pro Asp Gly Ser Leu Ser
195 200 205
Cys Leu Pro Gly Trp Thr Gly Lys Tyr Cys Asp Gln Pro Ile Cys Leu
210 215 220
Ser Gly Cys His Glu Gln Asn Gly Tyr Cys Ser Lys Pro Asp Glu Cys
225 230 235 240
Ile Cys Arg Pro Gly Trp Gln Gly Arg Leu Cys Asn Glu Cys Ile Pro
245 250 255
His Asn Gly Cys Arg His Gly Thr Cys Ser Ile Pro Trp Gln Cys Ala
260 265 270
Cys Asp Glu Gly Trp Gly Gly Leu Phe Cys Asp Gln Asp Leu Asn Tyr

275 280 285
Cys Thr His His Ser Pro Cys Lys Asn Gly Ser Thr Cys Ser Asn Ser
290 295 300
Gly Pro Lys Gly Tyr Thr Cys Thr Cys Leu Pro Gly Tyr Thr Gly Glu
305 310 315 320
His Cys Glu Leu Gly Leu Ser Lys Cys Ala Ser Asn Pro Cys Arg Asn
325 330 335
Gly Gly Ser Cys Lys Asp Gln Glu Asn Ser Tyr His Cys Leu Cys Pro
340 345 350
Pro Gly Tyr Tyr Gly Gln His Cys Glu His Ser Thr Leu Thr Cys Ala
355 360 365
Asp Ser Pro Cys Phe Asn Gly Gly Ser Cys Arg Glu Arg Asn Gln Gly
370 375 380
Ser Ser Tyr Ala Cys Glu Cys Pro Pro Asn Phe Thr Gly Ser Asn Cys
385 390 395 400
Glu Lys Lys Val Asp Arg Cys Thr Ser Asn Pro Cys Ala Asn Gly Gly
405 410 415
Gln Cys Gln Asn Arg Gly Pro Ser Arg Thr Cys Arg Cys Arg Pro Gly
420 425 430
Phe Thr Gly Thr His Cys Glu Leu His Ile Ser Asp Cys Ala Arg Ser
435 440 445
Pro Cys Ala His Gly Gly Thr Cys His Asp Leu Glu Asn Gly Pro Val
450 455 460
Cys Thr Cys Pro Ala Gly Phe Ser Gly Arg Arg Cys Glu Val Arg Ile
465 470 475 480
Thr His Asp Ala Cys Ala Ser Gly Pro Cys Phe Asn Gly Ala Thr Cys
485 490 495
Tyr Thr Gly Leu Ser Pro Asn Asn Phe Val Cys Asn Cys Pro Tyr Gly
500 505 510
Phe Val Gly Ser Arg Cys Glu Phe Pro Val Gly Leu Pro Pro Ser
515 520 525

<210> 956
<211> 498
<212> PRT
<213> Macaca fascicularis

<400> 956
Ser Gly Val Phe Gln Leu Gln Leu Gln Glu Phe Val Asn Glu Arg Gly
1 5 10 15
Val Leu Ala Ser Gly Arg Pro Cys Glu Pro Gly Cys Arg Thr Phe Phe
20 25 30
Arg Val Cys Leu Lys His Phe Gln Ala Val Val Ser Pro Gly Pro Cys
35 40 45
Thr Phe Gly Ser Val Ser Thr Pro Val Leu Gly Thr Asn Ser Phe Ala
50 55 60
Val Arg Asp Asp Ser Ser Gly Gly Gly Arg Asn Pro Leu Gln Leu Pro
65 70 75 80
Phe Asn Phe Thr Trp Pro Gly Thr Phe Ser Leu Ile Ile Glu Ala Trp
85 90 95
His Ala Pro Gly Asp Asp Leu Arg Pro Glu Ala Leu Pro Pro Asp Ala
100 105 110
Leu Ile Ser Lys Ile Ala Ile Gln Gly Ser Leu Ala Val Gly Gln Asn
115 120 125
Trp Leu Leu Asp Glu Gln Thr Ser Thr Leu Thr Arg Leu Arg Tyr Ser
130 135 140
Tyr Arg Val Ile Cys Ser Asp Asn Tyr Tyr Gly Asp Asn Cys Ser Arg
145 150 155 160
Leu Cys Lys Lys Arg Asn Asp His Phe Gly His Tyr Val Cys Gln Pro
165 170 175

Asp Gly Asn Leu Ser Cys Leu Pro Gly Trp Thr Gly Glu Tyr Cys Gln
180 185 190
Gln Pro Ile Cys Leu Ser Gly Cys His Glu Gln Asn Gly Tyr Cys Ser
195 200 205
Lys Pro Ala Glu Cys Leu Cys Arg Pro Gly Trp Gln Gly Arg Leu Cys
210 215 220
Asn Glu Cys Ile Pro His Asn Gly Cys Arg His Gly Thr Cys Ser Thr
225 230 235 240
Pro Trp Gln Cys Thr Cys Asp Glu Gly Trp Gly Gly Leu Phe Cys Asp
245 250 255
Gln Asp Leu Asn Tyr Cys Thr His His Ser Pro Cys Lys Asn Gly Ala
260 265 270
Thr Cys Ser Asn Ser Gly Gln Arg Ser Tyr Thr Cys Thr Cys Arg Pro
275 280 285
Gly Tyr Thr Gly Val Asp Cys Glu Leu Glu Leu Ser Glu Cys Asp Ser
290 295 300
Asn Pro Cys Arg Asn Gly Gly Ser Cys Lys Asp Gln Glu Asp Gly Tyr
305 310 315 320
His Cys Leu Cys Pro Pro Gly Tyr Tyr Gly Leu His Cys Glu His Ser
325 330 335
Thr Leu Ser Cys Ala Asp Ser Pro Cys Phe Asn Gly Gly Ser Cys Arg
340 345 350
Glu Arg Asn Gln Gly Ala Ser Tyr Ala Cys Glu Cys Pro Pro Asn Phe
355 360 365
Thr Gly Ser Asn Cys Glu Lys Lys Val Asp Arg Cys Thr Ser Asn Pro
370 375 380
Cys Ala Asn Gly Gly Gln Cys Leu Asn Arg Gly Pro Ser Arg Met Cys
385 390 395 400
Arg Cys Arg Pro Gly Phe Thr Gly Thr Tyr Cys Glu Arg His Val Ser
405 410 415
Asp Cys Ala Arg Asn Pro Cys Ala His Gly Gly Thr Cys His Asp Leu
420 425 430
Glu Ser Gly Leu Met Cys Thr Cys Pro Ala Gly Phe Ser Gly Arg Arg
435 440 445
Cys Glu Val Arg Thr Ser Ile Asp Ala Cys Ala Ser Ser Pro Cys Phe
450 455 460
Asn Arg Ala Thr Cys Tyr Thr Asp Leu Ser Thr Asp Thr Phe Val Cys
465 470 475 480
Asn Cys Pro Tyr Gly Phe Val Gly Ser Arg Cys Glu Phe Pro Met Gly
485 490 495
Leu Pro

<210> 957
<211> 498
<212> PRT
<213> Macaca mulatta

<400> 957
Ser Gly Val Phe Gln Leu Gln Leu Gln Glu Phe Val Asn Glu Arg Gly
1 5 10 15
Val Leu Ala Ser Gly Arg Pro Cys Glu Pro Gly Cys Arg Thr Phe Phe
20 25 30
Arg Val Cys Leu Lys His Phe Gln Ala Val Val Ser Pro Gly Pro Cys
35 40 45
Thr Phe Gly Ser Val Ser Thr Pro Val Leu Gly Thr Asn Ser Phe Ala
50 55 60
Val Arg Asp Asp Ser Ser Gly Gly Gly Arg Asn Pro Leu Gln Leu Pro
65 70 75 80
Phe Asn Phe Thr Trp Pro Gly Thr Phe Ser Leu Ile Ile Glu Ala Trp

85 90 95
His Ala Pro Gly Asp Asp Leu Arg Pro Glu Ala Leu Pro Pro Asp Ala
100 105 110
Leu Ile Ser Lys Ile Ala Ile Gln Gly Ser Leu Ala Val Gly Gln Asn
115 120 125
Trp Leu Leu Asp Glu Gln Thr Ser Thr Leu Thr Arg Leu Arg Tyr Ser
130 135 140
Tyr Arg Val Ile Cys Ser Asp Asn Tyr Tyr Gly Asp Asn Cys Ser Arg
145 150 155 160
Leu Cys Lys Lys Arg Asn Asp His Phe Gly His Tyr Val Cys Gln Pro
165 170 175
Asp Gly Asn Leu Ser Cys Leu Pro Gly Trp Thr Gly Glu Tyr Cys Gln
180 185 190
Gln Pro Ile Cys Leu Ser Gly Cys His Glu Gln Asn Gly Tyr Cys Ser
195 200 205
Lys Pro Ala Glu Cys Leu Cys Arg Pro Gly Trp Gln Gly Arg Leu Cys
210 215 220
Asn Glu Cys Ile Pro His Asn Gly Cys Arg His Gly Thr Cys Ser Thr
225 230 235 240
Pro Trp Gln Cys Thr Cys Asp Glu Gly Trp Gly Gly Leu Phe Cys Asp
245 250 255
Gln Asp Leu Asn Tyr Cys Thr His His Ser Pro Cys Lys Asn Gly Ala
260 265 270
Thr Cys Ser Asn Ser Gly Gln Arg Ser Tyr Thr Cys Thr Cys Arg Pro
275 280 285
Gly Tyr Thr Gly Val Asp Cys Glu Leu Glu Leu Ser Glu Cys Asp Ser
290 295 300
Asn Pro Cys Arg Asn Gly Gly Ser Cys Lys Asp Gln Glu Asp Gly Tyr
305 310 315 320
His Cys Leu Cys Pro Pro Gly Tyr Tyr Gly Leu His Cys Glu His Ser
325 330 335
Thr Leu Ser Cys Ala Asp Ser Pro Cys Phe Asn Gly Gly Ser Cys Arg
340 345 350
Glu Arg Asn Gln Gly Ala Ser Tyr Ala Cys Glu Cys Pro Pro Asn Phe
355 360 365
Thr Gly Ser Asn Cys Glu Lys Lys Val Asp Arg Cys Thr Ser Asn Pro
370 375 380
Cys Ala Asn Gly Gly Gln Cys Leu Asn Arg Gly Pro Ser Arg Met Cys
385 390 395 400
Arg Cys Arg Pro Gly Phe Thr Gly Thr Tyr Cys Glu Arg His Val Ser
405 410 415
Asp Cys Ala Arg Asn Pro Cys Ala His Gly Gly Thr Cys His Asp Leu
420 425 430
Glu Ser Gly Leu Met Cys Thr Cys Pro Ala Gly Phe Ser Gly Arg Arg
435 440 445
Cys Glu Val Arg Thr Ser Ile Asp Ala Cys Ala Ser Ser Pro Cys Phe
450 455 460
Asn Arg Ala Thr Cys Tyr Thr Asp Leu Ser Thr Asp Thr Phe Val Cys
465 470 475 480
Asn Cys Pro Tyr Gly Phe Val Gly Ser Arg Cys Glu Phe Pro Val Gly
485 490 495
Leu Pro

What is claimed is:

1. An isolated nucleic acid molecule encoding an antibody or antibody fragment which specifically binds human delta-like ligand 4 (hDll4), wherein the antibody or antibody fragment comprises heavy chain complementarity determining region (CDR) 1, CDR2 and CDR3 and light chain CDR1, CDR2 and CDR3, wherein the heavy chain CDR1, CDR2 and CDR3 comprise the amino acid sequences of SEQ ID NOS:431, 433 and 435, respectively.

2. A recombinant expression vector comprising the nucleic acid molecule of claim 1.

3. An isolated host cell comprising the expression vector of claim 1 An isolated nucleic acid molecule encoding an antibody or antibody fragment which specifically binds human delta-like ligand 4 (hDll4), wherein the antibody or antibody fragment comprises heavy chain complementarity determining region CDR1, CDR2 and CDR3 and light chain CDR1, CDR2 and CDR3, wherein the heavy chain CDR1, CDR2 and CDR3 comprise the amino acid sequences of SEQ ID NOS: 431, 433 and 435, respectively, and the light chain CDR1, CDR2 and CDR3 comprise the amino acid sequences of SEQ ID NOS: 439, 441 and 443, respectively.

4. The nucleic acid molecule of claim 1, wherein the antibody or antibody fragment comprises a heavy chain variable region (HCVR) comprising the amino acid sequence of SEQ ID NO:429 or 901.

5. The nucleic acid molecule of claim 4 comprising the nucleotide sequence of SEQ ID NO:428 or 900, or a substantially similar sequence having at least 95% homology thereof.

6. The nucleic acid molecule of claim 1, wherein the antibody or antibody fragment comprises a light chain variable region (LCVR) comprising the amino acid sequence of SEQ ID NO:437 or 903.

7. The nucleic acid molecule of claim 6 comprising the nucleotide sequence of SEQ ID NO:436 or 902, or a substantially similar sequence having at least 95% homology thereof.

8. An isolated nucleic acid molecule encoding an antibody or antibody fragment which specifically binds human delta-like ligand 4 (hDll4), wherein the antibody or antibody fragment comprises a HCVR comprising the amino acid sequence of SEQ ID NO:901 and a LCVR comprising the amino acid sequence of SEQ ID NO:903.

9. The nucleic acid molecule of claim 8, wherein the HCVR is encoded by a nucleotide sequence comprising SEQ ID NO: 900.

10. The nucleic acid molecule of claim 8, wherein the LCVR is encoded by a nucleotide sequence comprising SEQ ID NO: 902.

11. The nucleic acid molecule of claim 8 comprising the nucleotide sequences of SEQ ID NOS:900 and 902.

12. A method of producing an antibody or antibody fragment which specifically binds human delta-like ligand 4 (hDll4), comprising growing the host cell of claim 3 under conditions permitting production of the antibody or fragment thereof, and recovering the antibody or fragment thereof so produced.

13. A recombinant expression vector comprising the nucleic acid molecule of claim 8.

14. An isolated host cell comprising the expression vector of claim 13.

15. A method of producing an antibody or antibody fragment which specifically binds human delta-like ligand 4 (hDll4), comprising growing the host cell of claim 14 under conditions permitting production of the antibody or fragment thereof, and recovering the antibody or fragment thereof so produced.

16. A recombinant expression vector comprising the nucleic acid molecule of claim 11.

17. An isolated host cell comprising the expression vector of claim 16.

18. A method of producing an antibody or antibody fragment which specifically binds human delta-like ligand 4 (hDll4), comprising growing the host cell of claim 17 under conditions permitting production of the antibody or fragment thereof, and recovering the antibody or fragment thereof so produced.

19. An isolated nucleic acid molecule encoding an antibody or antibody fragment which specifically binds human delta-like ligand 4 (hDll4), wherein the antibody or antibody fragment comprises a HCVR comprising the amino acid sequence of SEQ ID NO:429 and a LCVR comprising the amino acid sequence of SEQ ID NO:437.

20. The nucleic acid molecule of claim 19, wherein the HCVR is encoded by a nucleotide sequence comprising SEQ ID NO: 428.

21. The nucleic acid molecule of claim 19, wherein the LCVR is encoded by a nucleotide sequence comprising SEQ ID NO: 436.

22. The nucleic acid molecule of claim 19 comprising the nucleotide sequences of SEQ ID NOS:428 and 436.