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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 (hDII4) and blocks hDII4 binding to a Notch receptor. The human anti hDII4 antibody or antibody fragment binds hDII4 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 (DIL4) (hereinafter "DIL4") 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). DIL4 is a ligand for Notch receptors, including Notch1 and Notch 4. The nucleic acid and amino acid sequences for human DIL4 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 (hDIL4). These antibodies are characterized by binding to hDIL4 with high affinity and by the ability to neutralize DIL4 activity. The antibodies of the invention are capable of blocking DIL4 binding to its Notch receptor(s), and thus inhibit signaling by DIL4. 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, 833, 857, 881, 901, 917, 933, 949, 965, 981, 997, 1013, 1029, 1045, 1061, 1077, 1093, 1109, 1125, 1141, 1157, 1173, 1189, 1205, 1221, 1237, 1253, 1269, 1285, 1301, 1317, 1333, 1349, 1365, 1381, 1397, 1413, 1429, 1445, 1461, 1477, 1493, 1509, 1525, 1541, 1557, 1573, 1589, 1605, 1621, 1637, 1653, 1669, 1685, 1701, 1717, 1733, 1749, 1765, 1781, 1797, 1813, 1829, 1845, 1861, 1877, 1893, 1909, 1925, 1941, 1957, 1973, 1989, 2005, 2021, 2037, 2053, 2069, 2085, 2101, 2117, 2133, 2149, 2165, 2181, 2197, 2213, 2229, 2245, 2261, 2277, 2293, 2309, 2325, 2341, 2357, 2373, 2389, 2405, 2421, 2437, 2453, 2469, 2485, 2501, 2517, 2533, 2549, 2565, 2581, 2597, 2613, 2629, 2645, 2661, 2677, 2693, 2709, 2725, 2741, 2757, 2773, 2789, 2805, 2821, 2837, 2853, 2869, 2885, 2901, 2917, 2933, 2949, 2965, 2981, 2997, 3013, 3029, 3045, 3061, 3077, 3093, 3109, 3125, 3141, 3157, 3173, 3189, 3205, 3221, 3237, 3253, 3269, 3285, 3301, 3317, 3333, 3349, 3365, 3381, 3397, 3413, 3429, 3445, 3461, 3477, 3493, 3509, 3525, 3541, 3557, 3573, 3589, 3605, 3621, 3637, 3653, 3669, 3685, 3701, 3717, 3733, 3749, 3765, 3781, 3797, 3813, 3829, 3845, 3861, 3877, 3893, 3909, 3925, 3941, 3957, 3973, 3989, 4005, 4021, 4037, 4053, 4069, 4085, 4101, 4117, 4133, 4149, 4165, 4181, 4197, 4213, 4229, 4245, 4261, 4277, 4293, 4309, 4325, 4341, 4357, 4373, 4389, 4405, 4421, 4437, 4453, 4469, 4485, 4501, 4517, 4533, 4549, 4565, 4581, 4597, 4613, 4629, 4645, 4661, 4677, 4693, 4709, 4725, 4741, 4757, 4773, 4789, 4805, 4821, 4837, 4853, 4869, 4885, 4901, 4917, 4933, 4949, 4965, 4981, 4997, 5013, 5029, 5045, 5061, 5077, 5093, 5109, 5125, 5141, 5157, 5173, 5189, 5205, 5221, 5237, 5253, 5269, 5285, 5301, 5317, 5333, 5349, 5365, 5381, 5397, 5413, 5429, 5445, 5461, 5477, 5493, 5509, 5525, 5541, 5557, 5573, 5589, 5605, 5621, 5637, 5653, 5669, 5685, 5701, 5717, 5733, 5749, 5765, 5781, 5797, 5813, 5829, 5845, 5861, 5877, 5893, 5909, 5925, 5941, 5957, 5973, 5989, 6005, 6021, 6037, 6053, 6069, 6085, 6101, 6117, 6133, 6149, 6165, 6181, 6197, 6213, 6229, 6245, 6261, 6277, 6293, 6309, 6325, 6341, 6357, 6373, 6389, 6405, 6421, 6437, 6453, 6469, 6485, 6501, 6517, 6533, 6549, 6565, 6581, 6597, 6613, 6629, 6645, 6661, 6677, 6693, 6709, 6725, 6741, 6757, 6773, 6789, 6805, 6821, 6837, 6853, 6869, 6885, 6901, 6917, 6933, 6949, 6965, 6981, 6997, 7013, 7029, 7045, 7061, 7077, 7093, 7109, 7125, 7141, 7157, 7173, 7189, 7205, 7221, 7237, 7253, 7269, 7285, 7301, 7317, 7333, 7349, 7365, 7381, 7397, 7413, 7429, 7445, 7461, 7477, 7493, 7509, 7525, 7541, 7557, 7573, 7589, 7605, 7621, 7637, 7653, 7669, 7685, 7701, 7717, 7733, 7749, 7765, 7781, 7797, 7813, 7829, 7845, 7861, 7877, 7893, 7909, 7925, 7941, 7957, 7973, 7989, 8005, 8021, 8037, 8053, 8069, 8085, 8101, 8117, 8133, 8149, 8165, 8181, 8197, 8213, 8229, 8245, 8261, 8277, 8293, 8309, 8325, 8341, 8357, 8373, 8389, 8405, 8421, 8437, 8453, 8469, 8485, 8501, 8517, 8533, 8549, 8565, 8581, 8597, 8613, 8629, 8645, 8661, 8677, 8693, 8709, 8725, 8741, 8757, 8773, 8789, 8805, 8821, 8837, 8853, 8869, 8885, 8901, 8917, 8933, 8949, 8965, 8981, 8997, 9013, 9029, 9045, 9061, 9077, 9093, 9109, 9125, 9141, 9157, 9173, 9189, 9205, 9221, 9237, 9253, 9269, 9285, 9301, 9317, 9333, 9349, 9365, 9381, 9397, 9413, 9429, 9445, 9461, 9477, 9493, 9509, 9525, 9541, 9557, 9573, 9589, 9605, 9621, 9637, 9653, 9669, 9685, 9701, 9717, 9733, 9749, 9765, 9781, 9797, 9813, 9829, 9845, 9861, 9877, 9893, 9909, 9925, 9941, 9957, 9973, 9989, 10005, 10021, 10037, 10053, 10069, 10085, 10101, 10117, 10133, 10149, 10165, 10181, 10197, 10213, 10229, 10245, 10261, 10277, 10293, 10309, 10325, 10341, 10357, 10373, 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12677, 12693, 12709, 12725, 12741, 12757, 12773, 12789, 12805, 12821, 12837, 12853, 12869, 12885, 12901, 12917, 12933, 12949, 12965, 12981, 12997, 13013, 13029, 13045, 13061, 13077, 13093, 13109, 13125, 13141, 13157, 13173, 13189, 13205, 13221, 13237, 13253, 13269, 13285, 13301, 13317, 13333, 13349, 13365, 13381, 13397, 13413, 13429, 13445, 13461, 13477, 13493, 13509, 13525, 13541, 13557, 13573, 13589, 13605, 13621, 13637, 13653, 13669, 13685, 13701, 13717, 13733, 13749, 13765, 13781, 13797, 13813, 13829, 13845, 13861, 13877, 13893, 13909, 13925, 13941, 13957, 13973, 13989, 14005, 14021, 14037, 14053, 14069, 14085, 14101, 14117, 14133, 14149, 14165, 14181, 14197, 14213, 14229, 14245, 14261, 14277, 14293, 14309, 14325, 14341, 14357, 14373, 14389, 14405, 14421, 14437, 14453, 14469, 14485, 14501, 14517, 14533, 14549, 14565, 14581, 14597, 14613, 14629, 14645, 14661, 14677, 14693, 14709, 14725, 14741, 14757, 14773, 14789, 14805, 14821, 14837, 14853, 14869, 14885, 14901, 14917, 14933, 14949, 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17253, 17269, 17285, 17301, 17317, 17333, 17349, 17365, 17381, 17397, 17413, 17429, 17445, 17461, 17477, 17493, 17509, 17525, 17541, 17557, 17573, 17589, 17605, 17621, 17637, 17653, 17669, 17685, 17701, 17717, 17733, 17749, 17765, 17781, 17797, 17813, 17829, 17845, 17861, 17877, 17893, 17909, 17925, 17941, 17957, 17973, 17989, 18005, 18021, 18037, 18053, 18069, 18085, 18101, 18117, 18133, 18149, 18165, 18181, 18197, 18213, 18229, 18245, 18261, 18277, 18293, 18309, 18325, 18341, 18357, 18373, 18389, 18405, 18421, 18437, 18453, 18469, 18485, 18501, 18517, 18533, 18549, 18565, 18581, 18597, 18613, 18629, 18645, 18661, 18677, 18693, 18709, 18725, 18741, 18757, 18773, 18789, 18805, 18821, 18837, 18853, 18869, 18885, 18901, 18917, 18933, 18949, 18965, 18981, 18997, 19013, 19029, 19045, 19061, 19077, 19093, 19109, 19125, 19141, 19157, 19173, 19189, 19205, 19221, 19237, 19253, 19269, 19285, 19301, 19317, 19333, 19349, 19365, 19381, 19397, 19413, 19429, 19445, 19461, 19477, 19493, 19509, 19525, 19541, 19557, 19573, 19589, 19605, 19621, 19637, 19653, 19669, 19685, 19701, 19717, 19733, 19749, 19765, 19781, 19797, 19813, 19829, 19845, 19861, 19877, 19893, 19909, 19925, 19941, 19957, 19973, 19989, 20005, 20021, 20037, 20053, 20069, 20085, 20101, 20117, 20133, 20149, 20165, 20181, 20197, 20213, 20229, 20245, 20261, 20277, 20293, 20309, 20325, 20341, 20357, 20373, 20389, 20405, 20421, 20437, 20453, 20469, 20485, 20501, 20517, 20533, 20549, 20565, 20581, 20597, 20613, 20629, 20645, 20661, 20677, 20693, 20709, 20725, 20741, 20757, 20773, 20789, 20805, 20821, 20837, 20853, 20869, 20885, 20901, 20917, 20933, 20949, 20965, 20981, 20997, 21013, 21029, 21045, 21061, 21077, 21093, 21109, 21125, 21141, 21157, 21173, 21189, 21205, 21221, 21237, 21253, 21269, 21285, 21301, 21317, 21333, 21349, 21365, 21381, 21397, 21413, 21429, 21445, 21461, 21477, 21493, 21509, 21525, 21541, 21557, 21573, 21589, 21605, 21621, 21637, 21653, 21669, 21685, 21701, 21717, 21733, 21749, 21765, 21781, 21797, 21813, 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24117, 24133, 24149, 24165, 24181, 24197, 24213, 24229, 24245, 24261, 24277, 24293, 24309, 24325, 24341, 24357, 24373, 24389, 24405, 24421, 24437, 24453, 24469, 24485, 24501, 24517, 24533, 24549, 24565, 24581, 24597, 24613, 24629, 24645, 24661, 24677, 24693, 24709, 24725, 24741, 24757, 24773, 24789, 24805, 24821, 24837, 24853, 24869, 24885, 24901, 24917, 24933, 24949, 24965, 24981, 24997, 25013, 25029, 25045, 25061, 25077, 25093, 25109, 25125, 25141, 25157, 25173, 25189, 25205, 25221, 25237, 25253, 25269, 25285, 25301, 25317, 25333, 25349, 25365, 25381, 25397, 25413, 25429, 25445, 25461, 25477, 25493, 25509, 25525, 25541, 25557, 25573, 25589, 25605, 25621, 25637, 25653, 25669, 25685, 25701, 25717, 25733, 25749, 25765, 25781, 25797, 25813, 25829, 25845, 25861, 25877, 25893, 25909, 25925, 25941, 25957, 25973, 25989, 26005, 26021, 26037, 26053, 26069, 26085, 26101, 26117, 26133, 26149, 26165, 26181, 26197, 26213, 26229, 26245, 26261, 26277, 26293, 26309, 26325, 26341, 26357, 26373, 26389, 26405, 26421, 26437, 26453, 26469, 26485, 26501, 26517, 26533, 26549, 26565, 26581, 26597, 26613, 26629, 26645, 26661, 26677, 26693, 26709, 26725, 26741, 26757, 26773, 26789, 26805, 26821, 26837, 26853, 26869, 26885, 26901, 26917, 26933, 26949, 26965, 26981, 26997, 27013, 27029, 27045, 27061, 27077, 27093, 27109, 27125, 27141, 27157, 27173, 27189, 27205, 27221, 27237, 27253, 27269, 27285, 27301, 27317, 27333, 27349, 27365, 27381, 27397, 27413, 27429, 27445, 27461, 27477, 27493, 27509, 27525, 27541, 27557, 27573, 27589, 27605, 27621, 27637, 27653, 27669, 27685, 27701, 27717, 27733, 27749, 27765, 27781, 27797, 27813, 27829, 27845, 27861, 27877, 27893, 27909, 27925, 27941

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:429/437 or 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; 763/765/767; 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, 114, 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, 828, 844, 860, 876, 892, 908, 924, 940, 956, 972, 988, 1004, 1020, 1036, 1052, 1068, 1084, 1100, 1116, 1132, 1148, 1164, 1180, 1196, 1212, 1228, 1244, 1260, 1276, 1292, 1308, 1324, 1340, 1356, 1372, 1388, 1404, 1420, 1436, 1452, 1468, 1484, 1500, 1516, 1532, 1548, 1564, 1580, 1596, 1612, 1628, 1644, 1660, 1676, 1692, 1708, 1724, 1740, 1756, 1772, 1788, 1804, 1820, 1836, 1852, 1868, 1884, 1900, 1916, 1932, 1948, 1964, 1980, 1996, 2012, 2028, 2044, 2060, 2076, 2092, 2108, 2124, 2140, 2156, 2172, 2188, 2204, 2220, 2236, 2252, 2268, 2284, 2300, 2316, 2332, 2348, 2364, 2380, 2396, 2412, 2428, 2444, 2460, 2476, 2492, 2508, 2524, 2540, 2556, 2572, 2588, 2604, 2620, 2636, 2652, 2668, 2684, 2700, 2716, 2732, 2748, 2764, 2780, 2796, 2812, 2828, 2844, 2860, 2876, 2892, 2908, 2924, 2940, 2956, 2972, 2988, 3004, 3020, 3036, 3052, 3068, 3084, 3100, 3116, 3132, 3148, 3164, 3180, 3196, 3212, 3228, 3244, 3260, 3276, 3292, 3308, 3324, 3340, 3356, 3372, 3388, 3404, 3420, 3436, 3452, 3468, 3484, 3500, 3516, 3532, 3548, 3564, 3580, 3596, 3612, 3628, 3644, 3660, 3676, 3692, 3708, 3724, 3740, 3756, 3772, 3788, 3804, 3820, 3836, 3852, 3868, 3884, 3900, 3916, 3932, 3948, 3964, 3980, 3996, 4012, 4028, 4044, 4060, 4076, 4092, 4108, 4124, 4140, 4156, 4172, 4188, 4204, 4220, 4236, 4252, 4268, 4284, 4300, 4316, 4332, 4348, 4364, 4380, 4396, 4412, 4428, 4444, 4460, 4476, 4492, 4508, 4524, 4540, 4556, 4572, 4588, 4604, 4620, 4636, 4652, 4668, 4684, 4700, 4716, 4732, 4748, 4764, 4780, 4796, 4812, 4828, 4844, 4860, 4876, 4892, 4908, 4924, 4940, 4956, 4972, 4988, 5004, 5020, 5036, 5052, 5068, 5084, 5100, 5116, 5132, 5148, 5164, 5180, 5196, 5212, 5228, 5244, 5260, 5276, 5292, 5308, 5324, 5340, 5356, 5372, 5388, 5404, 5420, 5436, 5452, 5468, 5484, 5500, 5516, 5532, 5548, 5564, 5580, 5596, 5612, 5628, 5644, 5660, 5676, 5692, 5708, 5724, 5740, 5756, 5772, 5788, 5804, 5820, 5836, 5852, 5868, 5884, 5900, 5916, 5932, 5948, 5964, 5980, 5996, 6012, 6028, 6044, 6060, 6076, 6092, 6108, 6124, 6140, 6156, 6172, 6188, 6204, 6220, 6236, 6252, 6268, 6284, 6300, 6316, 6332, 6348, 6364, 6380, 6396, 6412, 6428, 6444, 6460, 6476, 6492, 6508, 6524, 6540, 6556, 6572, 6588, 6604, 6620, 6636, 6652, 6668, 6684, 6700, 6716, 6732, 6748, 6764, 6780, 6796, 6812, 6828, 6844, 6860, 6876, 6892, 6908, 6924, 6940, 6956, 6972, 6988, 7004, 7020, 7036, 7052, 7068, 7084, 7100, 7116, 7132, 7148, 7164, 7180, 7196, 7212, 7228, 7244, 7260, 7276, 7292, 7308, 7324, 7340, 7356, 7372, 7388, 7404, 7420, 7436, 7452, 7468, 7484, 7500, 7516, 7532, 7548, 7564, 7580, 7596, 7612, 7628, 7644, 7660, 7676, 7692, 7708, 7724, 7740, 7756, 7772, 7788, 7804, 7820, 7836, 7852, 7868, 7884, 7900, 7916, 7932, 7948, 7964, 7980, 7996, 8012, 8028, 8044, 8060, 8076, 8092, 8108, 8124, 8140, 8156, 8172, 8188, 8204, 8220, 8236, 8252, 8268, 8284, 8300, 8316, 8332, 8348, 8364, 8380, 8396, 8412, 8428, 8444, 8460, 8476, 8492, 8508, 8524, 8540, 8556, 8572, 8588, 8604, 8620, 8636, 8652, 8668, 8684, 8700, 8716, 8732, 8748, 8764, 8780, 8796, 8812, 8828, 8844, 8860, 8876, 8892, 8908, 8924, 8940, 8956, 8972, 8988, 9004, 9020, 9036, 9052, 9068, 9084, 9100, 9116, 9132, 9148, 9164, 9180, 9196, 9212, 9228, 9244, 9260, 9276, 9292, 9308, 9324, 9340, 9356, 9372, 9388, 9404, 9420, 9436, 9452, 9468, 9484, 9500, 9516, 9532, 9548, 9564, 9580, 9596, 9612, 9628, 9644, 9660, 9676, 9692, 9708, 9724, 9740, 9756, 9772, 9788, 9804, 9820, 9836, 9852, 9868, 9884, 9900, 9916, 9932, 9948, 9964, 9980, 10000, 10016, 10032, 10048, 10064, 10080, 10096, 10112, 10128, 10144, 10160, 10176, 10192, 10208, 10224, 10240, 10256, 10272, 10288, 10304, 10320, 10336, 10352, 10368, 10384, 10400, 10416, 10432, 10448, 10464, 10480, 10496, 10512, 10528, 10544, 10560, 10576, 10592, 10608, 10624, 10640, 10656, 10672, 10688, 10704, 10720, 10736, 10752, 10768, 10784, 10800, 10816, 10832, 10848, 10864, 10880, 10896, 10912, 10928, 10944, 10960, 10976, 10992, 11008, 11024, 11040, 11056, 11072, 11088, 11104, 11120, 11136, 11152, 11168, 11184, 11200, 11216, 11232, 11248, 11264, 11280, 11296, 11312, 11328, 11344, 11360, 11376, 11392, 11408, 11424, 11440, 11456, 11472, 11488, 11504, 11520, 11536, 11552, 11568, 11584, 11600, 11616, 11632, 11648, 11664, 11680, 11696, 11712, 11728, 11744, 11760, 11776, 11792, 11808, 11824, 11840, 11856, 11872, 11888, 11904, 11920, 11936, 11952, 11968, 11984, 12000, 12016, 12032, 12048, 12064, 12080, 12096, 12112, 12128, 12144, 12160, 12176, 12192, 12208, 12224, 12240, 12256, 12272, 12288, 12304, 12320, 12336, 12352, 12368, 12384, 12400, 12416, 12432, 12448, 12464, 12480, 12496, 12512, 12528, 12544, 12560, 12576, 12592, 12608, 12624, 12640, 12656, 12672, 12688, 12704, 12720, 12736, 12752, 12768, 12784, 12800, 12816, 12832, 12848, 12864, 12880, 12896, 12912, 12928, 12944, 12960, 12976, 12992, 13008, 13024, 13040, 13056, 13072, 13088, 13104, 13120, 13136, 13152, 13168, 13184, 13200, 13216, 13232, 13248, 13264, 13280, 13296, 13312, 13328, 13344, 13360, 13376, 13392, 13408, 13424, 13440, 13456, 13472, 13488, 13504, 13520, 13536, 13552, 13568, 13584, 13600, 13616, 13632, 13648, 13664, 13680, 13696, 13712, 13728, 13744, 13760, 13776, 13792, 13808, 13824, 13840, 13856, 13872, 13888, 13904, 13920, 13936, 13952, 13968, 13984, 14000, 14016, 14032, 14048, 14064, 14080, 14096, 14112, 14128, 14144, 14160, 14176, 14192, 14208, 14224, 14240, 14256, 14272, 14288, 14304, 14320, 14336, 14352, 14368, 14384, 14400, 14416, 14432, 14448, 14464, 14480, 14496, 14512, 14528, 14544, 14560, 14576, 14592, 14608, 14624, 14640, 14656, 14672, 14688, 14704, 14720, 14736, 14752, 14768, 14784, 14800, 14816, 14832, 14848, 14864, 14880, 14896, 14912, 14928, 14944, 14960, 14976, 14992, 15008, 15024, 15040, 15056, 15072, 15088, 15104, 15120, 15136, 15152, 15168, 15184, 15200, 15216, 15232, 15248, 15264, 15280, 15296, 15312, 15328, 15344, 15360, 15376, 15392, 15408, 15424, 15440, 15456, 15472, 15488, 15504, 15520, 15536, 15552, 15568, 15584, 15600, 15616, 15632, 15648, 15664, 15680, 15696, 15712, 15728, 15744, 15760, 15776, 15792, 15808, 15824, 15840, 15856, 15872, 15888, 15904, 15920, 15936, 15952, 15968, 15984, 16000, 16016, 16032, 16048, 16064, 16080, 16096, 16112, 16128, 16144, 16160, 16176, 16192, 16208, 16224, 16240, 16256, 16272, 16288, 16304, 16320, 16336, 16352, 16368, 16384, 16400, 16416, 16432, 16448, 16464, 16480, 16496, 16512, 16528, 16544, 16560, 16576, 16592, 16608, 16624, 16640, 16656, 16672, 16688, 16704, 16720, 16736, 16752, 16768, 16784, 16800, 16816, 16832, 16848, 16864, 16880, 16896, 16912, 16928, 16944, 16960, 16976, 16992, 17008, 17024, 17040, 17056, 17072, 17088, 17104, 17120, 17136, 17152, 17168, 17184, 17200, 17216, 17232, 17248, 17264, 17280, 17296, 17312, 17328, 17344, 17360, 17376, 17392, 17408, 17424, 17440, 17456, 17472, 17488, 17504, 17520, 17536, 17552, 17568, 17584, 17600, 17616, 17632, 17648, 17664, 17680, 17696, 17712, 17728, 17744, 17760, 17776, 17792, 17808, 17824, 17840, 17856, 17872, 17888, 17904, 17920, 17936, 17952, 17968, 17984, 18000, 18016, 18032, 18048, 18064, 18080, 18096, 18112, 18128, 18144, 18160, 18176, 18192, 18208, 18224, 18240, 18256, 18272, 18288, 18304, 18320, 18336, 18352, 18368, 18384, 18400, 18416, 18432, 18448, 18464, 18480, 18496, 18512, 18528, 18544, 18560, 18576, 18592, 18608, 18624, 18640, 18656, 18672, 18688, 18704, 18720, 18736, 18752, 18768, 18784, 18800, 18816, 18832, 18848, 18864, 18880, 18896, 18912, 18928, 18944, 18960, 18976, 18992, 19008, 19024, 19040, 19056, 19072, 19088, 19104, 19120, 19136, 19152, 19168, 19184, 19200, 19216, 19232, 19248, 19264, 19280, 19296, 19312, 19328, 19344, 19360, 19376, 19392, 19408, 19424, 19440, 19456, 19472, 19488, 19504, 19520, 19536, 19552, 19568, 19584, 19600, 19616, 19632, 19648, 19664, 19680, 19696, 19712, 19728, 19744, 19760, 19776, 19792, 19808, 19824, 19840, 19856, 19872, 19888, 19904, 19920, 19936, 19952, 19968, 19984, 20000, 20016, 20032, 20048, 20064, 20080, 20096, 20112, 20128, 20144, 20160, 20176, 20192, 20208, 20224, 20240, 20256, 20272, 20288, 20304, 20320, 20336, 20352, 20368, 20384, 20400, 20416, 20432, 20448, 20464, 20480, 20496, 20512, 20528, 20544, 20560, 20576, 20592, 20608, 20624, 20640, 20656, 20672, 20688, 20704, 20720, 20736, 20752, 20768, 20784, 20800, 20816, 20832, 20848, 20864, 20880, 20896, 20912, 20928, 20944, 20960, 20976, 20992, 21008, 21024, 21040, 21056, 21072, 21088, 21104, 21120, 21136, 21152, 21168, 21184, 21200, 21216, 21232, 21248, 21264, 21280, 21296, 21312, 21328, 21344, 21360, 21376, 21392, 21408, 21424, 21440, 21456, 21472, 21488, 21504, 21520, 21536, 21552, 21568, 21584, 21600, 21616, 21632, 21648, 21664, 21680, 21696, 21712, 21728, 21744, 21760, 21776, 21792, 21808, 21824, 21840, 21856, 21872, 21888, 21904, 21920, 21936, 21952, 21968, 21984, 22000, 22016, 22032, 22048, 22064, 22080, 22096, 22112, 22128, 22144, 22160, 22176, 22192, 22208, 22224, 22240, 22256, 22272, 22288, 22304, 22320, 22336, 22352, 22368, 22384, 22400, 22416, 22432, 22448, 22464, 22480, 22496, 22512, 22528, 22544, 22560, 22576, 22592, 22608, 22624, 22640, 22656, 22672, 22688, 22704, 22720, 22736, 22752, 22768, 22784, 22800, 22816, 22832, 22848, 22864, 22880, 22896, 22912, 22928, 22944, 22960, 22976, 22992, 23008, 23024, 23040, 23056, 23072, 23088, 23104, 23120, 23136, 23152, 23168, 23184, 23200, 23216, 23232, 23248, 23264, 23280, 23296, 23312, 23328, 23344, 23360, 23376, 23392, 23408, 23424, 23440, 23456, 23472, 23488, 23504, 23520, 23536, 23552, 23568, 23584, 23600, 23616, 23632, 23648, 23664, 23680, 23696, 23712, 23728, 23744, 23760, 23776, 23792, 23808, 23824, 23840, 23856, 23872, 23888, 23904, 23920, 23936, 23952, 23968, 23984, 24000, 24016, 24032, 24048, 24064, 24080, 24096, 24112, 24128, 24144, 24160, 24176, 24192, 24208, 24224, 24240, 24256, 24272, 24288, 24304, 24320, 24336, 24352, 24368, 24384, 24400, 24416, 24432, 24448, 24464, 24480, 24496, 24512, 24528, 24544, 24560, 24576, 24592, 24608, 24624, 24640, 24656, 24672, 24688, 24704, 24720, 24736, 24752, 24768, 24784, 24800, 24816, 24832, 24848, 24864, 24880, 24896, 24912, 24928, 24944, 24960, 24976, 24992, 25008, 25024, 25040, 25056, 25072, 25088, 25104, 25120, 25136, 25152, 25168, 25184, 25200, 25216, 25232, 25248, 25264, 25280, 25296, 25312, 25328, 25344, 25360, 25376, 25392, 25408, 25424, 25440, 25456, 25472, 25488, 25504, 25520, 25536, 25552, 25568, 25584, 25600, 25616, 25632, 25648, 25664, 25680, 25696, 25712, 25728, 25744, 25760, 25776, 25792, 25808, 25824, 25840, 25856, 25872, 25888, 25904, 25920, 25936, 25952, 25968, 25984, 26000, 26016, 26032, 26048, 26064, 26080, 26096, 26112, 26128, 26144, 26160, 26176, 26192, 26208, 26224, 26240, 26256, 26272, 26288, 26304, 26320, 26336, 26352, 26368, 26384, 26400, 26416, 26432, 26448, 26464, 26480, 26496, 26512, 26528, 26544, 26560, 26576, 26592, 26608, 26624, 26640, 26656, 26672, 26688, 26704, 26720, 26736, 26752, 26768, 26784, 26800, 26816, 26832, 26848, 26864, 26880, 26896, 26912, 26928, 26944, 26960, 26976, 26992, 27008, 27024, 27040, 27056, 27072, 27088, 27104, 27120, 27136, 27152, 27168, 27184, 27200, 27216, 27232, 27248, 27264, 27280, 27296, 27312, 27328, 27344, 27360, 27376, 27392, 27408, 27424, 27440, 27456, 27472, 27488, 27504, 27520, 27536, 27552, 27568, 27584, 27600, 27616, 27632, 27648, 27664, 27680, 27696, 27712, 27728, 27744, 27760, 27776, 27792, 27808, 27824, 27840, 27856, 27872, 27888, 27904, 27920, 27936, 27952, 27968, 27984, 28000, 28016, 28032, 28048, 28064, 28080, 28096, 28112, 28128, 28144, 28160, 28176, 28192, 28208, 28224, 28240, 28256, 28272, 28288, 28304, 28320, 28336, 28352, 28368, 28384, 28400, 28416, 28432, 28448, 28464, 28480, 28496, 28512, 28528, 28544, 28560, 2857

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 by 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 hDII4, 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^a is Pro or Arg; and X^b is Thr.

[0032] In a fourth aspect, the invention features a fully human antibody or antibody fragment which binds hDII4 with an IC₅₀ of less than about 10 nM, as measured in *in vitro* assay or ELISA-based DII4 blocking assay (described below). In a preferred embodiment, the antibody of the invention exhibits an IC₅₀ of about 500 pM or less. In an even more preferred embodiment, the antibody of the invention exhibits an IC₅₀ of about 100 pM or less.

[0033] In one embodiment, the invention provides a fully human monoclonal antibody which specifically binds and inhibits human DII4 and exhibits an IC₅₀ of less than or equal to about 150 pM, 100 pM, 75 pM, or 50 pM, as measured by Notch-inducible luciferase bioassay with hDII4-Fc. As shown in the experimental section below, the anti-hDII4 antibodies of the invention do not cross-react with closely related delta proteins, such as hDII1 and hDII3.

[0034] In one embodiment, the invention provides an isolated human antibody, or an antigen-binding portion thereof, that binds hDII4 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 hDII4 (Table 2).

[0035] The invention encompasses anti-hDII4 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-hDII4 antibodies which bind specific epitopes of hDII4 and are capable of blocking the biological activity of hDII4. The extracellular domain of DII4 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 hDII4 (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.

[0038] 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 interconnected 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 $1 \times 10^{-3} \text{ s}^{-1}$ or less, preferably $1 \times 10^{-4} \text{ s}^{-1}$ 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. (1986) *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. 20:6267-6295) 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 hDII4 is substantially free of antibodies that specifically bind antigens other than hDII4). An isolated antibody that specifically binds hDII4 may, however, have cross-reactivity to other antigens, such as hDII4 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* (Bränden & Tooze, eds., 1991, Garland Publishing, NY); and Thomson 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 16 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 mutant 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 cytotoxicity (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 60 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 hDII4 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 DII4.

[0081] Mice may be immunized by any method known in the art (see, for example, Harlow and Lane *supra*). In one embodiment, hDII4 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 DII4 (nM)	K_D DII4-Fc (nM)	IC_{50} DII4-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	0.853	0.28
VAW 8A10-14	1.41	0.648	0.08
VAW 8G1-12	8.09	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	58.10	0.555	0.10

TABLE 2

Antibody	K_D DII4 (nM)	K_D DII4-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	0.185	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	6.88	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 IC₅₀ 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-B	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-hDII4 antibodies to block DII4 binding to Notch was also evaluated with the ELISA-based immunoassay described above, modified by replacing 25 pM of biotin-DII4-hFc with 30 pM of biotin-DII4-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 DII4 mediated cellular function was also tested *in vitro* using DII4 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 2×10^5 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, Applied 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
hDJ4-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 MCD8-131 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 4×10^3 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
VAWBA10-14	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-A6	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 2×10^4 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 hDII4-hFc	1.5 nM hDII4-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-hDII4 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 hDII4-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 x10⁵ cells/well in 2.0 ml total media volume. Immediately following cell seeding, anti-hDII4 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-hDII4 antibodies were able to entirely block the Notch1 cleavage induced by plate coated hDII4-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 hDII4 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 hDII4; (6) engineered HT1080 cells expressing eGFP; (7) engineered HT1080 cells expressing hDII4; and (8) HT29. Human DII4 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% CO₂ 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 hDII4 (col. 5), which exhibited the highest hDII4 expression among all cell lines (as determined by immunoprecipitation/Western blot and flow cytometry). The maximum cell cytotoxicity in the C6-hDII4 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% CO₂ 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 DII4 proteins were generated in which specific human DII4 domains were substituted into a mouse DII4 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-Q289); #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 hDII4, mDII4, 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 DII4 proteins, hDII4-mFc, and mDII4-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 hDII4; VAW3A7-2 bound an epitope between Q283-E400 hDII4; and 15E10 bound an epitope between E252-D282 of hDII4.

TABLE 9

Antibody	hDII4-mFc	mDII4-mFc	Chimeric Proteins			
			#1	#2	#3	#4
22G12	+	-	+	+	+	+
VAW3A7-2	+	-	-	-	-	+
15E10	+	-	-	-	+	+

[0096] Binding specificity of purified test mAb to hDII4, mDII4 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 DII4 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 mDII4-mFc was used as a positive control (positive control= 6C10). The results (Table 10) show that REGN279 bound an epitope between S27-Q218 of hDII4; REGN287 bound between Q283-E400 of hDII4; REGN289, REGN290 and REGN306 bound between S27-E400 of hDII4.

TABLE 10

Antibody	hDII4-mFc	mDII4-mFc	Chimeric human-mouse DII4 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 DII4 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	hDII4-mFc	mDII4-mFc	Chimeric human-mouse DII4 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 DII4 was determined by Western blot. Briefly, hDII4-mFc (200 ng per lane), mDII4-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 hDII4-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 hDII4 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 hDII4 and REGN281, in a molar ratio of 1:5, or hDII4 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 hDII4 that were protected from protease digestion by the binding of REGN281 to hDII4. 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	hDII4 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	760.8	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 DII4.

[0102] The binding affinities of selected purified antibodies to hDII4, *M. fascicularis* DII4 (mDII4, SEQ IN NO:956), and *M. mulatta* DII4 (mmDII4, 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, hDII4 (from 12.5 nM to 100 nM), mDII4 (from 3.13 nM to 100 nM), or mmDII4 (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 ⁻¹ s ⁻¹)			kd (s ⁻¹)			K _D (nM)		
	hDII4	mDII4	mmDII4	hDII4	mDII4	mmDII4	hDII4	mDII4	mmDII4
REGN281	1.56 x 10 ⁵	6.64 x 10 ⁴	9.27 x 10 ⁴	2.30 x 10 ⁻⁵	2.04 x 10 ⁻⁵	3.05 x 10 ⁻⁵	0.146	0.307	0.329
REGN421	1.63 x 10 ⁵	7.28 x 10 ⁴	9.70 x 10 ⁴	2.17 x 10 ⁻⁵	2.02 x 10 ⁻⁵	3.23 x 10 ⁻⁵	0.133	0.278	0.333
REGN422	1.64 x 10 ⁵	8.01 x 10 ⁴	9.27 x 10 ⁴	2.36 x 10 ⁻⁵	2.88 x 10 ⁻⁵	3.41 x 10 ⁻⁵	0.144	0.380	0.375

[0103] The binding affinities of anti-hDII4 antibodies toward hDII4 and mmDII4 dimers were also determined using a BIACORE™ 2000 and the method describe above, except that hDII4 was replaced with hDII4-mFc (from 3.13 nM to 100 nM), or mmDII4 with mmDII4-mFc (from 0.78 nM to 25 nM) as analyte (Table 14).

TABLE 14

	ka (M ⁻¹ s ⁻¹)		kd (s ⁻¹)		K _D (nM)	
	hDII4-mFc	mmDII4-mFc	hDII4-mFc	mmDII4-mFc	hDII4-mFc	mmDII4-mFc
REGN281	3.02 x 10 ⁵	3.16 x 10 ⁵	4.96 x 10 ⁻⁵	4.64 x 10 ⁻⁵	0.0163	0.0147
REGN421	3.43 x 10 ⁵	3.35 x 10 ⁵	4.70 x 10 ⁻⁵	3.80 x 10 ⁻⁵	0.0137	0.013
REGN422	3.46 x 10 ⁵	4.23 x 10 ⁵	4.60 x 10 ⁻⁵	4.15 x 10 ⁻⁵	0.0133	0.0098

Example 8. Cross-Reactivity of Antibodies With hDII1, hDII3, mDII4, or mfDII4.

[0104] Cross-reactivity of the antibodies to human delta-like ligand 1 (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 hDII4-hFc or hDII1-hFc protein at 100 µg/ml were used as analyte injected over the antibody surfaces. All three anti-hDII4 antibodies only bound to hDII4-hFc, and did not bind hDII1-hFc.

[0105] An alternative BIACORE™ format was used to assess cross-reactivity between anti-hDII4 antibody and either hDII1-hFc or hDII3-hFc. Briefly, ligands hDII4-hFc, hDII1-hFc, and hDII3-hFc were each covalently linked to a CM-5 chip, through amine coupling, to an RU range of about 8,000 to 10,000. REGN421, at 300 µg/ml, was injected over the surface of each chip. REGN421 bound only to hDII4-hFc; no binding was observed to either hDII1-hFc or hDII3-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-hDII4 antibodies and hDII4-hFc, hDII3-hFc, hDII1-hFc, mfDII4-mmh, or mDII4-mFc. Briefly, streptavidin 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 hDII4-hFc or hDII3-hFc, hDII1-hFc, or mDII4-mFc, at 200 nM, or mfDII4-mmh at 100 nM, for 10 min at 30°C. Changes in the thickness of the biological layer after each incubation were measured. Human DII4-hFc and mfDII4-mmh bound to anti-hDII4 antibody-bound biosensors, whereas hDII3-hFc, hDII1-hFc, and mDII4-mFc did not bind to anti-hDII4 antibody-bound biosensors.

Example 9. Effect of Anti-hDII4 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 DII4 protein (SCIDxhDII4). Briefly, the humanized DII4 mouse was made by replacing the entire extracellular domain of the mouse DII4 gene with the corresponding extracellular region of the human DII4 gene (7kb) in embryonic stem (ES) cells. Homozygous hDII4 mice were generated and bred into SCID background. Each mouse was then implanted subcutaneously (SC) with 2.5×10^6 human HT1080 tumor cells. After the tumors were established in the mice (~ 100-150 mm³ 18 days after implantation), mice were measured and treated with hFc, hDII4-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 hDII4-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 $l \times w^2/2$. 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 mDII4 (n=2) was implanted with tumor cells and treated with hDII4-Fc (25 mg/kg) following the same dosing schedule.

TABLE 15

Mouse	Treatment	Tumor Size (mm ³)				
		Day 16	Day 18	Day 20	Day 22	Day 25
SCID	hDII4-hFc	162.0	232.8	320.0	336.0	253.1
SCID	hDII4-hFc	22.5	117.0	117.0	408.0	66.8
SCIDxhDII4	hDII4-hFc	288.0	320.0	352.0	446.0	320.0
SCIDxhDII4	hFc	162.0	288.0	320.0	500.0	550.0
SCIDxhDII4	hFc	162.0	220.5	352.0	662.0	661.5
SCIDxhDII4	hFc	93.8	135.0	179.6	352.0	726.0
SCIDxhDII4	REGN421	144.0	245.0	320.0	162.0	144.0
SCIDxhDII4	REGN421	87.5	162.0	153.0	225.0	135.0
SCIDxhDII4	REGN421	144.0	196.0	272.0	162.0	152.5

TABLE 16

Mouse	Treatment	Tumor Size (mm ³)
SCID	hDII4-hFc	308.0
SCID	hDII4-hFc	105.0
SCIDxhDII4	hDII4-hFc	480.0
SCIDxhDII4	hFc	924.0
SCIDxhDII4	hFc	1020.0
SCIDxhDII4	hFc	792.0
SCIDxhDII4	REGN421	168.0
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 Trp Val Ala Val Ser Leu Gly Val Gly Leu Ala Val Leu Leu Val Leu
 530 535 540
 Leu Gly Met Val Ala Val Ala Val Arg Gln Leu Arg Leu Arg Arg Pro
 545 550 555 560
 Asp Asp Gly Ser Arg Glu Ala Met Asn Asn Leu Ser Asp Phe Gln Lys
 565 570 575
 Asp Asn Leu Ile Pro Ala Ala Gln Leu Lys Asn Thr Asn Gln Lys Lys
 580 585 590
 Glu Leu Glu Val Asp Cys Gly Leu Asp Lys Ser Asn Cys Gly Lys Gln
 595 600 605
 Gln Asn His Thr Leu Asp Tyr Asn Leu Ala Pro Gly Pro Leu Gly Arg
 610 615 620
 Gly Thr Met Pro Gly Lys Phe Pro His Ser Asp Lys Ser Leu Gly Glu
 625 630 635 640
 Lys Ala Pro Leu Arg Leu His Ser Glu Lys Pro Glu Cys Arg Ile Ser
 645 650 655
 Ala Ile Cys Ser Pro Arg Asp Ser Met Tyr Gln Ser Val Cys Leu Ile
 660 665 670
 Ser Glu Glu Arg Asn Glu Cys Val Ile Ala Thr Glu Val
 675 680 685

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

<220>
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<400> 3
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 tctgtgcag cctctggatt cacctttagc acctatgga tgaactgggt cgcaccggct 120
 ccaggggaagg ggcctggagtg ggtggccaac ataaaccaag atggaaglga gaaalactat 180
 glggactcag tgaaggcccg aatcaccalc tccagagaca acgccaagaa ctcaclgtat 240
 ctgcaaatga acagccagag aglogaggac accgctgtat ailaclglc gagaaaatgg 300
 aacaactgga acccggagga gaactggggc cagggaaacc tggtcacogt ctctcag 358

<210> 4
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 4

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

<210> 5

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 5

ggattcacct ttaglaccta ttgg 24

<210> 6

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 6

Gly Phe Thr Phe Ser Thr Tyr Trp
1 5

<210> 7

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 7

ataaaccaag atggaagtga gaaa 24

<210> 8

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 8

Ile Asn Gln Asp Gly Ser Glu Lys
1 5

<210> 9

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 9

gcgagaaaal ggaacaactg gaaccoggag gagaac 36

<210> 10

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 10

Ala Arg Lys Trp Asn Asn Trp Asn Pro Glu Glu Asn
1 5 10

<210> 11

<211> 337

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 11

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atctcctgca ggtctagica gaccctctg cataalaglg galacaactt ttggatgg 120
lacctgcaga agccagggca gctccacaa ctctgalct atttggttc taalcgggcc 180
tccggggtcc ctgacaggit caglggcagl ggalcaggca cagatttac actgaagatc 240
agaagagtgg aggctgagga lgtlgggait tattacigca tgcaagctct acacactcc 300
tacactttg gccaggggac caaggtggag alcaaac 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
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<210> 14
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
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<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
 llgcgttcl 9

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

<220>
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<400> 16
 Leu Arg Ser
 1

<210> 17

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

<220>
<223> Synthetic

<400> 17
algcaagc tccacac tcaact 27

<210> 18
<211> 9
<212> PRT
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<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
gaggcagc tggggagc tggggaggc tggccagc ctggggggtc cclgagactc 60
lclgtgtag cclgtggtt caccitlagl agctatgga tgacctgggt ccgccaggct 120
ccaggggaagg ggctggagt ggiggccaac ataaaacaag alggaagga gaaalactat 180
gggactctg lgaagggccg attcaaccgc tccagagaca acgccaagaa ctcaglgat 240
ctgcaaalga gcagctlgag agccgaggac acggctgtg altactgic gagagaltg 300
aactalggc ccgattacta clactaccac ggttggacg tctggggcca agggaccacg 360
gtcaacglt 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 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 itgg 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
 alaaaacaag alggaaglga 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 taclactacc acggtttgga cglc 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 lgaccocaglc lccglccctcc cgtctcglat cgtaggaga cagagtcacc 60
alcacttgcc gggcaagtca gggcattaga aalgattag gctgglltca gcagaaacca 120
gggaaagccc ctaagcgcc galctalgcl gcalccagtl tgcaaagtgg ggloccatca 180
aggltcagcg gcagtggaic lggacagaa ttactctca caalcagcag cctgctcct 240
gaagatttg caactlalta cgtctacag cataatactt acccgtacac tttggccag 300
gggaccaagc tggagalcaa 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 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 gaaalgal 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
gctgcalcc 9

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

<220>
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<400> 32
Ala Ala Ser
1

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

<220>
<223> Synthetic

<400> 33
ctacagcata alacclacc 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 tgggggagtc tgggggaggc ggggiccagc ctgggaggtc cctgagactc 60
tcctggaag calctggall cagttcaga agltaaggca tgcactgggl ccgccaggct 120
ccaggcaggg gacgggaglg gatggcaglt attggtaag atggcagtaa gacataclat 180
acagagtcog tgacgggccc altcaccalc lccagagaca altccaagaa caccclatal 240
ctgcaaataa acagccagag agcccaggac acggcgtttt attactgic gagcggttt 300
tcagtgctg ccacgatcct tgacaactgg gcccaggaa cctgggiclc cglctctca 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 lggc 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
 atttggtaag alggcagtaa gaca 24

<210> 40
 <211> 8
 <212> PRT
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<220>
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<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
 gcgagcgggt ttccaglgcc lgccacgac cllgacaac 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
gacalccaga tgaaccagtc lccalccctcc ctgtctgcal ctglaggaga cagagtcacc 60
alcacttgcc gggcaaglca gggcattaga aalgattlag gctggtlca gcagaaacca 120
gggaaagccc claaccgct galctatgga gcalccagit tgaagggtg ggtcccalca 180
aggttcagcg gcagtggatc tggacagat ttactctca caatcagcag cctgcagcca 240
gaagatttg caactatla ctglclacag cataattct acccgtggac gtccggccaa 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
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<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
ggagcalcc 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
clacagcala attcttacc gggacg 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

cagglgcagc lgggggaglc lgggggaggc gtagtccagc ctgggagglc cctgagactc 60
 tctgtgcag cgtcggatt caccitcagl agclalggca tgcactgggl ccgccaggct 120
 ccaggcaagg ggctggagtg ggllggcagtt alalgglalq alggaaataa taaatactal 180
 atagactccg tgaagggccg atlcaccatc tccagagaca attccaagaa cagcctgtat 240
 ctgcaaalga acagcctgag agccgaggac accgctgtgt attactgtgc gagagaccgt 300
 ggalalagtg gclaccaggg atacttcgat cctcggggcc gllggaccct ggtcactgic 360
 tctcag 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

ggaitcacct tcagtagcta lggc 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
atatgglatg atggaaalaa laaa 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 gggatalag tggctacgag ggatactcg 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 lgaccacgac cccagactcc ctggctgigt cctcggggcga gagggccacc 60
ctcaactgla aglccagcca gagtgttita tacagctcca acaataagaa clactlagct 120

tggtaccagc agaaaccagg acagccctct aagctgctca ttaactgggc aactaccgg 180
gaalccgggg lccctgaccg atcagtgcc agcgggtctg ggacagatt cactctacc 240
alcagcagcc tgcaggctga agatgtggca gttatctct gtcagcaata ttalactact 300
tggacgttcg gccaggggac caaggltgaa alcaaac 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
cagaglttt talacagctc caacaataag aactac 36

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

<220>
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<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

tgggcalct

9

<210> 64

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 64

Trp Ala Ser

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<210> 65

<211> 24

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<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

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 tctctgcag cctctgcalc caccctcagc aggcctggca tgcactgggt cggccaggct 120
 ccaggcaagg gactggaglg ggtggcagtt atatcatalg atggaaataa laaatactat 180
 gtgactcag tgaagggcag atcaccalc tccagagaca attccaagaa cacgctglat 240
 ctgcaaalga atagcctgag aactgacgac acggctgltg attattgttc gaaagagta 300
 gtagglatc ctggaaacct ggtctactac tactactacg gaatggacgt ctggggccaa 360
 gggaccacgg tcaccgctc ctacg 385

<210> 68

<211> 128

<212> PRT

<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
tcgaaagagl taglagglal tactggaaac ctggtctact actactacta cggaaaggac 60
glc 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
gaaatgigl tgaocagtc tccaggcacc ctgclttgl ctccagggga aagagccacc 60
ciclcclgca gggccaglca gactatfac agcagctact taggctggla ccagcagaaa 120
cctggccagg ctcccagacl cctcalclal ggtgcalcca acagggccac tggcalccca 180
gacaglttca gtggcaglgg gtcgggaca gactcactc tcaccatcag cagactggag 240
cclgaagatt tgcaglgla ttactgtcaa caltalaaca actcacctta cactllggc 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>
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<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
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<220>
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<400> 80
Gly Ala Ser
1

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

<220>
<223> Synthetic

<400> 81
caacattata acaacacacc 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
caggtagcagc tgcaggagtc gggcccagga ctggggaagc cttcacagac cctgtccctc 60
accctgcactg tctctgggg ctcacaagc agtgggggtt actactggag ctggatccgc 120
cactaccag ggaagggcct ggaglggatt ggctacgtcc attacagtgg gaacacccac 180
lacaalacgt ccctcaagag ggcactacc atalcaalag acacgictaa gagccaallc 240
lccctggatc tgagetctgt gactgcccgg gacacggccg lgtallactg tgcgagagcc 300
ccccgggat accattactt tgcctactgg ggcacgggaa cccctggcac cgtctccca 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

<210> 85
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 85
 ggaggcicca taagcagtgg tggtaclac 30

<210> 86
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

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

<210> 87
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 87
 gtccattaca ggggaacac c 21

<210> 88
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

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

<210> 89

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

<220>
<223> Synthetic

<400> 89
gcgagagccc cccgaggala ccactacttt gcctac 36

<210> 90
<211> 12
<212> PRT
<213> Artificial Sequence

<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
<212> DNA
<213> Artificial Sequence

<220>
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<400> 91
gaaatgggt tgaegcagic tccaggcacc ctgtcttgt cccagggga aagagccacc 60
ctctctgca gggccagta gaggatagc agcagglact tagcctggta ccagcagaaa 120
ccggccagg ctccaggct cctcacttt ggtagatcca gcagggccac tggcalacca 180
gacaggitca gggcagigg gtcgggaca gactcactc lcaccatcag cagactggag 240
cctgaagatt ttgagtga ttactgtag cagtaggta gctaccgct cacttcggc 300
ggagggacca agglggagal caaac 325

<210> 92
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 92
Glu Ile Gly 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 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
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 93
cagagtatta gcagcaggta c 21

<210> 94
<211> 7
<212> PRT
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<220>
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<400> 94
Gln Ser Ile Ser Ser Arg Tyr
1 5

<210> 95
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
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<400> 95
ggtgcatcc 9

<210> 96
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 96
Gly Ala Ser
1

<210> 97
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 97
cagcaglatg gtagctcacc gctcact 27

58

<210> 98
<211> 9
<212> PRT
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<220>
<223> Synthetic

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

<210> 99
<211> 361
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 99
caggcgcagc tgcaggagtc gggcccagga cggggaagc cttcacagac cctgtccctc 60
acctgcactg lctcgggtgg ctccalcagc agtagigggt actactggag ttggatccgc 120
cagcaccacag ggaagggcct ggaggggatt gggtaagtc attacagtg gaacaccac 180
tacagcccgf cclcaagag logactacc alatacagtg acaagctaa gaaccagtc 240
tccctgaagc lgagctctgt gactgcgcg gacaagccg lgtallactg tgcgagagcc 300
ccccgggat accaltact tgcctactgg ggcagggaa cctggtaac cgtcctca 360
g 361

<210> 100
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 100
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 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
<211> 30
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 101

ggggccca tcagcagtag lggtaclac 30

<210> 102

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 102

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

<210> 103

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 103

glccattaca gtgggaacac c 21

<210> 104

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 104

Val His Tyr Ser Gly Asn Thr
1 5

<210> 105

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 105

gcgagagcgc ccgclggata ccattacttt gcclac 36

<210> 106

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 106

Ala Arg Ala Pro Arg Gly Tyr His Tyr Phe Ala Tyr
1 5 10

<210> 107

<211> 325

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 107

aaaaatgtgtgtagcgcagcctccaggcaccctgtctttgtciccagggga gagagocacc 60
ctctcctgca gggccagta gagltagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ciccaggct cctcacttt ggtagatca gcagggccac tggcaccca 180
gacaggtca gggcagtg gctgggcca gactcactc taccattag gagactggag 240
cctgaagatt tgggtgta ttactgtcag cagtatgta gttaccgct cacttcggc 300
ggagggacca aggtggagat caaac 325

<210> 108

<211> 108

<212> PRT

<213> Artificial Sequence

<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

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 109

cagagtatta gcagcagcta c 21

<210> 110

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

<220>
<223> Synthetic

<400> 110
Gln Ser Ile Ser Ser Ser Tyr
1 5

<210> 111
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 111
ggtgcalcc 9

<210> 112
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 112
Gly Ala Ser
1

<210> 113
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 113
cagcaglatg gtagtcacc gctcacl 27

<210> 114
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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<400> 114
Gln Gln Tyr Gly Ser Ser Pro Leu Thr
1 5

<210> 115

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

<220>
<223> Synthetic

<400> 115
cagggtcagl tgggacagtc tggagctgag ggaagaagc ctggggccctc agtgaaggtc 60
tctgcaagg ctctgggta cacctttcc acctatggla tcagctgggt ggcacaggcc 120
ccggacaag ggcttgagtg gatgggalgg atcagcgctt acgacaataa cggggactat 180
gcacagaact tccaggccag agtcaccalg accacagaca catccaagac cacagcctac 240
atggagctga ggagccctgag atctgacgac acggcccggt attactgtgc gaggtalgc 300
tgaactttc actgggtcga ccctggggc caggaaccc tggtcaccgl ctctcag 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 ttccaccta tggg 24

<210> 118
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 118
Gly Tyr Thr Phe Ser Thr Tyr Gly
1 5

<210> 119
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 119
alcagcgctt acgacaataa cgcg 24

<210> 120
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 120
Ile Ser Ala Tyr Asp Asn Asn Ala
1 5

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

<220>
<223> Synthetic

<400> 121
gcgaggtala gctggaactt tcaactggllc gacccc 36

<210> 122
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 122
Ala Arg Tyr Ser Trp Asn Phe His Trp Phe Asp Pro
1 5 10

<210> 123
<211> 325
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 123

gaaatgigt tgaagcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctctgca gggccagta gaggttagc agtacclact tagcctggta ccagcagcaa 120
octggccagg cccccaggt cclcalclal gglgcalcca gcaggggcac lggcatccca 180
gacaggttca gtggcagtg gtcctggaca gacttcactc lcaccalcag cagactggag 240
octgaagatt ttgcagtgta ttactgtcag cagtatggta actcaccgtg gacgttcggc 300
caagggacca agglggaal 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

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 125

cagagtgtta gcagtaccta c 21

<210> 126

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 126

Gln Ser Val Ser Ser Thr Tyr
1 5

<210> 127

<211> 9

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 127
ggtgcatcc 9

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

<220>
<223> Synthetic

<400> 128
Gly Ala Ser
1

<210> 129
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 129
cagcaglatg gtaactcaacc ggggacg 27

<210> 130
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 130
Gln Gln Tyr Gly Asn Ser Pro Trp Thr
1 5

<210> 131
<211> 358
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 131
cagggtcacc lgglgcaglc lggagctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgcaggg ctctcggila cacccttacc aactalgga tcacctgggl ggcacaggcc 120
cctggacaag ggcttgagtg gatgggatgg alcagcgctt acaglgglaa cacagactat 180
gcacagaagl ccaggccag aalcaccatg accacagaca calccaagac cacagccac 240
atggaaciga ggagcctgac alclgacgac acggccglgt attaclgtgc gaggtatagc 300
lggaacttc actgggtcga cccclggggc cagggaaacc lggtaaccgl ctccacag 358

<210> 132

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

<220>
<223> Synthetic

<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
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 133
ggttacacct ttaccaacta tggg 24

<210> 134
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 134
Gly Tyr Thr Phe Thr Asn Tyr Gly
1 5

<210> 135
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 135
alcagcgctt acaglggtaa caca 24

<210> 136
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

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

<210> 137
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 137
gcgagglala gctggaactt lcactggctc gacccc 36

<210> 138
<211> 12
<212> PRT
<213> Artificial Sequence

<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
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 139
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ctctctcgca gggccagica gaglgttagt agcagclact lagcctggla ccagcagaaa 120
cctggccagg ctcccaggcl cctcactcl ggtgcacca gcagggccac tggcaccaca 180
gacaggttca gggcagtggt gtcgggaca gactcactc lcaccalcag cagtctggag 240
cctgaagatt ttgcagtga ttactgcag cagtgtggg gctcaccgtg gacgttcggc 300
caagggacca ggggtgagal caaac 325

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

<220>
<223> Synthetic

<400> 140

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
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

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 141

cagagtgtta glagcagcta c 21

<210> 142

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 142

Gln Ser Val Ser Ser Ser Tyr
1 5

<210> 143

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 143

ggtgcalcc 9

<210> 144

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 144

Gly Ala Ser

1

<210> 145

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 145

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27

<210> 146

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 146

Gln Gln Cys Gly Gly Ser Pro Trp Thr

1

5

<210> 147

<211> 358

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 147

cagggtcaac tgggcagtc tgggctgag ggaagaagc ctggggcctc agtgaaggc 60
gcctgcaagg cttctggtt caccttacc caclatggtt tcacctgggt ggcacaggcc 120
cctggacaag ggcctgagtg gatgggatgg atcagcgctt acagtggica tacagactat 180
gcacggaagl tccaggccag aglcaccatg accacagaca ccttcaccgac cacagcctac 240
atggaactga ggagcctgag atcagcagac acggccggtt atactgtgc gagllatagc 300
tggaaacttc actgggttga cccctggggc cagggaaacc tggtcaccgt cctctcag 358

<210> 148

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<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

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 153

gcgagtlala gctggaactt tcactgggtc gacccc 36

<210> 154

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 154

Ala Ser Tyr Ser Trp Asn Phe His Trp Phe Asp Pro
1 5 10

<210> 155

<211> 325

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 155

caaattgtgt tgaccgagtc lccaggcacc ctgtctttgt ctcaggggga aagagccacc 60
ctcctctgca gggccagtca gagtgttagt accacctact tagcctggta ccagcagaaa 120
cttgccagg ctcocagctc cctcatctat gglacaloca ccagggccac tggcatocca 180
gacaggttca gggcagibg gctgggact gactcadc tcaccatcag cagactggag 240
cclgaagatt ttgcagigla ttactgicag cagtgtgtg gclcaccgig gacgttcggc 300
caaggacca agtgaaaal caaac 325

<210> 156

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<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

<210> 157
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 157
cagagtgta glaccaccta c 21

<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
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<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
cagcaglgg gtggctcacc gtggacg 27

<210> 162

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

<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
cagggcagc tggcgcagc tggggctgag gtaagaagc ctggggccgc tgtgaaggc 60
tcctgcaagg ctctggata caogtcacc aglalatgata tcaactgggl ggcacaggcc 120
actggacaag ggctgagtg galgggatgg alaaacccta acagtggtaa cacaggctat 180
gcacagaagt llcagggcag agtcacctg accaggaaca cctccataag cacagcctac 240
atggaactga gcagccgag atctgaggac acggccgtt attactgigc gagagagggg 300
tatttggtg gtagtgcta tgcctttag atctggggcc aagggaaca ggcaccgc 360
cttcag 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

ggalacaagt lcaccagtta lgat 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

ataaacocla acagtgglaa 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

gogagagagg gatattggg lgggatgic taigcilltg 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
gaaattggtg tgacacaalc tccagggcacc cggctcttgg cccaggggga aagagccacc 60
ctctccggca gggccaglca gaglgttagc agcagctacl tagcctggla ccagcagaaa 120
ccggccagg ccccaggct cctcatctt gglgcatcca gcagggccac tggcatcca 180
gacaggtlca gggcaglgg gtcctgggaca gacttcaclc tcaccatcag cagactggag 240
cctgaagatt ttgcagtga ttactgacag cagtatggla gctcacogcl cacttgggc 300
ggagggacca aggggagat 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
cagagtgta gcagcagcla 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

gglgcatcc 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 gclcacl 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 tgcaggaglc gggcccagga ctgggaagc ctctggagac ccgctccctc 60
accgcaactg tctctggtgg ctccatcagc agtagtagtt actacgggg ctggalccgc 120
cagccccag ggaaggggct ggaglggati gggaglaict attalagtg gagcaactac 180
lacaaccgt cctcaagag tcgaglcacc ataccglag acacgtcca gaaccagtc 240
lccctgaagc lgagctctgt gaccgcccga gacacggcig tgtattactg tgcggcaaac 300
lgggacgacg ccttctctt lgactactgg ggcaggga cctctgtcac 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

ggggcclcca tcagcaglag tagtactac 30

<210> 182

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 182

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

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

<220>
<223> Synthetic

<400> 183
atclattata ggggagcac 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
gcccgaact gggagcagc ctctcttt gaclac 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

gacatcaga tgaccaglc tcttcacc ctgtctgcal ctgtaggaga cagagtcacc 60
 alcacttgcc gggccaglca gactttagt agctgggtgg cctggatca gcagaaacca 120
 gggaaagccc cttagctcl galctalaag ggccttagt tagaaagtgg ggtccatca 180
 aggtcagcg gcagtgatc tggacagaa tcactclca ccalcagcag cctgcagct 240
 galgatitg caactlala ctgccaacag lataatagt atctglacac tttggccag 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
 cagaglatla glagctgg 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

aaggcglct

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 alagllatic 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

caggtagcagc tggtagcagtc lggggcagc gigaagaagc ctggggccctc aglgaaggtc 60
tccagcaagg ctctgggata cacctcacc ggclactata ttcactgggtc acgacaggcc 120
ccaggacaag gccttagtg gatgggatgg atcaacccta acagtgggtg cacaaactat 180
gcacagaagl ttcagggcag ggtcaccatg accagggaca cgtccatcac cacagcctac 240
alggagcga gcaggctgat atctgaccac accggcgtgt attactgtgc gagaggaccc 300
lggallctc ttgactactg gggccaggga acctgggca 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
ggalacacct tcaccggcta clat 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
alcaacccta acagtgggg 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
gacalcgtga tgaccacgic ccagacicc ctggelgtgt cctcgggcca gagggccacc 60
alcaactgca aglocagcca gagigttta lacagctcca acaalaagaa ctacttagct 120
lglaccagc agaaaccagg acagcctcct aagcigcica ttactlgggc atclaccogg 180
gaalccgggg tccclgacog attcaglggc agcgggicg ggacagatt caciclcacc 240
alcagcagcc lgcaggctga agalgtggca glttattact gtcagcaala tatagtacl 300
ccgtacactt lggccaggg gaccaagctg gagalcaaac 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 tatcacagctc 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
 tgggcaact 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 atagactcc glacact 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
caggcgcagc tggcgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgcaagg ctctggata caoctcacc ggctactata ttcactgggt acgacaggcc 120
cctggacaag gccttgagtg galgggatgg atcaacccla acagiggagg cacaaacal 180
gcacagaagl ttcagggcag ggtcaccatg accaggggaca cglccatcag cacagcctac 240
alggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gagaggacc 300
tgggattct tgaclactg gggccaggga accctggtca ccgtcctc 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

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 217
gcgagaggac cctgggallt cttgactac 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 tgaccacagc tccagactcc clggctgtgt ctctggggcga gagggccacc 60
atcaactgca agtccagcca gaglgtlta tacagctcca acaalaagaa ctacttagct 120
lglaccagg agaaaccagg acagcclecl aagctgtcca ttactlgggc alctaccgg 180
gaatccgggg tccctgaocg altcagtggc agcgggtcig ggacagatt cactctcacc 240
atcagcagcc lgcaggctga agatlggca gtttattact gtcagcaala ttatagtact 300
ccgtacactl tggccaggg 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
cagagtgtt latakagctc caacaalaag aaciac 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
lgggcalct 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

cagcaalatt ataglaclcc glacact

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
caggtagcagt tgcaggagtc gggcccagga ctggtagaagc ctccacagac cctgtccctc 60
acctgcactg tclclggtag cccatcggc aglggtagt aclactggag ctggatccgc 120
cagcaccag ggaagggcct ggagggatt gggtacgtcc attacagtg gaacaccac 180
tacaaccct cctcaagag tgcacttcc atalcaalag acagctclaa galccagtc 240
tccctgaagc tgagctclgt gactgccgcg gacacggcgg tgtattactg tgcgagagcc 300
ccccgggat accattact tgcclactgg ggccagggaa cccctggcac 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
ggggctcca toggcagtg gggttactac 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
gogagagccc cccgggala ccallacttt gcttac 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

gaaattggt tgcacaatc tccaggcacc ctgtcttgt ctcaggggga aagagccacc 60
ctctcctgca gggccaglca gaglgttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcalcttt ggtagalcca gcagggccac tggcatcca 180
gacaggtlca gtggcagttg gtcgggaca gacttcactc tcaccalcag cagactggag 240
cctgaagatt ttgagtgta ttactgtcag caglatgga gctcaccgct cacttccggc 300
ggagggacca agglggagat 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

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 237

cagagtgta gcagcagcla c

21

<210> 238
<211> 7
<212> PRT
<213> Artificial Sequence

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

<220>
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<400> 241
cagcaglatg gtagctcacc gctcact 27

<210> 242
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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<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
cagggtcagc tgcaggagtc gggcccagga ctggggaagc ctccacagac cctglccclc 60
accgcaactg tclclgggg ctccalcage aglgggggtt aclactggag clggatccgc 120
caglacccag ggaagggccl ggaglggalt ggttacgtcc attacaglgg gagcaccac 180
tacaaccogt cctcaagag tgcactacc atatcaatag acacgtclaa gagccagttc 240
tccclgaagc tgagctclgt gactgccgcg gacacggccg tglattacig tgcgagagcc 300
ccccgtgat accactactt tgcclactgg ggccagggaa cctcggtcac cglctclca 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
ggtggclcca tcagcaglgg tggllactac 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

glccattaca ggggagcac 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>

<223> Synthetic

<400> 249

gagagagccc ccgaggata ccattacllt gcclac 36

<210> 250

<211> 12

<212> PRT

<213> Artificial Sequence

<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

gaaattgtgtgtagcagcacc ctagctttgt cttcagggga aagagccacc 60
ctctctgtca gggccagtca gagggttagc agcaggtaact tagccctggla ccagcagaaa 120
cctggccagg ctcccaggct cctcaacttt ggtgcatcca gcagggccac iggcalacca 180
gacaggttca gggcagtgg gtcgggaca gactcactc lcaccalcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag caglatggla gctcaccgct cacltcggc 300
ggagggacca agglggagat 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

cagagtgta 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
gglgcatcc

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
cagcagtag 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
caggtgcagc lgcaggagtc gggcccagga ctggtgaagc cttcacagac cciglcoclc 60
acctgcactg tclctgggg ctccalcagc aglgggtggt actactggag ctggatccgc 120
cagcaccacag ggaagggcct ggaglggatt gggtaacatc attacaglgg gagcacclac 180
tacaaccogt cctcaagag tgaattalc atatcagtag acacgctaa gaaccagttc 240
lccctgaagc tgagctctgt gacigccgcg gacacggccg tgaattacig tgcgagagaa 300
ggggclatgg ttllgacta ctggggccag ggaaccclgg tcaccglctc 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 tcagcaglgg 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

alctattaca ggggagcac 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

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<220>

<223> Synthetic

<400> 265

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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

gacatccagl lgaccagtc lccalcctc ctgctgcat ctgtaggaga cagagtcacc 60
atcactgtc gggccagtc gggcattagc agtatllag cctggatca gcaaaaacca 120
gggaaagccc ctaaactcct gattatgct gcalccgct lgcaaagtg ggtccalca 180
agglicagcg gcaglggalc lggacagaa tcaclctca ccalcagcag cctgcagcc 240
gaagattlg caactatla ctgcaacag ctaalagt acccgtcac tttagccag 300
gggaccaagc tggagalca 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

gclgcatcc 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 atagtlacco 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
cagglgcagc tgcaggagtc gggcccagga ctgggtgaagc ctccacagac cctgiccctc 60
acctgcactg tctctggggg cccatcagc agtgggggtt actactggag ctggatccgc 120
cagcaccacag ggaagggcct ggaglggatt ggglacatct attacagtgg gagcaoctac 180
tacaaccctg cctcaagag tcaattatc alalcagtac acacgiclaa gaaccagttc 240
tcctgaagc tgagctctgt gactgccgog gacacggcog tglattactg tgcgagagaa 300
ggggctatgg ttttgacla ctggggccag ggaacctgg tcaccgtctc ctacg 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
 ggggctcca tcagcagtg ggttactac 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
 alclattaca gtgggagcac c 21

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

<220>
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<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 gggclalggi ttlgactac 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>
<223> Synthetic

<400> 283
gacatccagl lgaccacagtc tccalccttc ctgtctgcat ctglaggaga cagaglcacc 60
atcaactgct gggccaglca gggcattagc agttatttag cctgglaica gcaaaaacca 120
gggaaagccc ctaaactccl gatttatgct gcalccgctt tgcaaaglgg ggtcccalca 180
aggttcagcg gcagtggalc lgggacagaa tcaactlca ccatcagcag cctgcagccl 240
gaagattllg caactafta ctgtcaacag ctaaatagti acccghlac ttllggccag 300
gggaccaagc tggagalcaa 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
cagggcatla 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
gclgcatcc 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
caggTgcagc tgcaggagtc gggcccagga ctggTgaagc cttcacagac ccigtccctc 60
acctgcactg tctctggTgg cccalcagc agTggTggTt actactggac ctggatccgc 120
cagcaccag ggaagggccT ggagTggatt gggTacaTct attacagTgg gagcacctac 180
tacaaccogt cccTcaagag tggagTatc atatcagTag acacgtctaa gaaccagTtc 240
tccctgaagc Tgagctctgt gactgcccgc gacacggccg Tgtattactg Tgcgagagaa 300
ggggctatgg tttTgacta ctggggccag ggaaccctgg tcaacctctc ctacg 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 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 lcagcaggg lggttactac

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

atclattaca glggagcac c

21

<210> 296

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<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 gggclalgg tttgactac

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 tgaccocagtc lccalccttc ctgtctgcal ctgtaggaga cagagtcacc 60
atcacttgtc gggccaglca gggcattagc agttatttag cctgglatca gcaaaaacca 120
gggaaagccc claagctcct gatctatgct gcacccgctt tgcmaaagtg ggtcccalca 180
aggctcagcg gcagtgatc tgggacagaa tcaacttca caalcagcag cctgcagcct 240
gaagatttg caacttatta ctgtcaacag cttaatagtt acccgttcaac ttttgccag 300
gggaccaagc tggagalcaa 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 atagtaccg 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
caggtagcagc lgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60
acctgcactg tctctggtag ctcacacagc aglgggggt actactggac ctggatccgc 120
cagtagccag ggaagggccl ggagtagatt gggacatct attacagtag gagcaactac 180
tacaacccl cccccaagag tggagtagc atalcagtag acacgtctaa gaaccagttc 240
tccctgaggc lgagctcgt gactgccgcg gacacggccg tglattacg lgcgagagaa 300
ggggclatgg ttttgacla ctggggccag ggaaccclgg tcacctctc ctacg 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 lcagcagtagc lggllactac 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 gtagggagcac 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 gggctatggg tttgactac 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

gacatccagl tgaccacgic tccatccttc ctgctcgcac ctgtaggaga cagaglcacc 60
alcacttgct gggccagica gggcattagc agttatttag ccigglalca gcaaaaacca 120
gggaaagccc ctaagcctc galctatgcl gcatccgclt tgcaaaglgg ggtcccalca 180
aggllcagcg gcagtggaic tgggacagaa ttactctca caatcagcag ccigcagcct 240
gaagatttg caactatta ctglcaacag ctlaatagt acccgttcac ttggccag 300
gggaccaagc tggagalcaa 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
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<212> DNA
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<220>
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<400> 317
cagggcatta gcagtlat 18

<210> 318
<211> 6
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<220>
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<400> 318
Gln Gly Ile Ser Ser Tyr
1 5

<210> 319
<211> 9
<212> DNA
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<220>
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<400> 319
gctgcatcc

9

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

<220>
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<400> 320
Ala Ala Ser
1

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

<220>
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<400> 321
caacagctta atagttacc gttcact

27

<210> 322
<211> 9
<212> PRT
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<220>
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<400> 322
Gln Gln Leu Asn Ser Tyr Pro Phe Thr
1 5

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

<220>
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<400> 323
cagggtcacc tgggtcagtc tggagctgag gtaagaaga ctagggccctc agtgaaggtc 60
tcctgcaggg ctctgggta caccctaac aactatggta tcacctggg ggcacaggcc 120
cctggacaag ggctlgagt galgggatgg atcagcgcctc acagtggtaa cacagactct 180
gcacagaagt tccaggccag agtcaccatg accacagaca catccacgac cacagcctac 240
atggaactga ggagcctgag atctgacgac acggccgtgt atattgtgc gacgtatagt 300
tggaacltc actgggtcga ccctggggc cagggaacc tggtcaccgt ctcctcag 358

<210> 324
<211> 119

<212> PRT
<213> Artificial Sequence

<220>
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<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 lggt 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
alcagcgcta acagggtaa 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
gcgacglala gtlggaact lcactggtc gacccc 36

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

<220>
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<400> 330
Ala Thr Tyr Ser Trp Asn Phe His Trp Phe Asp Pro
1 5 10

<210> 331
<211> 325
<212> DNA
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<220>
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<400> 331
gaaattgtgt lgacgcaglc lccaggcact ctgctttgt ctccagggga aagagtcacc 60
ctctctgca gggccaglca gaglgtcagt accaactacl laacctgga ccagcagaaa 120
cctggccagg ctccaggct cctcatctal ggtgcalcca gcagggccac lggcatcca 180
gacaggllca gtggcaglgg gtcgggaca gactlcatc lcaccatcag aagltcggag 240
cctgaagait ttgcagtga ttactgicag cagtgtggtg gctcaccgtg gacgtcggc 300
caagggacca gggtggaat caaac 325

<210> 332
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<212> PRT
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<220>
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<400> 332

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<210> 337
<211> 27
<212> DNA
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<220>
<223> Synthetic

<400> 337
cagcaglgtg gggctcacc ggggacg 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
caggcgcagc lgggggagtc lgggggaggc ggggccagc clgggaggtc tctgagactc 60
lclgtgcag cglclggatt cacctcagl agctatggca lgcactgggt ccgccaggct 120
ccaggcaagg gacgggagtg gggggcagtt atatggatg atggaaglaa laaatat 180
ggagactccg lgaagggccg attcaccalc tccagagaca attccaagaa cagcclgtat 240
clgcaaalga acagcclgag agccgaggac acggcclgal aillactgtc gagagatgga 300
gtagaccgtg cttttgatat tlggggccaa gggacaacgg tcaccgtclc tcag 355

<210> 340
<211> 118
<212> PRT
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<220>
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<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

<220>

<223> Synthetic

<400> 345

gcgagagatg gagtagacgg tgccttgal 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 taccaccagtc tccalcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
ataacttggc gggcaagfca ggacattaga aatgatttag gctggatca gcagaaacca 120
gggaaagccc claaactcct gatctatgct gcattccagtt lacaaaglgg ggtcccatca 180
aggitcagcg gcaglggatc tggcacagat ttaactctca ccatcagcag actgcagcct 240
gaagatttg caactata ctgtcaacaa gattacaatt acctglatac tttagccag 300
gggaccaacc tggagalcaa 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
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 349
caggacatta gaaatgat 18

<210> 350
<211> 6
<212> PRT
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<220>
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<400> 350
Gln Asp Ile Arg Asn Asp
1 5

<210> 351
<211> 9
<212> DNA
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<220>
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<400> 351
gctgcatcc 9

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

<220>
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<400> 352
Ala Ala Ser
1

<210> 353
<211> 27
<212> DNA
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<220>
<223> Synthetic

<400> 353
caacaagatt acaattaccl glatacl 27

<210> 354
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
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<400> 354
Gln Gln Asp Tyr Asn Tyr Leu Tyr Thr
1 5

<210> 355
<211> 364
<212> DNA
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<220>
<223> Synthetic

<400> 355
gagglgcagl tgggggaglc ggggggaggc ttggtccagc ctgggggglc cctgagacle 60
lccctggaag cctctggatt caccttggat aactattata lgacctgggt cagccagact 120
ccaggggaagg ggcctggaglg ggtggccaac alaaaggaag alggaaalga tagalactal 180
glggactctg tgaagggcag ctccaccalc ccagagaca acgccaagca glcactgitt 240
ctacaaalga acaglcgag agccgaggac acggcigtit attactgtgc gagagaatt 300
lggaglggcc ctcaclacgg ttggacgic tggggccaag ggaccacggt caccgtctcc 360
lcag 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
85 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

ggattcaccl ttgalaacta 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 ttggagtgg cctcactac ggttggacg 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
gocctocaga tgaccocagtc tccatccctcc ctgtctgcac ctglaggcga cagagtcacc 60
atcacitgcc gggcaagtca ggacgttaga aataatllag gclggatca gcagaaacca 120
gggaatgcc ctaaafccct galctatgct gcalccagtt tacaaagtgg aalcccatca 180
aggltcagcg gcagtggtatc tggctcagal ttcactctca ccatcagcag octgcagcct 240
gaagatttg caactatta 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>
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<400> 365
caggacgta gaaataal 18

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

<220>
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<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>
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<400> 368
Ala Ala Ser
1

<210> 369
<211> 27
<212> DNA
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<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

cagggtgcagc tgggtggagtc tgggggaggc gtgggccagc ctgggaggtc cctgagactc 60
lccgtgcag cgctcgaat cacctcagt agtattggca tgcactgggt cggccaggct 120
ccaggcaagg ggctggagtg ggtggcagtt ttatggtag atggaagtaa laaaaactat 180
gtagactccg tgaagggccg atccaccatc tcaagagaca attccaagaa caagctgtat 240
ctgcaaatga acagcccgag agccgaggac acggctgltt attactglc gagagatcac 300
gatttagga ggggttatga ggggtggtc gaccctggg gccagggaac ctgggcacc 360
gtctctcag 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

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<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
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<220>
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<400> 375
ttatggtatg atggaagtaa laaa 24

<210> 376
<211> 8
<212> PRT
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<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 gaglggitat gagggglggl lcgacccc 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
gaaatgltg tgcacacagtc lccagccacc ctglctttgt ctccagggga aagagccacc 60

ciclcclgca gggccagtc gaggttgc agctacttag cctgglaaca acagaaacct 120
ggccaggctc ccaggctccl cabclalgal gcaccaaca gggccacagg calcccagcc 180
agggtcagtg gcaglggtc lggacagac ttcactclca ccacagcag cctagagcct 240
gaagatttg cagtlalta clgcagcac cglagcaact ggctcccac ttlogcgga 300
gggaccgagg tggaggcag 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
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<220>
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<400> 381
cagagtgctc gcagctac 18

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

<220>
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<400> 382
Gln Ser Val Arg Ser Tyr
1 5

<210> 383
<211> 9
<212> DNA
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<223> Synthetic

<400> 383
gatgcalcc

9

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

<220>
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<400> 384
Asp Ala Ser
1

<210> 385
<211> 27
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<400> 385
cagcacocgla gcaactggcc toccact

27

<210> 386
<211> 9
<212> PRT
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<220>
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<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
laccggctcc cgalgg

16

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

<220>
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<400> 388
 ggcggclaag gigtffga 19

 <210> 389
 <211> 22
 <212> DNA
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 <220>
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 <400> 389
 ttgggaalga ggaaagcaaa ct 22

 <210> 390
 <211> 18
 <212> DNA
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 <220>
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 <400> 390
 ctgaagtacc ggaggaga 18

 <210> 391
 <211> 20
 <212> DNA
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 <220>
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 <400> 391
 atcacgctgg tggctcttt 20

 <210> 392
 <211> 16
 <212> DNA
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 <220>
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 <400> 392
 gctgcggcga gtcctt 16

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

 <220>
 <223> Synthetic

 <400> 393
 ttgcaaatgc tggaccaac aca 23

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

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 394

gggtccggc alctgccc 19

<210> 395

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 395

gcagatgaaa aacgggaac ca 22

<210> 396

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 396

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accctggcca tctccggaga cagctctct agtgatagtg ctgctggaa ctggalcagg 120
cagctcccat cgagaggcct tgagggctg ggaaggacat actacaggtc caagtggat 180
aatgattaag cagtatctgt gaaaagtga ataacctca acccagatcc alccaagaac 240
cacatctccc tgcagctgaa ctctgtact ccgaggaca cggctatc taactgtgca 300
agagaggggg alaaltgaa ttacggctgg ctcgaccct ggggccaggg aaccacggtc 360
accgtctccl 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 tcctagtg 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
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<220>
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<400> 400
acatactaca gglocaagtg gtataal 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 tggotcgacc cc 42

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

<220>
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<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
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atcctcgcga ggctcagca gaggccctt cttagtaatg gatacaacta ttggattgg 120
tacctgcaga agccagggca gctccacaa cctctgact attlggttc taglccggcc 180
lccgggggcc ctgacaggt cagtggcagt ggalccggca cagatttac acigaaaac 240
agcagaglgg aggtcgagga ttgggaat tattattga tgaagctc acaaacccg 300
tacactttg gccgggggac caaggggaa 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
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<220>
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<400> 406
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<210> 407
<211> 11
<212> PRT
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<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
ttggtttcl 9

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

<220>
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<400> 409
Leu Val Ser
1

<210> 410
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<220>
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<400> 410
algcaagcic tacaactcc glacact 27

<210> 411
<211> 9
<212> PRT
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<220>
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<400> 411

Met Gln Ala Leu Gln Thr Pro Tyr Thr
1 5

<210> 412
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<220>
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<400> 412
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acctgcactg tctctgggg ctccgtcagc agtggaait actactggag ctggglccgc 120
caacaccag ggaagggccl ggagtggtt ggttacatca aaaacagtg gggcacctac 180
lacaaccgt cctcaagag lgaaltacc atatcagtag acacglctaa gaaccactc 240
lccctgaggc tgagctctat gacggccgcg gacacggccg tgtattactg tgcgagagcl 300
ggttcgggga gtcactactt tgactactgg ggccagggaa ccttggtcac cglctctca 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
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<210> 415
<211> 10

<212> PRT
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<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
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<220>
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<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
gcgagagcgc gtctgggggag tcactactt gactac 36

<210> 419
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<212> PRT
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<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>
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<400> 420
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ctctctcgca gggccagica gactgttagc agcaactact tagcctggta ccagcagaaa 120
ccgggcagg ccccaggct cctcaactat ggtgcacca gcagggccac tggcaiccca 180
gacaggttca gggcagtggt gtcgggaca gactcactc tcaccatcag cagactggag 240
cctgaagatt ggcagtgta ttactgtag cagtaagggt actcaccgat caccttggc 300
caagggacca agctggagal caaa 324

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

<220>
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<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
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<220>
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<400> 422
cagagtglla gcagcaacta c 21

<210> 423
<211> 7
<212> PRT
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<220>
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<400> 423
Gln Ser Val Ser Ser Asn Tyr
1 5

<210> 424
<211> 9
<212> DNA
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<220>
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<400> 424
ggtgcatcc 9

<210> 425
<211> 3
<212> PRT
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<220>
<223> Synthetic

<400> 425
Gly Ala Ser
1

<210> 426
<211> 27
<212> DNA
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<220>
<223> Synthetic

<400> 426
cagcagtaag gtlactacc gatcacc 27

<210> 427
<211> 9
<212> PRT
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<220>
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<400> 427
Gln Gln Tyr Gly Tyr Ser Pro Ile Thr
1 5

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

<220>
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<400> 428
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ccaggcaagg ggcctggagtg gglgtcatt ttatgglatg atggaactaa laaaaaactat 180
gtagagtcgg tgaagggccg atccaccatc lcaagagaca attccaagaa talgcgtat 240
ctggaaaiga acagccctgag agccgaggac acggcctgtl attactgigc gagagatcac 300
gatttagga ggggtalga ggggtggflic gacccctggg gccagggaac cctgggcacc 360
gltccca 369

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

<220>
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<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
ggallcaccl tcagtagtta tggc 24

<210> 431
<211> 8
<212> PRT
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<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

ttatgglatg 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

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<400> 434

gcgagagatc acgatlltag gaglggttat gaggggtggt togacccc 48

<210> 435

<211> 16

<212> PRT

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<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

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ggccaggctc ccaggctct catclalgal gcalccaaca gggccactgg catcccagcc 180
aggltcaglg gcaglgggc tgggacagac ttcaclctca ccalcagcag cclagagcc 240
gaagalttg cagtlatta ctgtcaaac cglagcaact ggccleccac ttlogggga 300
gggaccaagg tggaaatcaa a 321

<210> 437

<211> 107
<212> PRT
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<220>
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<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
cagagtgta gcagctac 18

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

<220>
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<400> 439
Gln Ser Val Ser Ser Tyr
1 5

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

<220>
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<400> 440
galgalcc 9

<210> 441
<211> 3

<212> PRT
<213> Artificial Sequence

<220>
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<400> 441
Asp Ala Ser
1

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

<220>
<223> Synthetic

<400> 442
caacaccgta gcaacaggcc tccact 27

<210> 443
<211> 9
<212> PRT
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<220>
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<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
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acctgctctg tctctgggg ctccalcagc agtgglaalt actactggac ctggatccgc 120
cagcaaccag ggaagggcct ggagggalt gggatcalca agaacagtg aagcgcctac 180
tacaatccgl ccccaagag tgcactacc atgcaatag acacgtctca gaaccactc 240
tcttgattt tgactctgt gactgccgcg gacacggcct talatfactg tgcgagagal 300
gaaaatalag cagttctca tgcctttgal atctggggcc aagggacalc ggtcacccgc 360
tcctca 366

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

<220>
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<400> 445

<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
gcgagagalg aaaatatagc agtcgcat gctttgata tc 42

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

<220>
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<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>
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<400> 452
gaaatagigt tgacacagtc lccaggcgcc ctgtcttgt ctccaggaga aagagccacc 60
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cclggccagg ctccagget cctcatclat ggtacalcca gcggggccac tggcatcca 180
gacaggitca glggcagtg gctggggaca gacttcaclc tcaccatcac cagactggag 240
ccigaagatt ttcaalala ttactgicag cagtcggit actcacctct cacttccgc 300
ggagggacca aglggaaat caaa 324

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

<220>
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<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

<220>

<223> Synthetic

<400> 458

cagcagtcg gttactcacc tctcact 27

<210> 459

<211> 9

<212> PRT

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<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

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acclgcactg tctctgatga ctccalcaac aalgctgaat cctactggac ctggatcgc 120
caacaccag ggaagggccl ggagiggait ggatacalca aatacactgg gggcatccac 180
talaaccogl cctcaagag tgcactgcc atalcagtg acacglcaaa gaaccagtc 240
tccctgaaaa lgaactcgt gactgcccg gacacggcca aatattactg tgcgagagca 300
cglggaagtc atactllga tgtctggggc caggggacaa cggtcaccgt cctctca 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>
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<400> 462
gagactcca lcaacaatgl tgaatcctac 30

<210> 463
<211> 10
<212> PRT
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<220>
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<400> 463
Asp Asp Ser Ile Asn Asn Val Glu Ser Tyr
1 5 10

<210> 464
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<220>
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<400> 464
alcaaalaca ctgggggcat c 21

<210> 465
<211> 7
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<220>
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<400> 465
Ile Lys Tyr Thr Gly Gly Ile
1 5

<210> 466
<211> 33
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<400> 466
gcgagagcac gtggaagtca tactttgat gtc 33

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

<210> 468
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cctggccagg ctccccgact cctcattal ggtgcaccca gcaggglogc lggcatccca 180
gacaggitca gtggcagtgg gtcgggaca gactlcactc lcaccalcag cagactggag 240
cctgaagall ttgcactgla ttattgacag caalatagta ggtcaccgat cacctloggc 300
caagggacca agctggagat caaa 324

<210> 469
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
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<400> 469
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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
<212> DNA
<213> Artificial Sequence

<220>
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<400> 470
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<210> 471
<211> 7
<212> PRT
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<220>
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<400> 471
Gln Ser Val Ser Ser Asn Tyr
1 5

<210> 472
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<220>
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<400> 472
gggcalcc 9

<210> 473
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<212> PRT
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<220>
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<400> 473
Gly Ala Ser
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<210> 474
<211> 27
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<220>
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<400> 474
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<210> 475
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<400> 475

Gln Gln Tyr Ser Arg Ser Pro Ile Thr
1 5

<210> 476
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cagcaccagc ggaggggccc agagtggalt gggalcalca aaltcagtg gagcacctac 180
tacaaccctg cctcaaggg tggaglcacc atalcaglgg acacglclaa gaaccaatc 240
tccctaaaa taactctgt gactgccgcg gacacggccg tgtllactg tgcgagagcl 300
lclggaagtc alactttga talctggggc caagggacaa tggtcaccgl ctcctca 357

<210> 477
<211> 119
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<220>
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<400> 477
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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
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<220>
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<400> 478
ggtagcctca lcaacagtgt tacllactac 30

<210> 479
<211> 10
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<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

alcaaattca ggggagcac c 21

<210> 481

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

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<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

gcgagagcct cgggaaglca tactttgat atc 33

<210> 483

<211> 11

<212> PRT

<213> Artificial Sequence

<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>

<223> Synthetic

<400> 484

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ggccaggcic ccaggcicc caictalga acatcctaca gggccactga cglcccagcc 180
aggitcaglg gcaggggic lggacagac ttcactctca ccalcaaaa cctagagccl 240
gaagatttg cagttalta ctgcagcag cglagcgcct ggccgclcag ctccggcgga 300
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<210> 485

<211> 107

<212> PRT

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<220>

<223> Synthetic

<400> 485

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 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
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Ser Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
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<210> 486

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 486

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<210> 487

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<212> PRT

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Gln Ser Ile Ser Gly Tyr
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<210> 488
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<220>
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<400> 488
gatacalcc 9

<210> 489
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Asp Thr Ser
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<210> 490
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<400> 490
cagcagcgtg ggcactggcc gtcagc 27

<210> 491
<211> 9
<212> PRT
<213> Artificial Sequence

<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
cagglgcagc tgcaggaglc gggcccagga ctgglggaagc cttcacagac cctglccclc 60
accgcaclg lclclggtgg ctccalcaac aglgtactt actaclggac ctggatccgc 120
cagcaccocag ggaggggocct agaglggatt ggglacatca aatlcaglgg gagcacclac 180

tacaaccggt cccccaaggg togaglcacc atalcaglgg acaagctctaa gaaccaatc 240
tcccttaaaa ttaactctgt gactgccggg gacacggccg lgttttactg lgcgagagct 300
btgggaaglc atactttga taltgggggc caagggacaa tgglcaccgt ctctca 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
gglggctcca tcaacagtg l tactactac 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 glgggagcac 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

gcgagagcct ctggaagtca tactttgat alc

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

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ctctctgca gggccagta gagtgttagc aacagclact tagcctggta ccagcagaaa 120
ccggccagg ctccaggct cctcctctt ggtagctca gcagggtcac lggcalcca 180
gacaggltca gtggcagtg gctgggaca gactcactc lcaccatcag cagactggag 240
cctgaagatt ttggaatgla ttactgicag caglalagla ggcaccgat cacctcggc 300
caagggacca agglggaaat 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

cagagtgta 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

gglgcglcc 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 galcacc 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
gagggtcagc tgggtcagtc tggagctgag gtgaagaagc clggggccdc aglgaaggtc 60
tcctgcaagg ctctgggta ctctttacc agcttgggt tcagctgggt ggcacaggcc 120
ccggacaag gactgagtg gctgggatgg atcagcgctt acagtggtga cacagaclat 180
gcacagaagl tccagggcag aglcaccclg accactgaca calccacgac caclgcctac 240
alggagctga ggagccigag atctgacgac acggccgtct attactgtgc gogalalaac 300
tggaacclcc actggttoga ccctggggc cagggaaacc tggtcaccgt ctctca 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 tgggt 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
 alcagcgctt acaglggga 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
gcgcgatala ac1ggaacct ccactgg1tc 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
gacatcogga tgaccagtc tccaggcate ctg1ctt1gt c1ccagggga aagagccacc 60
ct1c1ctgca gggccag1ca gaatattaaa agcaactact tagc1gg1a ccagcagaaa 120
cctggccagg c1cccaggct cctc1c1ttt gglacatcca acagggccac 1gocall1ca 180
gacagg1ca g1ggcag1gg gtctgggaca gactcctt1 taccalca1g cagac1ggag 240
cctgaagatt ttgcag1g1a ttactgtcag cag1algg1a actcaccgtg gacgt1cggc 300
caagggacca aag1ggalal 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

<400> 522
cagcaglatg gtaactcacc ggggacg

27

<210> 523
<211> 9
<212> PRT
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<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
caggtagcagc tgcaggagtc gggcccagga cggggaagc ctccacagac cctgtccctc 60
accagcactg tctcagatgg ctccatcaac agtgltgaat cctactggac ctggatccgc 120
cagcaccacag ggaagggcct ggaglggatl ggatacatca aatacactgg gggcalccac 180
tataaccogt cctcaagag tcgactigcc atalcaglgg acacgtcaaa gaaccagllc 240
tccclgaaaa tgagctctgt gactgccgcg gacacggccg tglatalctg tggagagca 300
cgtggaagtc alacttllga lgtcggggc caggggacaa lggicaccgt clctca 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
galggctcca tcaacaglg lgaalccctac 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
atcaaalaca clgggggcal 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 tactttgat 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

gaaatgagc tgactcagtc lccaggcacc cigtcttggc cccaggggga aagagccacc 60
ctctctgca gggccagtc gagtattagc aglaactact tagccctggta ccagcagaaa 120
ccctggccagg ccccagact cctcattat ggtgcaccca gcagggtcac tggcatcca 180
gacaggttca gtggcagtg gctggggaca gacttcacac lcaccatcag cagactggag 240
cctgaagatt ttgcactgta ttattgtag cagtatagta ggtcaccgat caccttcggc 300
caagggacca aagtgatata 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

cagaglalla gcagtaacta c

<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
cagcaglata gtagglcacc galcacc 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
caggcgcagc tgcaggaglc gggcccagga ctggtgaagc cttcacagac cctglcctc 60
acctgcactg tctcggggg ctcgcagc agtgglaat actacggag cggatccgc 120
cagcaccag ggaaggcct ggagtggtt gggacatca aaaacaggg gggcacctac 180
lacaaccgt cctcaagag tcaatlac atatcagtag acacgctaa gaaccactc 240
tccctgaggc tgagctctat gaaggccgc gacacggccg tgtallactg tgcagagct 300
ggctcgggga gtcactact tgaactcgg ggcagggaa cctgggtcac 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
ggcggctccg tcaagcaggg taactactac 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

alcaaaaaca ggggggcac 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 lcactactt 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 tcacggcacc ctgctcttgt ctcagggga aagagccacc 60
 ctcctctgca gggccagica gaglgtagc agcagctact tagcctggla ccagcagaaa 120
 cctggccagg ctcacaggct cctcatctat ggtgcatcca gcagggccac lggcatccca 180
 gacaggctca glggcaglgg gtcctgggaca gactcactc tcaccatcag cagactggag 240
 cctgaagatt glgcaglgla ttactgicag cagtatggtt actcaccgat caactcggc 300
 caagggacca aggtggaat 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

cagagtgta 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
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 553
Gly Ala Ser
1

<210> 554
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 554
cagcagatg gttactcacc galcacc

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
gaaglgcagc lggigcagtc tgggggaggc gtggccagc ctgggaggtc cctgagactc 60
tcclgtacag cgtctggatl cacctcagl agctatgcc tglactgggt ccgccaggct 120
ccaggcaagg ggcctggagtg ggtggcagtt atalgglatg atggaagtaa laaaaactat 180
gcagactccg tgaagggccg atcaccalc tccagagaca attccaagaa cacactgtat 240
ctgcaagtga acagcctgag agccgaggac acggclgtgt attacgtgic gagagatcac 300

gattlittga gtggtatga ggggltgtc gacccclggg gacagggaac cclggcacc 360
gtcclctca 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 lcagtagcta tggc 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
alatggtalg algaagtaa 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
gcgagagalc acgattttt gagtggttal gagggglgt tgcacccc 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
gaaattgtc tgactcaglc tccagccacc ctgctttgt ctccagggga aagagocacc 60
ctctctgca gggccaglca gagtqtlagl agctactiag cctggtacca acagaaacct 120
ggccaggcic ccaggclccl catctalgat gcatccaaca gggccaclgg catcccagcc 180
aggitcaglg gcaglgggtc tyggacagac ttcactlca ccatcaglag cclagagcct 240
gaagatttg cagttatla ctgcagcaa cglagcaact ggcclcccac ttccggcgga 300
gggaccaaag tggatalcaa 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

cagagtgta glagctac 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>

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<400> 570

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27

<210> 571

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 571

Gln Gln Arg Ser Asn Trp Pro Pro Thr

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<210> 572

<211> 375

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 572

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lctlgcaagg ctctggta caccttacc acctatgga tcaactgggt ggcacagggc 120
ccggacaag ggcttgaglg galgggatgg atcagcgcct lcaalgggga cacaaactt 180
gcacagaacc tccagaacag aglcacctg accacagaca calccaclag cacagcctal 240
atggaactga ggagcctgag alctgacgac acggccgtt attactgtc gagaggggga 300
ggagcgcgc cggggaactl ctctctac ggtatggaag tclggggcca ggggaccacg 360
gtcaaccglcl cclca 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
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<220>
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<400> 574
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<210> 575
 <211> 8
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<400> 575
 Gly Tyr Thr Phe Thr Thr Tyr Gly
 1 5

<210> 576
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<220>
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<400> 576
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<210> 577
 <211> 8
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<220>
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<400> 577
 Ile Ser Ala Phe Asn Gly Asp Thr
 1 5

<210> 578
<211> 54
<212> DNA
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<400> 578
gcgagagggg gaggagclog lccggggaac ttctttctt acgglalga cglc 54

<210> 579
<211> 18
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<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
galgttga tgactcaglc lccagccaacc ctgcttltgt ctccagggga aagagccacc 60
ctctcclgla gggccaglca gagttlgcc agctactlag cctgglaacca acagaaacct 120
ggccaggctc ccaggcctct catctatgal accctctaca gggccactgg cglcccagcc 180
aggttcagtg gcaglggglc tgggacagac ttactctca acalcagcaa cclggagcct 240
gaagatttg cagittaita ctgtcagcaa cgtggcaact ggcccctcac ttccggcgga 300
gggaccaagg lggaaalcaa 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

<220>

<223> Synthetic

<400> 586

cagcaacgtg gcaactggcc gctcacl

27

<210> 587

<211> 9

<212> PRT

<213> Artificial Sequence

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<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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tctgcaagg cttctgglia caccttlagc tacaatggig tcactlgggl acgacaggcc 120
cctggacaag ggcttgaglg galgggatgg atcagcgtt acgatggtaa cacagaclat 180
gcacagaagt lccaagacag aalcaccalg accacagaca calccacgag tacagcctac 240
atggaactga ggagccttag alctgacgac acggcctct attactgtgc gaggtalagt 300
tgaacaacc actggttoga cccctggggc caggaaccc lggtaacct 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 ttgctacaa tgg| 24

<210> 591
<211> 8
<212> PRT
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<220>
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<400> 591
Gly Tyr Thr Phe Ser Tyr Asn Gly
1 5

<210> 592
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
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<400> 592
atcagcgctt acgatggtaa caca 24

<210> 593
<211> 8
<212> PRT
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<220>
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<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
gcgaggatata gttggaacaa ccactgggtc gacccc 36

<210> 595

174

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

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<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
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ctctcttga gggccagica gagtgttcc ggcagctact lagcctgga ccagcagaaa 120
cclggccagg ctccaggct cclcattat ggtgatcca acagggccac lggcatcca 180
gacaggtica ctggcagtg gctgggaca gacttcac tcaccatcag cagactggag 240
cclgaagait ttgcagtga ttctgtcag cagagtgct tctaccgtg gaagtcggc 300
caagggacca agcggagat 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
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<220>
<223> Synthetic

<400> 598
cagagtgltt ccggcagcla c 21

<210> 599
<211> 7
<212> PRT
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<220>
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<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
gglgcalcc 9

<210> 601
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 601
Gly Ala Ser
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<210> 602
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 602
cagcagagtg ctttclcacc gggagc 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 tgggtcagtc tgggggaggc ttggtacagc ctgggggggc cctgagactc 60
loctgtgcag cctctggatt caccttcagl atgtacgaca tgcactgggl ccgccaactc 120
ataggaaaag gctgggagtg ggtctcagca atgggtactg ctgglgacac atactalcca 180
ggctccglga agggccgalt caccalctoc agagaaaatg ccaagaactc ctgtttctt 240
caaalgaaca gcttgagagc cggggacacg gctgtttait actgtgtaag atccgggact 300
acagagtgtt togacccttg gggccagga accccggta ctgtctcc 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
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<223> Synthetic

<400> 606
ggaltcacct lcaglatgla cgac 24

<210> 607
<211> 8
<212> PRT
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<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

atggtaclg ctggtagac 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

glaagalccg ggaclacaga ggggtcga 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

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 atcactgic ggaogaglca ggglatiagt agctggitag cctggialca gcagaaacca 120
 ggaaaagccc ctaacctcct galctatgcl gcalccagtl lacaagtg ggloccalca 180
 aggtlcagcg gcagtgatc tgggacagal tcaclctca ccatcagcag cctgcagcct 240
 gaagatttg caacttacta tfgctacag gctaacagtl tccogtacac ttltggccag 300
 gggaccaagg tggagalcaa 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

caggglatgta glagctgg 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
gctgcalcc 9

<210> 617
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 617
Ala Ala Ser
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<210> 618
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 618
ctacaggcta acagttccc glacact 27

<210> 619
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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<400> 619
Leu Gln Ala Asn Ser Phe Pro Tyr Thr
1 5

<210> 620
<211> 369
<212> DNA
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<220>
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<400> 620
caggccagc tggcagtc lggggaggc ggggtccagc clgggaggc cctgagact 60
tcctgtcag cgtctggtt cacctcagl agttaggca lgcactggg cgcacaggct 120
ccaggcaagg ggcctggagtg ggtggcagtt ttagglalg alggaaglaa laaaaactat 180
gtagactccg tgaagggocg atcaccatc tcaagagaca allccaagaa cacgcttat 240

ctgcaaatga acagcctgag agccgaggac acggctgigt aitatigtgc gagagatcat 300
gatttagga gtggilatga ggggtgggtc gaccctggg gccagggaac cclggtcacc 360
glcclcca 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
ggatcacct lcagtagta tggc 24

<210> 623
<211> 8
<212> PRT
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<220>
<223> Synthetic

<400> 623
Gly Phe Thr Phe Ser Ser Tyr Gly
1 5

<210> 624
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 624

ttatggatg atggaaglaa laaa

24

<210> 625

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 625

Leu Trp Tyr Asp Gly Ser Asn Lys

1 5

<210> 626

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

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<400> 626

gcgagagatc atgatttag gagtggfai gaggggtggt tgcacccc 48

<210> 627

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<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

gaaattgic tgaacaglc lccagccacc ctgtcttigi ctccagggga aagagccacc 60
ctctctgca gggccagica gagtgtcgc agctactlag cctgglacca acagaaacct 120
ggccaggctc ccaggciccl calctatgat gcatccaaca gggccactgg catcccagcc 180
aggitcaglg gcagtggtc lgggacagac ttcactclca ccalcagcag cctagagcct 240
gaagatttg cagltatta ctgcaaacac cglagcaact ggccleccac 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

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<223> Synthetic

<400> 630

cagaglgitc gcagctac 18

<210> 631

<211> 6

<212> PRT

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<220>

<223> Synthetic

<400> 631

Gln Ser Val Arg Ser Tyr

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<210> 632

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 632

galgalcc 9

<210> 633

<211> 3

<212> PRT

<213> Artificial Sequence

<220>
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<400> 633
Asp Ala Ser
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<210> 634
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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<400> 634
caacaccgla gcaactggcc lcccacl 27

<210> 635
<211> 9
<212> PRT
<213> Artificial Sequence

<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>
<223> Synthetic

<400> 636
caggtaaccl tgaaggaglc gggcccagga clggtaagl ctccggagac cclgtccctc 60
acilgcactg tctctactgg clccalcagc agtagtagt actactgggc clggatccgc 120
cagccccag ggaagggact ggagtggatt gggagtalcl atalatgig gagtaaatic 180
tacagcccgl ccccaagag fogagtcacc atalacgllg acacglcaa gaatcagttc 240
lccclgcaac tgagctcggg gacggccgca gacacggctg lalattactg tgcgagacag 300
gtcggtgcaa tctllgacta clggggccag ggaaccclgg lcaccgtctc ctca 354

<210> 637
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<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
 acggcctcca lcagcagtag lagttactac 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
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<210> 641
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 641
 Ile Tyr Tyr Ser Gly Ser Lys
 1 5

<210> 642
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
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<400> 642
gogagacagg tcgggcaat cttgacac 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>
<223> Synthetic

<400> 644
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gggaaagccc ctaaactct gctctataag ggtctagtt tagaaaglgg ggtccatca 180
aggltcagcg gcaglggac lgggacagag ttcactctca ccacacagc cctgcagcct 240
galgalfttg caactatta ctgccaacag lalaatagtt attctggac gtcggccaa 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> 8
<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
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 649
Lys Ala Ser
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<210> 650
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 650
caacagiala alagttattc tgggacg 27

<210> 651
<211> 9
<212> PRT
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<220>
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<400> 651
Gln Gln Tyr Asn Ser Tyr Ser Arg Thr
1 5

<210> 652
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
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<400> 652
gaggtagcagc tggtagcagtc tggagctgag gtagagaagc ctagggccctc agtagaaggtc 60
lccagcaagg cctctgggta cacctllaac atclatggta lcagctgggt acgacaggcc 120
ccctggacaag ggcctgaglg gatgggalgg atcagcgcctt acaatggtaa cacaaactat 180
gcacagaaac lccagggcag agtcaccatg accacagaaa catccacgac cacagccctac 240
atggagtga ggagccctgag atctgacgac acggccgtgt attactglc gagagattct 300
gattggggaa ctcctacca ctactacggt atggacgtct ggggccaagg gaccacggtc 360
accgtctct ca 372

<210> 653
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
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<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 ttaacalcla lggt 24

<210> 655
<211> 6
<212> PRT
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<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>
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<400> 656
atcagcgctt acaatgglaa caca 24

<210> 657
<211> 8
<212> PRT
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<220>
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<400> 657
Ile Ser Ala Tyr Asn Gly Asn Thr
1 5

<210> 658
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
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<400> 658
gagagagatt ctgatgggg aactccctac cactactacg gtagggacgt c 51

<210> 659
<211> 17

<212> PRT
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<220>
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<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>
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<400> 660
gatattgtga tgaccacgic lccagactcc cgggcgtgt cctcgggcga gagggccacc 60
alcaacigca agtccagcca gaalattta lacacclcca acaalaagaa ctactagct 120
tggaccagc agaaccagg acagcctcct aagcgtcctc ttactgggc attaccocg 180
aaatccgggg lccclgaccg atccaglggc agcgggictg ggacagaltt cactctacc 240
atcagcagcc tgcaggctga agalgggca gtttattact gtcagcaata ttataatct 300
cctcggaogt lggccaagg gaccaaagtg galatcaaa 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

cagaatatt tatcaacctc caacaataag aectac

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 ataactctc tcggacg

27

<210> 667

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<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
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acctgcactg tctctgatgg ctccalcaac agtgggtggt cclactggag ctggatccgc 120
cagcaccocgg ggaagggocct ggagtggtat gggatcaatca aalacagtgg gggcgtccac 180
lalaaccocgl ccccaagag tgaalcaacc atatcagtgg acaogtctaa gaaccattc 240
lccclgaaaa tgacctctgt gactgcccgc gacacggccg tglattctg tggagagca 300
octggaaglc acacittga tatctggggc caggggacaa tggtaacogt ctttca 357

<210> 669
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<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
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<220>
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<400> 670
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<210> 671

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

<220>
<223> Synthetic

<400> 671
Asp Gly Ser Ile Asn Ser Gly Gly Ser Tyr
1 5 10

<210> 672
<211> 21
<212> DNA
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<220>
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<400> 672
alcaaataca glgggggcgt c 21

<210> 673
<211> 7
<212> PRT
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<220>
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<400> 673
Ile Lys Tyr Ser Gly Gly Val
1 5

<210> 674
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
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<400> 674
gcgagagcac clggaagtca cactttgal alc 33

<210> 675
<211> 11
<212> PRT
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<220>
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<400> 675
Ala Arg Ala Pro Gly Ser His Thr Phe Asp Ile
1 5 10

<210> 676

<211> 324
<212> DNA
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<220>
<223> Synthetic

<400> 676
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ctctcctgca gggccagtc gagtgtagc aacaactact tagcctggla ccagcagaaa 120
cctggccagg ctccagact cctcalclat ggtacatcca atagggicag tggcalocca 180
gacaggllca glggcaglgg gctcgggaca gactcactc tcaccalcag cagactggag 240
cctgaagatt tgaactala ttattgicag caglalagta ggtaccgal cacctcggc 300
caagggacac gactggagal laaa 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>
<223> Synthetic

<400> 678
cagagtgta 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>
<223> Synthetic

<400> 680
gglacatcc 9

<210> 681
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 681
Gly Thr Ser
1

<210> 682
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 682
cagcaglata gtaggtcacc galcaacc 27

<210> 683
<211> 9
<212> PRT
<213> Artificial Sequence

<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>
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<400> 684
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lccclgacg cclclggali caccttaac aacttgoca lgaccgggl cgcocaggct 120
ccaggaagg gctggagtg ggclcaact atlaggga gggcgltga cacalactgc 180
gcagaciccg lgaagggccg gllcaccalc tccagagaca attccaagaa cacactglat 240
ctgcaaalga acagcctgag agccgaggac acggccglal atlaclgfgc gaaagalggc 300
gcclclata gtgglacga acaclactgg ggccagggaa caatgglaac cglctoctca 360

<210> 685
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<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 taacaactt 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

attagtgga gggcggtga caca 24

<210> 689

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 689

Ile Ser Gly Ser Gly Val Asp Thr
1 5

<210> 690

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 690

gcgaaagalg ggccttcta tagtggtac 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>

<223> Synthetic

<400> 692

gaaacgacac tcacgcaglc tccaggcacc ctgtcttltg ctccagggga aagagccacc 60
ctctcttga gggccagta gaggttagc agcagctac tagcctgga ccagcagaaa 120
cctggccagg ctcccaggct cctcctcctt gglacatcca acagggcctc tggcatcca 180
gacaggctca ttggcaglg gtcgggaca gactcactc tcaaccatcag cagactggag 240
tcgaagatt ttgcagtga ttactgtcag caglatggta gctcacctcg gacgttcggc 300
caagggacca aagtggalat 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
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<220>
<223> Synthetic

<400> 694
cagagtgta gcagcagcla c 21

<210> 695
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<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
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<220>
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<400> 697
Gly Thr Ser
1

<210> 698
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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<400> 698
cagcagialg gtagctcacc lgggacg 27

<210> 699
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<400> 699
Gln Gln Tyr Gly Ser Ser Pro Arg Thr
1 5

<210> 700
<211> 363
<212> DNA
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<220>
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<400> 700
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lccctgicag cgtctggait cacctcagt agctatggca tgcactgggt cggccaggct 120
ccaggcaagg ggcctggagtg ggtggcagtt atalgglatg atggaagtaa taaalactal 180
gcagactcgg tgaaggccg attcaccalc tccagagaca attccaagaa catgctgtal 240
ctgcaaatga acagcccgag agccgaggac accgctgigt allactgtgc ggcttacgal 300
atttgatlg gtattcccc ggttgactac tggggccagg gaaccctggt caccgtelec 360
tca 363

<210> 701
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
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<400> 701
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 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
 ggaltcaccl tcagtagcga tggc 24

<210> 703
 <211> 8
 <212> PRT
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<220>
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<400> 703
 Gly Phe Thr Phe Ser Ser Tyr Gly
 1 5

<210> 704
 <211> 24
 <212> DNA
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<220>
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<400> 704
 atatggtatg atggaagtaa taaa 24

<210> 705
 <211> 8
 <212> PRT
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<220>
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<400> 705
Ile Trp Tyr Asp Gly Ser Asn Lys
1 5

<210> 706
<211> 42
<212> DNA
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<220>
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<400> 706
gaggcttacg alattllgat tggttatloc 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>
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<400> 708
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ctctctgca gggccagtca gacigttagl agcaacttag cctgggtcca gcagaaaccl 120
ggccaggctc ccagactcct calctalgal gcatccacca gggccacigc latcccagcc 180
agglicagtg gcagtgggc tgggacagaa ttcactctca ccatcagcag cctgcaglcl 240
gaagatttg cagllatta ctgtcagcag tataataact ggtacacclt tggccagggg 300
accaagctgg agatcaaa 318

<210> 709
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
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<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 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
 <213> Artificial Sequence

<220>
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<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>
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<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

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acctgcactg lclctgglgg ctccattacc aglgggggtt aclactggac ctggatccgc 120
cagcaccacag ggaagggcct ggaatggait ggatacalca aatttaglgg gaacacctac 180
lacaaccogt cctcaggag togagtcacc atalcactg acacgiclaa gaalcagttc 240
tcctgaata lgacctlgl gactgccgcg gacaogggcg tgtattattg tgcgagagca 300
cctggaaglc ataacttga calctggggc caagggacaa tggtcaccgl ccttca 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

<210> 718
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 718
 ggaggctcca ttaccaggg tggtaclac 30

<210> 719
 <211> 10
 <212> PRT
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<220>
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<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>
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<400> 720
 atcaaattta ggggaacac c 21

<210> 721
 <211> 7
 <212> PRT
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<220>
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<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 cgggaagtca taaclllgac 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
ggcatccggg tgaaccagtc tccagacacc ctgtctttgt ciccagggga aagagocacc 60
ctctctgca gggccagtg gagtattagt aataactatt tagcctggta ccagcagaaa 120
ccggccagg ctcccaggct cctcalclat ggtgcatoca gcagggccac tggcatocca 180
gacaggttca glggcaglgg gtcgggaca gacttcactc tcaccalcag aagactggag 240
lctgcagatt ttgcaccgta ttactgtcag caatalagta ggtcaccgat caccttcggc 300
caaggacac gactggagat laaa 324

<210> 725
<211> 108
<212> PRT
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<400> 725
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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

glgaglaatta gaalaacta l

21

<210> 727

<211> 7

<212> PRT

<213> Artificial Sequence

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<400> 727

Val Ser Ile Ser Asn Asn Tyr

1 5

<210> 728

<211> 9

<212> DNA

<213> Artificial Sequence

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<400> 728

gglgcalcc

9

<210> 729

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<400> 729

Gly Ala Ser

1

<210> 730

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 730

cagcaalata glagglcacc galcacc

27

<210> 731

<211> 9

<212> PRT

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<220>

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<400> 731
Gln Gln Tyr Ser Arg Ser Pro Ile Thr
1 5

<210> 732
<211> 357
<212> DNA
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<400> 732
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accggcactg tctcgggg cttccalcaac agtgttactt actactggac cgggatccgc 120
cagcaccocag ggaggggocct agagtggtatt gggatataca aattcagtg gaggacclac 180
tacaaccocgl ccccaaggg toagatcacc alatacgtgg acacgtctaa gaaccaattc 240
tccctaaaa ttaactctg gactggccgc gacacggccg tgtttactg tggagagcl 300
tctgaaglc atactttga tatcgggggc caagggacaa tggtcaccgi ctcclea 357

<210> 733
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
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<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
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<220>
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<400> 734
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<210> 735
<211> 10

<212> PRT
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<220>
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<400> 735
Gly Gly Ser Ile Asn Ser Val Thr Tyr Tyr
1 5 10

<210> 736
<211> 21
<212> DNA
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<220>
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<400> 736
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<210> 737
<211> 7
<212> PRT
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<220>
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<400> 737
Ile Lys Phe Ser Gly Ser Thr
1 5

<210> 738
<211> 33
<212> DNA
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<220>
<223> Synthetic

<400> 738
gcgagagcct ctggaaglca tactttgat atc 33

<210> 739
<211> 11
<212> PRT
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<220>
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<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>
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<400> 740
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c|ct|c|t|g|c|a gggccag|t|c|a g|a|g|t|g|t|a|g|c aacag|t|a|c|t| t|a|g|c|t|g|g|g|a ccagcagaaa 120
c|c|t|g|g|c|c|a|g|g| c|c|c|c|a|g|g|c|t| c|c|c|a|c|t|c|t| g|g|t|g|c|g|l|c|c|a g|c|a|g|g|g|t|c|a|c|c| l|g|g|c|a|t|c|c|c|a 180
g|a|c|a|g|g|t|t|c|a g|t|g|g|c|a|g|g|g| g|t|c|t|g|g|g|a|c|a g|a|c|t|c|a|c|t|c|c| t|a|c|c|a|c|a|g|c|a|g|a|c|t|g|g|a|g| 240
c|c|t|g|a|a|g|a|t|t| t|g|g|a|a|g|t|a| t|t|a|c|t|g|c|a|g| c|a|g|t|a|t|a|g|t|a| g|g|l|a|c|a|c|o|g|a|t| c|a|c|c|l|c|g|g|c| 300
c|a|a|g|g|g|a|c|c|a| a|g|c|t|g|g|a|g|a|t| c|a|a|a| 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
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<220>
<223> Synthetic

<400> 742
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<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
ggg⁹gcg⁹lcc

<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
cagcag²⁷lala g²⁷iagg²⁷lacc gat²⁷cacc

<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
gagg⁶⁰tg⁶⁰cagc tgg⁶⁰tcag⁶⁰lc lgg⁶⁰ggg⁶⁰ag⁶⁰gc ttg⁶⁰glac⁶⁰agc clgg⁶⁰cagg⁶⁰tc cct⁶⁰gag⁶⁰actc
tccl¹²⁰gl¹²⁰cag ccl¹²⁰gg¹²⁰agl cac¹²⁰ctgg¹²⁰at gat¹²⁰atg¹²⁰cca lgc¹²⁰actgg¹²⁰gl ccg¹²⁰gca¹²⁰agcl

ccaggaagg gccggaglg ggcclcaagt atagltgga atagtggtag tataggctat 180
gaggactctg lgaagggccg ctcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaatga acagctlgag agcigaggac acggcctgtl attaciglgc aaaagatggg 300
tgaaccctg aclacttga ctatggggc caggaataa oggaccctg cccclca 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
ggagtcaoct lggatgatta lgcc 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

atagttgga atagtgtag 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 gglggaaccc glaclacttt gactat

36

<210> 755

<211> 12

<212> PRT

<213> Artificial Sequence

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<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

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atcactgccc gggcaagica gggcattaga aglgatttag gctggatca gcagaaacca 120
gggaaagccc ctaagcgcc l gatclatget gcalccagtt tgc aaagtg ggloccatca 180
aggttcagcg gcaglggalc tggacagaa ttcactctca caalcagcag cctgcagcc 240
gaagatttg caactata ctgctacag calaatagtl aacctctcac ttccggcgga 300
gggaccaagg tggaaalcaa a 321

<210> 757

<211> 107

<212> PRT
<213> Artificial Sequence

<220>
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<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
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<220>
<223> Synthetic

<400> 758
cagggcatta gaagtgat 18

<210> 759
<211> 6
<212> PRT
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<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
gctgcalcc 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

ctacagcaca atagtaccc tctcacl 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

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acctgcgccg tctctgggta ctcctcagc agtggtaatt actactggag clggatccgc 120
caacacccag ggaagggcct ggaglggatt ggglacatca agtacacigc gagcaacctac 180
tacaacccgt cctcaagag tggagttatt alattagtag acacgictaa gaccagttc 240
tcctgaagc tgagctcigt gaalgccgcg gacacggccg lglattactg tgcgagagca 300
cctggaactc algcttttga tglttggggc caagggacaa lggtcaccgt cctctca 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 taatctac 30

<210> 767
 <211> 10
 <212> PRT
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<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
 alcaagtaca ctggagcac 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 lgcittgat gtt 33

<210> 771
<211> 11
<212> PRT
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<220>
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<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 lcacgcagtc lccaggcacc clgtcttgt ttccagggga aagagccacc 60
ctctcclgca gggccagica gaglgttagc aglagctact tagcctggta ccagcagaaa 120
cctggccagg clcccaggct cctcactial ggigcaloca gcagggccac lggcatcca 180
gcaggltca gtggcagtggt gctgtgaca gacccactc tcaccalcag cagcctggag 240
cctgaagatt ttgcagtga ttactgtaag cagtalagta gglaaccgat cacctcggc 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
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 774
 cagagtgta 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
 gglgcatcc 9

<210> 777
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 777
 Gly Ala Ser
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<210> 778
 <211> 27
 <212> DNA
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<220>

<223> Synthetic

<400> 778

cagcaglatg gtaggtcacc galcaacc

27

<210> 779

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 779

Gln Gln Tyr Ser Arg Ser Pro Ile Thr

1 5

<210> 780

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 780

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ccaggggaagg gccctggagtg ggtctcaact attagtgga gggcggtga cacalactgc 180
gcagactcog tgaagggccg glicaccatc tccagagaca atccaagaa cacactgtat 240
ctgcaaalga acagcctgag agccgaggac acggccgat attactgtc gaaagatggc 300
gccctctata gttgctacga acaclactgg ggcagggaa ccaeggtcac cglcctca 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
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 782
ggattcaact taacaactt tgcc 24

<210> 783
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
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<400> 783
Gly Phe Thr Phe Asn Asn Phe Ala
1 5

<210> 784
<211> 24
<212> DNA
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<220>
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<400> 784
atttagtgga gtggcgttga caca 24

<210> 785
<211> 8
<212> PRT
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<220>
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<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 gcgccctcta laglggctac gaacactac 39

<210> 787

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

<220>
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<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
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ctctcclgca gggccaglca gaggtttagc agcagclact tagcctgga ccagcagaaa 120
cctggccagg ctcccaggct cclcatctat ggtacatcca acagggccac tggcalcca 180
gacaggttca gggcaglgg gtcgggaca gacttcactc tcaccatcag cagacggag 240
tctgaagat ttgcagtgta ttactgicag caglatgga gctcaactcg gacgtcggc 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
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<210> 791
<211> 7
<212> PRT
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<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>
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<400> 792
ggtacatcc 9

<210> 793
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<220>
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<400> 793
Gly Thr Ser
1

<210> 794
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<400> 794
cagcagtatg glagctcacc tcggacg 27

<210> 795
<211> 9
<212> PRT
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<220>
<223> Synthetic

<400> 795
Gln Gln Tyr Gly Ser Ser Pro Arg Thr

1 5

<210> 796
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
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<400> 796
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cctggacaag ggcctgagtg galgggaggg atcagcgctt acgagglaa cacagactat 180
gcacagaagl tccaagacag aalcaccalg accacagaca catcclogac cacagoclac 240
atggaactga ggagcctgag atctgacgac acggccgtct attactgtc gaggtatgt 300
tgaacaagc actgggtoga cccclggggc cagggaaaca tggtcaccgl ctctca 357

<210> 797
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 797
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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
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<212> DNA
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<400> 798
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<210> 799
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<212> PRT
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<220>

<223> Synthetic

<400> 799

Gly Tyr Thr Phe Thr Tyr Tyr Gly
1 5

<210> 800

<211> 24

<212> DNA

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<220>

<223> Synthetic

<400> 800

alcagcgctt acgatgglaa caca 24

<210> 801

<211> 8

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<220>

<223> Synthetic

<400> 801

Ile Ser Ala Tyr Asp Gly Asn Thr
1 5

<210> 802

<211> 36

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<213> Artificial Sequence

<220>

<223> Synthetic

<400> 802

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<220>

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<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>

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<400> 804

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 cctggccagg ctcccagact cctcalctat ggtgcattcca acagggcac tggcatcca 180
 gacaggtlca ctggcaglgg gtctgggaca gacttcactc tcaccatcag cagaactggag 240
 cctgaagatt ttgcaglga ttctgtcaa cagtctgctt lctaacogtg gacgllggc 300
 caggggacca aggtggaal 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

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<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
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9

<210> 809
<211> 3
<212> PRT
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<220>
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<400> 809
Gly Ala Ser
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<210> 810
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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<400> 810
caacagctg ctctcacc gggacg

27

<210> 811
<211> 9
<212> PRT
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<220>
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<400> 811
Gln Gln Ser Ala Phe Ser Pro Trp Thr
1 5

<210> 812
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
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<400> 812
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tctgtcag cctctggagt cacctggal gattalgcca tgcactgggt ccggcaagct 120
ccagggaagg gctggagtg ggtctcaagt attagttgga atagtgtag talaggctat 180
gcgacictg tgaagggccg ctccaccatc tccagagaca acgccaagaa ctccolgtat 240

ctgcaaalga acagtcigag agctgaggac acggccctgt attactlggc aaaagatggg 300
tggaaaccogt aclacttga ctallggggc cagggaaalac cggtcaccgl ctctca 357

<210> 813
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
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<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>
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<400> 814
ggagtcacct tggatgalla 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
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<220>
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<400> 816
attagtggg atagtggtag tala

24

<210> 817
<211> 8
<212> PRT
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<220>
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<400> 817
Ile Ser Trp Asn Ser Gly Ser Ile
1 5

<210> 818
<211> 36
<212> DNA
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<220>
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<400> 818
gcaaaagatg ggggaaacc gactacttt gactat 36

<210> 819
<211> 12
<212> PRT
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<220>
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<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
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atcactgcc gggcaagtc gggcallaga aglgattag gctgglatca gcagaaacca 120
gggaaagccc claagocct gatlatgct gcalccagtt tcaaaagtg gglcccatca 180
agglicagcg gcagtgyalc tgggacagaa ttcacitca caalcagcag cctgcagcct 240
gaagatttg caacctata ctgtclacag calaatagtt accctctac ttccggcgga 300
gggaccaagc tggagalcaa a 321

<210> 821
<211> 107
<212> PRT
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<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>
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<400> 825
Ala Ala Ser
1

<210> 826
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 826
ctacagcata alagttaccc tctcaact 27

<210> 827
<211> 9
<212> PRT
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<220>
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<400> 827
Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 828
<211> 357
<212> DNA
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<400> 828
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acctgcgctg tclctggtga ctccitcagc agtgglaatt aclactggag ctggatccgc 120
caacaccocag ggaaggccct ggagtggaat gggtagatca aglacacagg gagcaacctac 180
lacaaccogt ccltcaagag tggagtlacc atattagtag acacgclaa gaccacagtc 240
tccctgaagc tgagcctgt gactgcgcgc gacacggccg tglattactg tgcgagagca 300
ccltgaactc alglttttga tgtctggggc caagggacaa tggcaccgt ccltca 357

<210> 829
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
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<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
 ggtgactoct lcagcagigg laattactac 30

<210> 831
 <211> 10
 <212> PRT
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<220>
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<400> 831
 Gly Asp Ser Phe Ser Ser Gly Asn Tyr Tyr
 1 5 10

<210> 832
 <211> 21
 <212> DNA
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<220>
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<400> 832
 alcaagtaca ctgggagcac c 21

<210> 833
 <211> 6
 <212> PRT
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<220>
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<400> 833
 Lys Tyr Thr Gly Ser Thr
 1 5

<210> 834
<211> 33
<212> DNA
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<220>
<223> Synthetic

<400> 834
gcgagagcac clggaacica tgttttgat 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>
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<400> 836
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cctcctcgca gggccagica gagtgtagc agtagclatt tagcctggla ccagcagaaa 120
ccggccagg ctcocagget cctcaictal gglgcalcca gcagggccac tggcatocca 180
gacaggtca gggcagtg gclclgaca gacitcacc tcaccatcag cagccolggag 240
cctgaagatt ttgcaglgta ttacigtacag caglatagta ggicaocgal cacctcggc 300
caagggacca agglggagat caaa 324

<210> 837
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
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<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

Ile Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 85 90 95
 100 105

<210> 838
<211> 21
<212> DNA
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<220>
<223> Synthetic

<400> 838
cagagtgta gcagtagcta l 21

<210> 839
<211> 7
<212> PRT
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<220>
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<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
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<210> 842
<211> 27
<212> DNA
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<220>
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<400> 842
cagcagata gtaggtcaac galcaac

27

<210> 843
<211> 9
<212> PRT
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<220>
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<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
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accgcaactg lctctgggg ctccatcagc aglgggggtt aclactggag ttggatccgc 120
cagcaccag ggaagggcct ggagtgall gggtaclcc attatagtg gaacaccac 180
tacaatccga cctcaagag tgaatlacc atalcagtag acacgclaa gaaccagllc 240
tccctgagg lgaactctg gacgcccgc gacacggccg tataclactg tgcgaggaal 300
alggllcggg gaggllcactg gttcgacccc tggggccagg gaaccacggt caccgtclcc 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
ggggctcca tcagcaglgg tggtaclac 30

<210> 847
<211> 10
<212> PRT
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<220>
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<400> 847
Gly Gly Ser Ile Ser Ser Gly Gly Tyr Tyr
1 5 10

<210> 848
<211> 21
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<220>
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<400> 848
atccattala ggggaacac c 21

<210> 849
<211> 7
<212> PRT
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<220>
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<400> 849
Ile His Tyr Ser Gly Asn Thr
1 5

<210> 850
<211> 39
<212> DNA
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<220>
<223> Synthetic

<400> 850
gcgaggaata tggltcgggg agltcactgg llcgacccc 39

<210> 851
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<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

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ctctctgtt gggccagtc gagtgtagc agcagclact tagcctgga ccagcagaaa 120
cctggccagg ctcccaggct cctcclctt ggtgcacca gcagggccac tggcaccaca 180
gacaggtca gtggcagtg gtcgggaca gactcactc lcaccalcag cagactggag 240
cctgaagatt ttgcagata ttctgcaa cagtataga gtcaccgct cacttlogc 300
ggaggacca agctggagal 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

cggaglgta gcagcagcla c

21

235

<210> 855
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<212> PRT
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<220>
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<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
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<220>
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<400> 858
caacaglala glagtcacc gctcacl 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 cllcacagac colgtcccic 60
accTgcactg tctctagTga ctccalcagc agTggTlaata actactggac ctggalccc 120
cagcaccagcag ggaggggcccl ggagTggalt gggtacatca aalacacTgg gagcggccac 180
tacaaccogt cccTcaagag TcgagTcacc algtcagTtag acacgtctaa gaalccagTtc 240
tcctTgaaaa TgaccTctgt gactgaocgc gacacggccg Tgtattattg Tcgaggggca 300
ccTggaagcc attctTllTga talatggggc cgaggggacaa TggTcaccgt cTctca 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 Talaactac 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

atcaaalaca clgggagcgc 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 clggaagcca ttctttgat ala 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

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cctggccagg ccccaggct cctcalclat ggtgcatcca gcagggccac tggcatcca 180
gacaggtca gtggcagtgg gctgaggaca gacttactc tcaacatcag cagactggag 240
cctgaagatt ttgactgta ttactgtag cagtalagta ggtcaccgat caacttcggc 300
caaggacac gactggagal 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

cagagtgta 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>
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<400> 872
ggtgcatcc 9

<210> 873
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
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<400> 873
Gly Ala Ser
1

<210> 874
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 874
cagcaglala 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
cagggtcagc tggtcagtc tgggggaggc ttggtacaac ctgggggggc cctaagactc 60
tcctgagcag cctctggait cactctaac aacttgcca tgacctgggt cggccaggct 120
ccaggggaagg gcctggagtg ggtctcaact attagtgga glggcgltga cacalactgc 180
gcagactcog tgaagggcgg gtlcaccalc tccagagaca altccaagaa cacactgtat 240
ctgcaaatga acagcctgag agtcgaggac acggccgtat attactgtc laaagalggc 300
gcctctata glggctacga acactactgg ggccagggaa ccttggcac cgtctctca 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
ggattcaacct caacaact lgcc 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
atlagtgga gtggcgtga 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
gctaaagalg gcgcctcta tagtggtac 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
galgtgtga tgaccagtc tccaggcacc ctgctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtc gagtgtagc agcagctact tagcctggta ccagcagaaa 120
ccggccagg ctccaggct cctcatctat ggtacatcca acagggcctc lggcatocca 180
gacaagtca ttggcaglg gctcgggaca gactcactc tcaccatcag cagactggag 240
ctgaagat ttgcagtga ttactgcag caglatgga gctcactcg gacgttcggc 300
caagggacca aagtgatc caaa 324

<210> 885
<211> 108
<212> PRT
<213> Artificial Sequence

<223> Synthetic

<400> 889
Gly Thr Ser
1

<210> 890
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 890
cagcagtatg gtagctcacc tgggacg 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
accatgcaacg tctccggcgg cccatcggc tccggcggt actactggc ctggalccgg 120
cagcaccocg gcaagggcct ggagtggalc ggclacgic actactccgg caacacctac 180
tacaaccccl cctgaagtc cgggtgacc atcctcggg acacclocaa gaaccagtc 240
tccctgaagc tglccicgl gaccgcggcc gacaccgcg tglactacg cggccgggccc 300
ccccggggt accactactl cgcctacgg ggcaggcca cctggtagc cgtglccccc 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

244

<223> Synthetic

<400> 896

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cagglgcagc tggtagagtc cggcggcggc ggggagcagc cgggcgggc cclggggctg 60
tctgcgocg cclccggctt caccttclcc tclacggca tgcactgggl gggcaggcc 120
cccgcaagg gccggagtg gggggccgtg clgggtagc acggcaccac caagtactac 180
ggcgactcgg tgaaggccg gllcaccatc lccggggaca actccaagaa caccclgtac 240
ctgcagatga acclccctgcg ggccgaggac accgcogtgt actclgcgc ccgggaccac 300
gactlccgtt ccggctacga gggctgggtc gacccctggg gccagggcac cctggtgacc 360
glglcclcc                                     369

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<210> 897

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 897

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

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<210> 898

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 898

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gagalogtgc lgaccagtc cccggccacc ctglccctgl cccccggcga gggggcacc 60
clgtctgcc gggcclcca gtcgltgc tctacctgg cclggtagca gcagaagccc 120
ggccaggccc ccggctgtct galctacgac gctccaacc gggccaccgg calccccgc 180
cggitctccg gctcggctc cggcaccgac taccctga ccalclctc cclggagccc 240
gaggacttcg ccglglacla clgcagcac cggccaact ggccccccac ctccggcggc 300
ggcaccaagg tggagatcaa g                                     321

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<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

cagglgcagc tggaggaglc tgggggagge gggglocagc ctgggaggtc colgagaclc 60
tctgtgcag cglctggatt caccttcagt agttalggca tgcactgggt cggccaggcl 120
ccaggcaagg ggcctggaglg ggtgtcaitt ttatgglaig atggaactaa taaaaactat 180
glagagtcog tgaagggccg atccaccalc tcaagagaca attccaagaa tatgctgtat 240
clggaaatga acagocctag agccgaggac accggctgtgl attactgtgc gagagatcac 300
gattttagga glgglalga ggggltgltc gacccctggg gccagggaaac cctggtcacc 360
glctccca 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
gaaatagtg igacacagtc tccagccacc ctgctttgt ctccagggga aagagccacc 60
ctctctgca gggccaglca gaglgtagc agctacttag cclggtagca acagaaaccl 120
ggccaggctc ccaggctcct calclatgat gcalccaaca gggccacigc calcccagcc 180
aggltcagtg gcaglgggtc lgggacagac ttcactctca ccatcagcag cclagagccl 240
gaagalltg cagittatta ctgtcaaacac cgtagcaact ggctcccac ttccggcgga 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
cagggtcagc lgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60
acctgcactg tclctgggtg ctccalcagc agtgggtggt aclactggag lggatccgc 120
cagcaccagc ggaagggccl ggagtggalt ggglacalcc attalagtgg gaacaccac 180
tacaatccga cctcaagag lcaaltacc atatcagtag acacglclaa gaaccagtc 240
tccttgagg tgaactcgt gactgccgog gacacggcog talactacig tgcgaggaal 300
algggtcggg gagtccactg gllcgacccc lggggccagg gaaccacggt caccglclcc 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 tcaaggcacc ctgctttgt ctccagggga gagagccacc 60
ctcttcigt gggccagtcg gagtgtagc agcagctact tagccggta ccagcagaaa 120
ccggccagg ctccaggct cctcatctt gglgcalcca gcagggccac tggcalcca 180
gacaggttca gggcagtgg gtcgggaca gacttcac tcaccalcag cagactggag 240
cctgaagatt ttgcagala ttctgcaa cagtatagta gttaccgct cactttggc 300
ggagggacca agcggagal 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
caggtagcagc tgcaggagtc cggccccggc ctggtgaagc cclcccagac cclgtccctg 60
acctgcaccg tglccggcgg clccalcctc tccggcggct actactggtc ctggatccgg 120
cagcaccctcg gcaagggcct ggagtggaic ggclacatcc actactccgg caacacctac 180
tacaaccctc cctgaagtc cgggtgacc atccctggg acacctccaa gaaccagtic 240
tccctgaagc lgtctccgt gaccgccgc gacaccgcg tglactactg cggccggaac 300
algglgcggg gctgcactg gttegacccc lggggccagg gcacctggt gaccgtgccc 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 igaccacgic ccccgccacc ctglccclgt ccccgggga gggggccacc 60
ctglccctgc gggcctcccg gtcctgtccc tctcctacc lggcctggta ccagcagaag 120
cccggccagg cccccggct gctgalctac ggccctctc cccgggccac cggcatcccc 180

gacgggtlcl ccggctccgg ctccggcacc gactcacc tgaccatctc ccggclggag 240
cccgaggact lcgccgtgta ctacigccag cagtaclcll cctcccccl gaccltggc 300
ggggccacca agglggagat 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
cagggtcagc lgcaggagtc gggcclagga ctggtgaagc cttcacagac cctglccctc 60
acctgcactg lctctgggg etccalcagc agtgggtggt aclaclggag ttggalccgc 120
cagcaccocag ggaagggccl ggaglggalt ggglacalcc attalaglgg gaacaccocac 180
lacaalccga ccccaagag lcgaaftacc alalcaglag acacgtctaa gaaccagtic 240
lccctlgagg tgaacclgt gactgcocgc gacaogocg lataclactg lgcgaggaal 300
atggttggg gagltcactg gttcgacccc lggggccagg gaaccclggt cacogtctcc 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
 gaaalaglgf tgacacagtc tccaggcacc ctglcttltgl ctccagggga gagagccacc 60
 ctctctgtt gggccaglog gagtgttagc agcagctact lagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatctct gglgcalcca gcagggccac tggcalcca 180
 gacaggitca gtggcaglgg gtcgggaca gaettcactc tcaccalcag cagactggag 240
 cctgaagat tgcagata ttctgtcaa caglatagla gtcaccgct cacttggc 300
 ggaggacca agglgaaat 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> 367
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 916

cagglgcagc lgcaggaglc cggccccggc ctggggaagc cclcccagac cctglccctg 60
acctgcaccg tctccggcgg ccccatcacc lccggcggct actactggc ctggatccgg 120
cagcaccocg gcaagggccl ggaggggac ggctacatca agtctccgg caacacclac 180
lacaacccl cctgaagtc ccgggtgacc atctccggg acaccfcaa gaaccagtc 240
lccctgaagc tgtctccgt gaccgcggc gacaccgocg lgtactactg cggccggcc 300
cccggclccc acaacticga catctggggc cagggcacca lggtagccgt gtcclcc 357

<210> 917

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 917

Gln Val Gln Leu 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 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

gagatcgtc lgcaccagtc ccccgccacc ctglccctgt cccccggcga gcgggccacc 60
ctgtctgcc gggccctcgt gcccactcc aacaactacc lggccggta ccagcagaag 120
cccggccagg cccccggcl gctgalctac ggccclctt cccgggccac cggcatccc 180
gaccgllcl ccggctccgg ctccggcacc gactcaccc tgaccalccg gggcgggag 240
ccgaggact lggccccla ctactgccag cagtactccc ggcccccal cactcggc 300
cagggcacc ggctgggat 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
 gagglgcagc tggtagagtc cggcgggggc ctggtgcagc ccggcgggctc cctgcggctg 60
 lccctgcgcc cctcgggctt cacctcaac aactlogcca tgcctgggt gggcagggcc 120
 ccggcaagg gctggagtg ggtgccc acccggct ccggcgigga cacclactac 180
 gccgactccg tgaagggccg gttcaccatc tccgggaca actccaagaa caccctglac 240
 ctgcagalga actccctgcg ggccgaggac accgccglg actactgctc caaggacggc 300
 gcctctact ccggctacga gcaclacigg ggccagggca ccttggtagc cgtgctctcc 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
gagatcglgc lgaoccagtc ccccggcacc ctgtccctgl cccccggcga gggggccacc 60
ctglcctgcc gggcctccca glccgtgtcc tctctctacc tggcctggta ccagcagaag 120
cccggccagg cccccggct gctgacttac ggcacclct cccgggccac cggcatccc 180
gaccggttct ccggctcgg ctccggcacc gacttcacc lgaccatct ccggtggag 240
cccaggact tgcctglgla ctactgccag cagtacggct cctcccccg gaccttggc 300
cagggcacca aglggagat 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
cagglgcagc tggcgcagtc cggcgcagag glgaagaagc cgggcgcctc cglgaaggcg 60
tctgcaagg cctcggcta cacttcacc taclacggca tctctgggl gggcaggcc 120
cccggccagg gactggagtg gatggctgg atctcggct acgacggcaa caccaactac 180
gcccagaagc tgcagggccg ggigaccatg accaccgaca cctccacctc caccgcctac 240
atggagctgc gglccctgag gtcgacagac accgccgtgt actactgcgc cggctactcc 300
tgaacaagc actggctgga cccctggggc cagggcacc tggtagccgt glcctcc 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 lgaccacagtc ccccggcacc ctgtccctgt cccccggaga gggggcacc 60
clglcctgcc ggccctccca gtcctgacc ggctcclacc tggcctgga ccagcagaag 120
ccggccagg cccccggct gctgalctac ggccctct cccgggccac cggcatccc 180
gaccggtcl ccgctccgg ctccggcacc gactcacc tgaccalc cggctggag 240
ccgaggact lcgccglga ctactgccag caglcgcct lctccccctg gacttggc 300
cagggcacca agtggagat 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
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

cagglgcagc lgcaggagc gggcccagga ctggggaagc cllcacagac cctgtccctc 60
accgtcaclg tcctgggag cccattacc agtgggggtt aciaclggac ctggalccgc 120
cagcaccacag ggaagggccl ggaatggatt ggalacalca aatttaglgg gaacacctac 180
lacaaccogt cctcaggag tggagtcacc atalcactlg acaccgictaa gaatcagttc 240

tcctgaata tgacctcigt gactgccgcg gacacggccg tglattatg tgcgagagca 300
cctggaagtc alaacttga cactcggggc caagggacaa tggcaccgt ctctca 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
gaaatogtgt tgaccagtc tcagacacc cigtcttgt cccagggga aagagccacc 60
ctcctcga gggccagtg gactatagt aataaclat tagcctggta ccagcagaaa 120
cclggccagg ccccaggct cctcactat ggtgcaccca gcagggccac tggcaccoca 180
gacaggttca gtggcagtgg giclgggaca gactcactc tcaccatcag aagactggag 240
ctgcagatt ttgcaccgta ttaclgtcag caatatagta ggcaccgat caactcggc 300
caagggacac gactggagal 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 lgggggagtc tgggggagcc ttggtacaac cgggggggtc cclgagactc 60
 lccclgicag cctctggatt caccttlaac aactttgoca tgacctgggt cggccaggct 120
 ccaggaagg gactggagtg ggtctcaact attagtgga gtggcgtga cacalactgc 180
 gcagactcog lgaagggccg gttcaccalc tccagagaca attccaagaa cacactglat 240
 clgcaaalga acagcclgag agccgaggac acggccglal attactgttc gaaagalggc 300
 gccttctafa gggclacga acactactgg ggccaggga ccttggtcac cglctctca 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

gaaattgigc tcaagcagtc tccagggcaac ctgictttgt ciccagggga aagagccacc 60
ctcctctgca gggccagtc gagtgtagc agcagctact tagcctggta ccagcagaaa 120
cclggccagg ccccaggcl cctcatctat gglacalcca acagggccac tggcatocca 180
gacaggttca gggcaglgg gctgggaca gactcactc tcaccalcaq cagactggag 240
ctgaagatt tgcaglgta ttactlcaq caglalggta gctcacctcg gacgtloggc 300
caagggacca agglggagal 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 tgggtcagtc tggacctgag gtaagaagc clggggcctc agtgaagtc 60
lctgcaagg ctctgglla caccttacc tactalggla tcagttggal acgacagacc 120
cctggacaag ggctgagtg gatgggatgg atcagcgctt acgatgglaa cacagactat 180
gcacagaagt lccaagacag aatcaccalg accacagaca catcclogac cacagcctac 240
atggaactga ggagcclgag atctgaagac aaggccgtct attactgigc gagglatagi 300
tgaacaagc actggttoga cccclggggc cagggaaacc tggtcaccgt cictca 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

<220>

<223> Synthetic

<400> 946

caggtagcagt tgcaggagtc gggcccagga ctggtagaagc cticacagac cctgtccctc 60
acctgcactg tctctggggc ctccatcggc agtgggtggt actactggag ctggatccgc 120
cagcaccag ggaagggccl ggagtggtt gggtagctcc attacagtg gaacaccac 180
tacaaccgcl ccccaagag tgcacttcc atatcaatag acacgtctaa galccagttc 240
lccctgaagc tgagctcgt gactgccgcg gacacggccg lglattactg tgcgagagcc 300
ccccgggal accattactl tgcclactgg ggcagggaa cctgtgtcac cgtctctca 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

gaaatgtgt tgacacaatc tccaggcaac ctgtcttgtl cccagggga aagagccacc 60
ctctctgca gggccagtca gagtgttagc agcagctact tagccttgta ccagcagaaa 120
cctggccagg clcccaggcl cctcalctt ggtagatcca gcagggccac tggcatcca 180
gacaggitca gtggcagtg gctgggaca gacttcaatc tcaccalcag cagactggag 240
cclgaagalt ttgcagtgta ttaactgac caglatggta gctcacogcr caclitggc 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 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 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 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
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 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
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 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 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

270

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 (hDII4), 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 (hDII4), 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 (hDII4), 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 (hDII4), 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.