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MORIN et al.

(54) **PET IMAGING WITH PD-L1 BINDING POLYPEPTIDES**

(71) Applicant: **BRISTOL-MYERS SQUIBB COMPANY**, Princeton, NJ (US)

(72) Inventors: **Paul E. MORIN**, Pennington, NJ (US); **David DONNELLY**, Doylestown, PA (US); **Dasa LIPOVSEK**, Pepperell, MA (US); **Jochem GOKEMEIJER**, Wayland, MA (US); **Maria N. JURE-KUNKEL**, Plainsboro, NJ (US); **David FABRIZIO**, South Hamilton, MA (US); **Martin C. WRIGHT**, Belmont, MA (US); **Douglas DISCHINO**, Middlefield, CT (US); **Samuel J. BONACORSI, Jr.**, Flemington, NJ (US); **Ralph Adam SMITH**, Yardley, PA (US); **Virginie LAFONT**, Lawrence Township, NJ (US); **Daniel COHEN**, New York, NY (US); **David K. LEUNG**, West Windsor, NJ (US)

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(60) Provisional application No. 62/344,258, filed on Jun. 1, 2016.

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C07K 16/28	(2006.01)

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

CPC ***A61K 51/088*** (2013.01); ***C07B 59/00*** (2013.01); ***C07K 16/2818*** (2013.01)

(57) **ABSTRACT**

Provided herein are novel ^{10}Fn3 domains which specifically bind to PD-L1, as well as imaging agents based on the same for diagnostics.

Specification includes a Sequence Listing.

Core sequences

WT	VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVDYTITVYAVTGRGDSPASSKPISINYRT
ATI-963	VSDVPRDLEVVAATPTSLLISWIAFFYNVIYYRITYGETGGNSPVQEFTVPGTGYTATISGLKPGVDYTITVYAVTDGASIASYAFPISINYRT
ATI-964	VSDVPRDLEVVAATPTSLLISWSYDGSIERYYRITYGETGGNSPVQEFTVPPDQKTATISGLKPGVDYTITVYAVRLEEAHYYRESPISINYRT
ATI-967	VSDVPRDLEVVAATPTSLLISWQGQLSPSFYYRITYGETGGNSPVQEFTVPVASGTATISGLKPGVDYTITVYAVTSHGIYFYAPISINYRT
A02	VSDVPRDLEVVAATPTSLLISWSYDGPIDRYYRITYGETGGNSPVQEFTVPPDQKTATISGLKPGVDYTITVYAVRLEEAHYNREFPISINYRT
E01	VSDVPRDLEVVAATPTSLLISWRAQLSPSFYYRITYGETGGNSPVQEFTVPNDVMTATISGLKPGVDYTITVYAVTTHGVYFYSPISINYRT
ATI-965	VSDVPRDLEVVAATPTSLLISWTAYDSVDKYYRITYGETGGNSPVQEFTVGPRHHTATISGLKPGVDYTITVYAVYHTEPGYHAHMPISINYRT
ATI-966	VSDVPRDLEVVAATPTSLLISWHRFSSIMAYYRITYGETGGNSPVQEFTVAGSVNTATISGLKPGVDYTITVYAVTIHNVSFPISINYRT

Figure 1

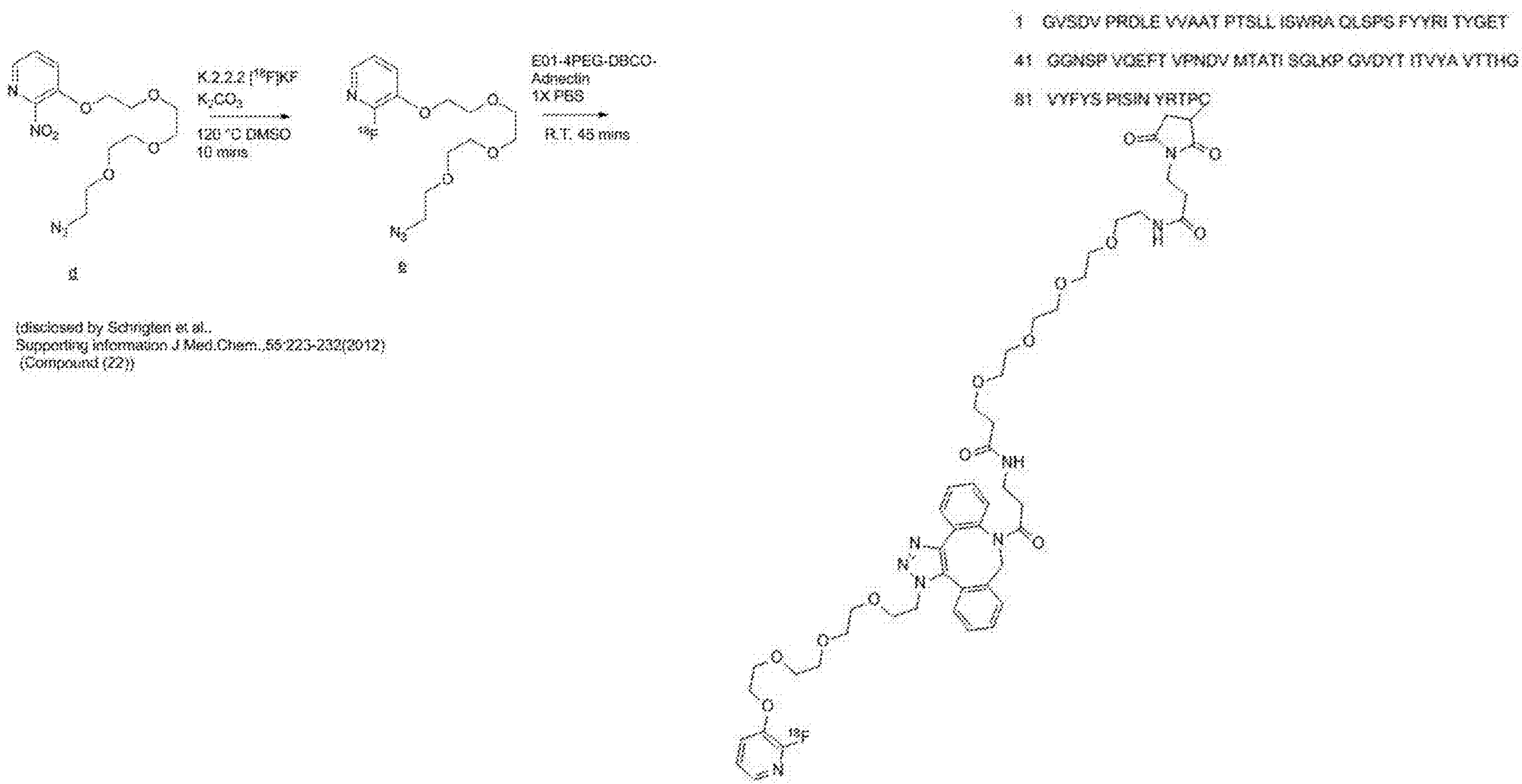

K.2.2.2 [18F]KF
K2CO3
120 °C DMSO
10 mins
E01-4PEG-DBCO-
Adnectin
1X PBS
R.T. 45 mins
d
e
(disclosed by Schrigten et al.,
Supporting information J Med.Chem.,55:223-232(2012)
(Compound (22))
1 GVSDV PRDLE VVAAT PTSLL ISWRA QLSPS FYYRI TYGET
41 GGNSP VQEFT VPNDV MTATI SGLKP GVDYT ITVYA VTTHG
81 VYFYS PISIN YRTPC

Figure 2

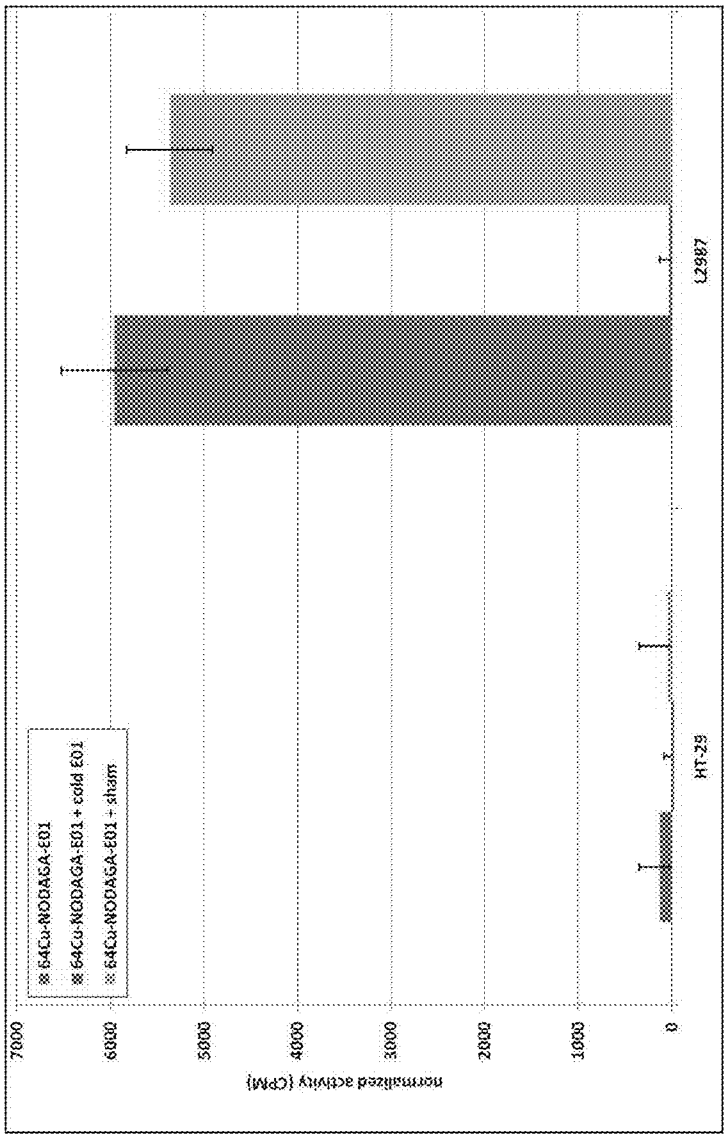

64Cu-NODAGA-E01
64Cu-NODAGA-E01 + cold E01
64Cu-NODAGA-E01 + sham
normalized activity (CPM)
7000
6000
5000
4000
3000
2000
1000
0
HT-29
L2987

Figure 3

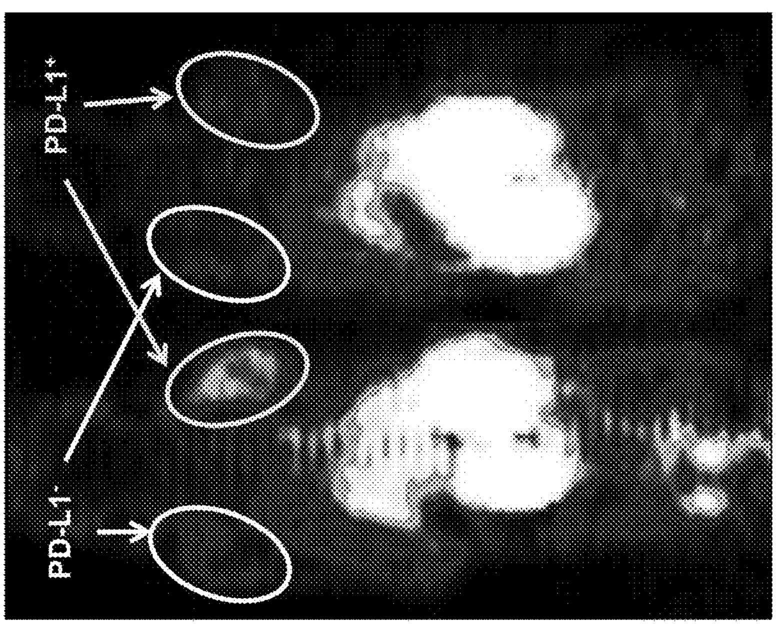


Figure 4A

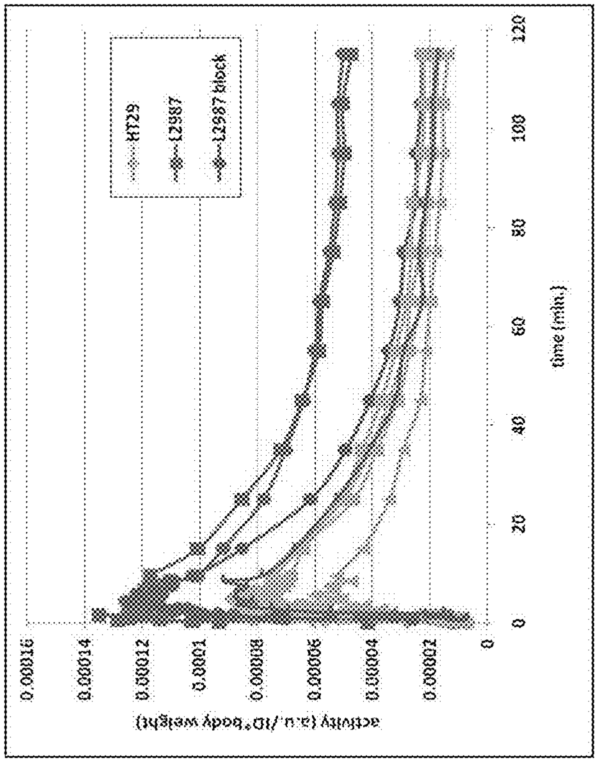


Figure 4B

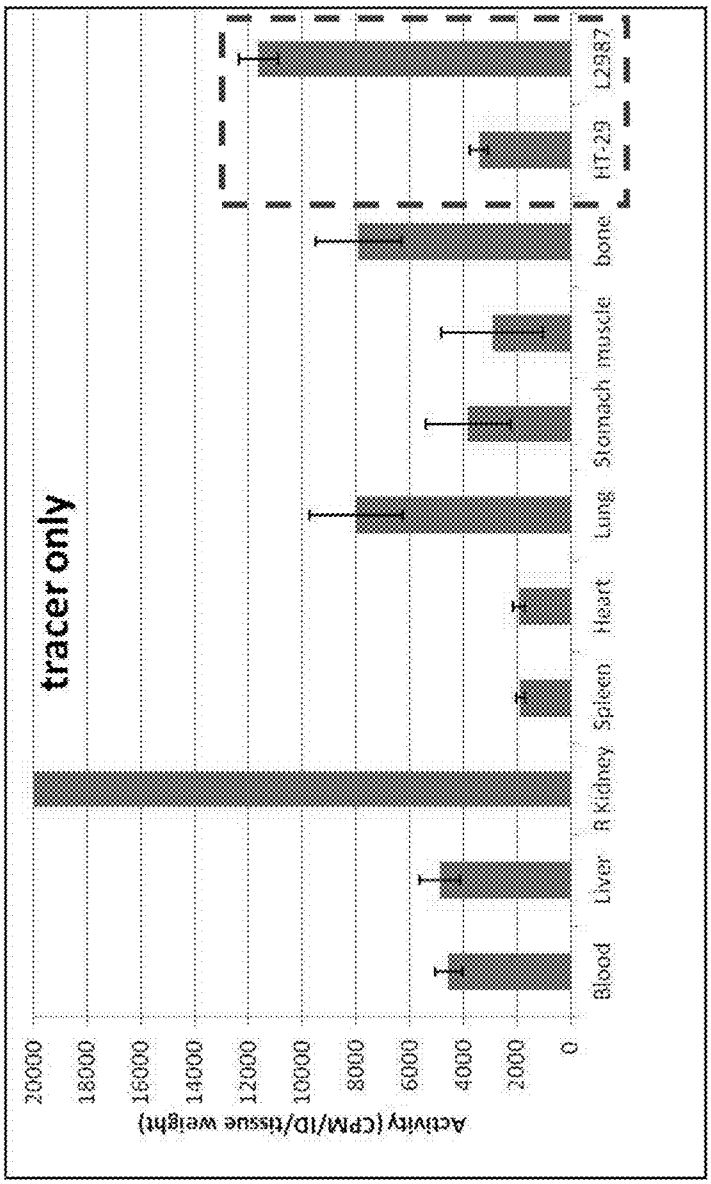

tracer only
Activity (CPM/ID/tissue weight)
20000
18000
16000
14000
12000
10000
8000
6000
4000
2000
0
Blood
Liver
R Kidney
Spleen
Heart
Lung
Stomach
muscle
bone
HT-29
L2987

Figure 5

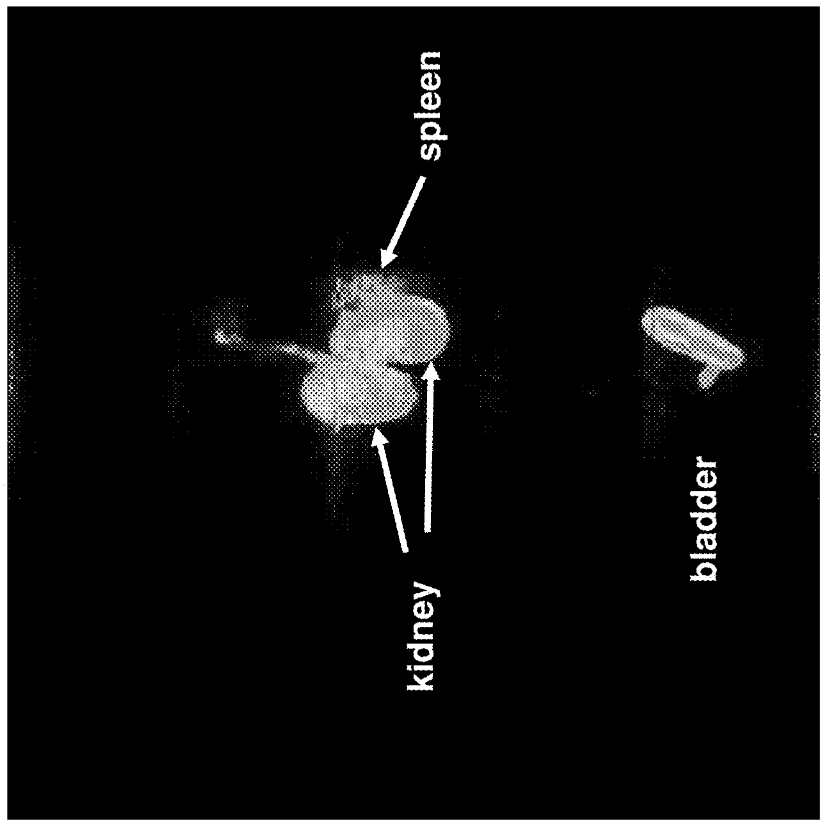
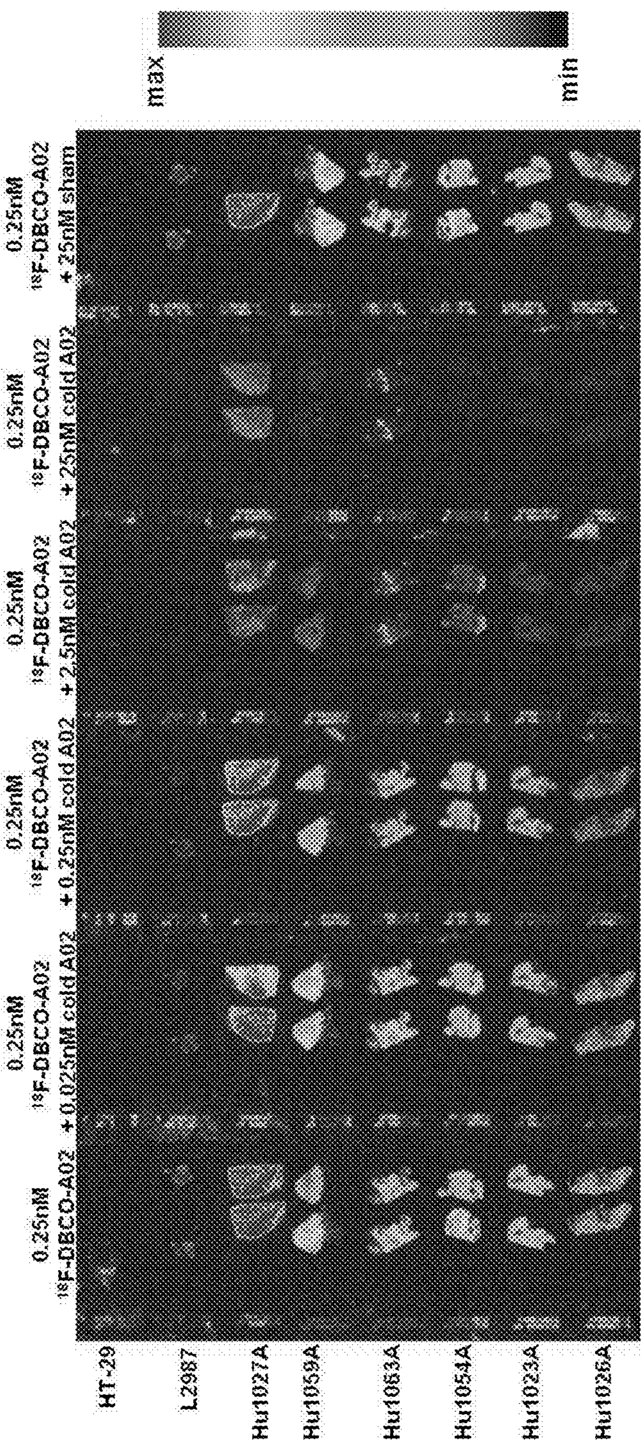


Figure 6



max
min
0.25nM
^{18}F-DBCO-A02
0.25nM
^{18}F-DBCO-A02
+ 0.025nM cold A02
0.25nM
^{18}F-DBCO-A02
+ 0.25nM cold A02
0.25nM
^{18}F-DBCO-A02
+ 2.5nM cold A02
0.25nM
^{18}F-DBCO-A02
+ 25nM cold A02
0.25nM
^{18}F-DBCO-A02
+ 25nM sham
HT-29
L2987
Hu1027A
Hu1059A
Hu1063A
Hu1054A
Hu1023A
Hu1026A

Figure 7

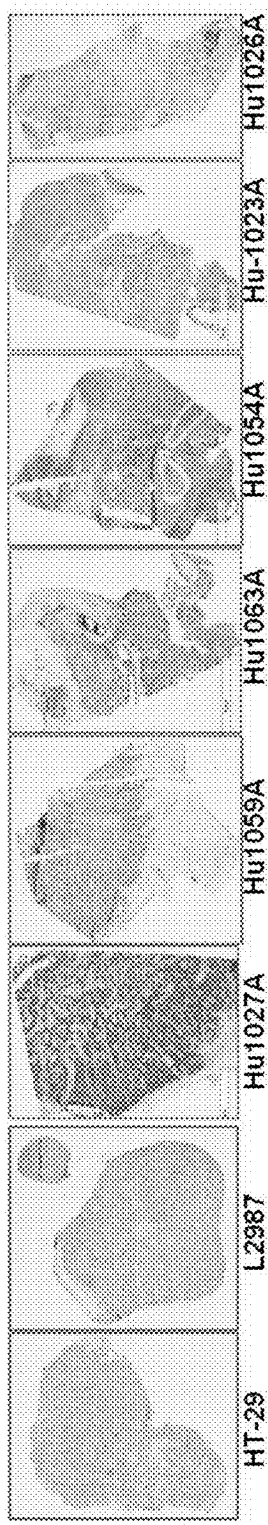

HT-29
L2987
Hu1027A
Hu1059A
Hu1063A
Hu1054A
Hu-1023A
Hu1026A

Figure 8

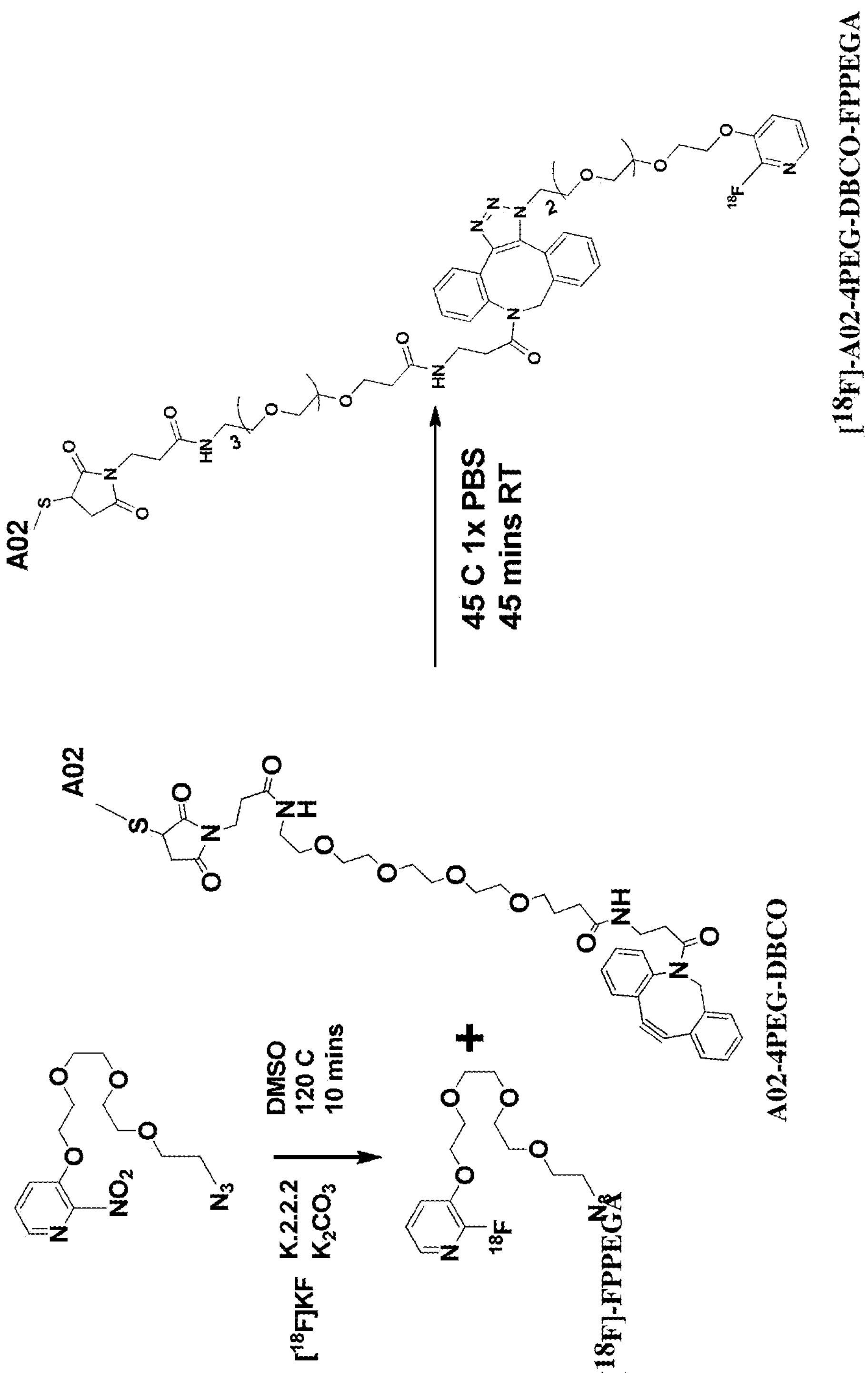

[18F]KF
K.2.2.2
K2CO3
DMSO
120 C
10 mins
[18F]-FPPEGA
A02-4PEG-DBCO
45 C 1x PBS
45 mins RT
[18F]-A02-4PEG-DBCO-FPPEGA

Figure 9

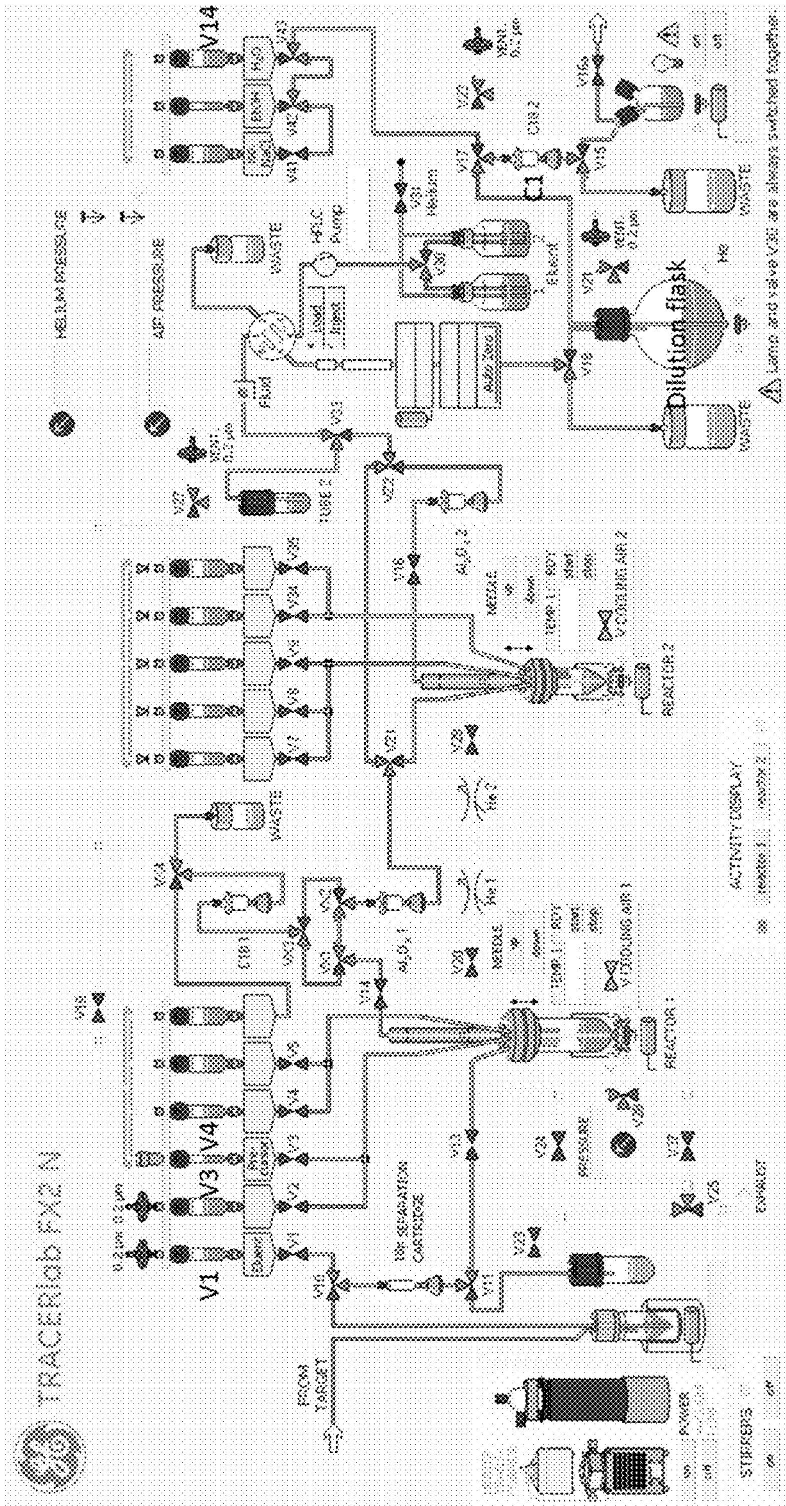

TRACERlab FX2 N
V1
V3
V4
V14
Dilution flask
WASTE
REACTOR 1
REACTOR 2

Figure 10

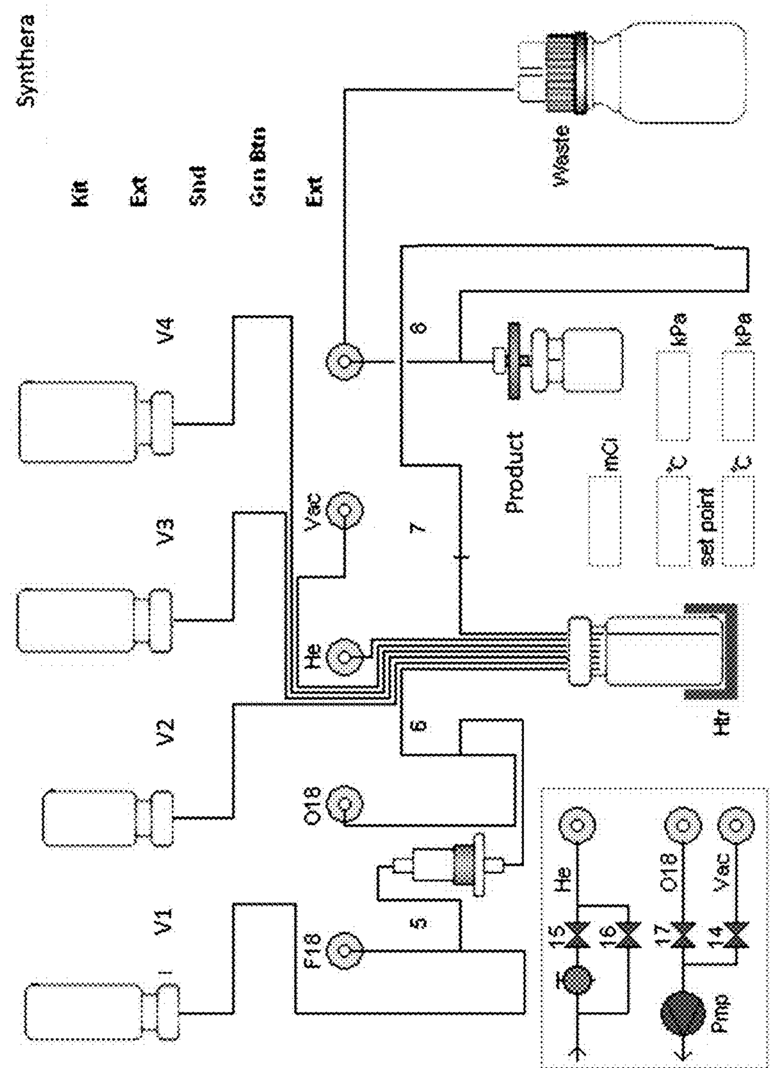

Synthera
Kit
Ext
Snd
Grn Btn
Ext
V1
V2
V3
V4
F18
O18
He
Vac
5
6
7
8
Waste
Product
mCi
°C
°C
set point
kPa
kPa
Htr
He
O18
Vac
15
16
17
14
Pmp

Figure 11

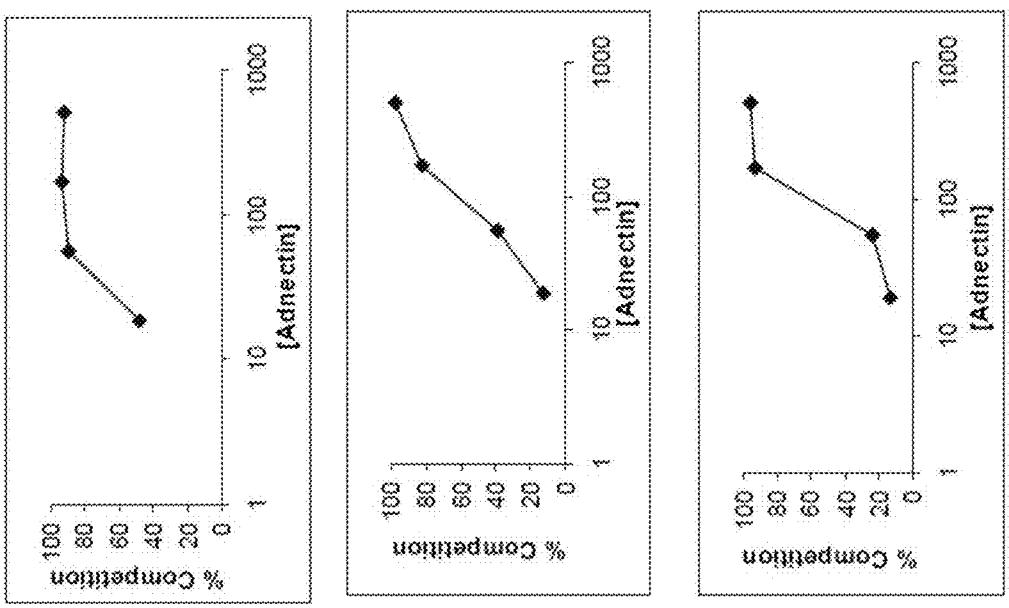


Figure 12

PET IMAGING WITH PD-L1 BINDING POLYPEPTIDES

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application is a divisional of U.S. patent application Ser. No. 16/305,284, filed Nov. 28, 2018, which is a 35 U.S.C. 371 national stage filing of International Application No. PCT/US2017/035227, filed May 31, 2017, which claims priority to U.S. Provisional Application No. 62/344,258, filed Jun. 1, 2016. The contents of the aforementioned applications are hereby incorporated by reference.

SEQUENCE LISTING

[0002] The instant application contains a Sequence Listing which has been submitted via EFS-Web and is hereby incorporated by reference in its entirety. Said ASCII copy, created on Apr. 2, 2022, is named Sequence_Listing_MXI_549USDV.txt and is 457,797 bytes in size.

BACKGROUND

[0003] Programmed Death Ligand-1 (PD-L1) is a surface glycoprotein ligand for PD-1, a key immune checkpoint receptor expressed by activated T and B cells and mediates immunosuppression, which is found on both antigen-presenting cells and human cancers and down regulates T cell activation and cytokine secretion by binding to PD-1 (Freeman et al., 2000; Latchman et al, 2001). Inhibition of the PD-L1/PD-1 interaction allows for potent anti-tumor activity in preclinical models, and antibodies that disrupt this interaction have entered clinical trials for the treatment of cancer (U.S. Pat. Nos. 8,008,449 and 7,943,743; Brahmer et al., 2010; Topalian et al., 2012b; Brahmer et al., 2012; Flies et al., 2011; Pardoll, 2012; Hamid and Carvajal, 2013).

[0004] PET, or Positron Emission Tomography, is a non-invasive, nuclear medicine technique that produces a three-dimensional image of various molecular processes within the body, or the location of proteins associated with disease pathology. The methodology detects pairs of gamma rays emitted indirectly by a positron-emitting radionuclide (tracer) introduced into the body on a biologically active molecule. PET imaging tools have a wide variety of uses for drug development and have a unique translational medicine advantage, in that the same tool could be used both preclinically and clinically. Examples include direct visualization of in vivo saturation of targets; monitoring uptake in normal tissues to anticipate toxicity or patient to patient variation; quantifying diseased tissue; tumor metastasis; monitoring drug efficacy over time, or resistance over time, and more.

[0005] Described herein are novel anti-PD-L1 Adnectins suitable for use as diagnostic/imaging agents, for example, for use in positron emission tomography.

SUMMARY

[0006] The present invention is based, at least in part, on the discovery of new anti-human PD-L1 Adnectins which are useful as diagnostic/imaging agents, for example, for use in positron emission tomography, and its methods of administration to subjects. These agents are useful in, e.g., the differentiation of PD-L1 expressing cells from non-PD-L1 expressing cells, e.g., tumor cells or tumor infiltrating lymphocytes (TILs), and the differentiation of PD-L1 expressing tissue from non-PD-L1 expressing tissue, e.g., cancer tissue.

[0007] In one aspect, provided herein is a polypeptide comprising a fibronectin type III tenth domain (^{10}Fn3), wherein (a) the ^{10}Fn3 domain comprises AB, BC, CD, DE, EF, and FG loops, (b) the ^{10}Fn3 has at least one loop selected from loop BC, DE, and FG with an altered amino acid sequence relative to the sequence of the corresponding loop of the human ^{10}Fn3 domain (SEQ ID NO: 1), and (c) the polypeptide specifically binds to PD-L1. In certain embodiments, the polypeptide binds to PD-L1 with a K_D of 500 mM or less, for example, 100 mM or less.

[0008] In certain embodiments, the ^{10}Fn3 domain comprises BC, DE, and FG loops comprising the amino acid sequences of:

[0009] (1) SEQ ID NOs: 6, 7, and 8, respectively;

[0010] (2) SEQ ID NOs: 21, 22, and 23, respectively;

[0011] (3) SEQ ID NOs: 36, 37, and 38, respectively;

[0012] (4) SEQ ID NOs: 51, 52, and 53, respectively;

[0013] (5) SEQ ID NOs: 66, 67, and 68, respectively;

[0014] (6) SEQ ID NOs: 81, 82, and 83, respectively;

[0015] (7) SEQ ID NOs: 97, 98, and 99, respectively;

[0016] (8) SEQ ID NOs: 113, 114, and 115, respectively;

[0017] (9) SEQ ID NOs: 124, 125 and 126, respectively;

[0018] (10) SEQ ID NOs: 135, 136 and 137, respectively;

[0019] (11) SEQ ID NOs: 146, 147 and 148, respectively;

[0020] (12) SEQ ID NOs: 157, 158 and 159, respectively;

[0021] (13) SEQ ID NOs: 168, 169 and 170, respectively;

[0022] (14) SEQ ID NOs: 179, 180 and 181, respectively;

[0023] (15) SEQ ID NOs: 190, 191 and 192, respectively;

[0024] (16) SEQ ID NOs: 201, 202 and 203, respectively;

[0025] (17) SEQ ID NOs: 212, 213 and 214, respectively;

[0026] (18) SEQ ID NOs: 223, 224 and 225, respectively;

[0027] (19) SEQ ID NOs: 234, 235, and 236, respectively;
[0028] (20) SEQ ID NOs: 245, 246 and 247, respectively;
[0029] (21) SEQ ID NOs: 256, 257 and 258, respectively;
[0030] (22) SEQ ID NOs: 267, 268 and 269, respectively;
[0031] (23) SEQ ID NOs: 278, 279 and 280, respectively;
[0032] (24) SEQ ID NOs: 289, 290 and 291, respectively;
[0033] (25) SEQ ID NOs: 300, 301 and 302, respectively;
[0034] (26) SEQ ID NOs: 311, 312 and 313, respectively;
[0035] (27) SEQ ID NOs: 322, 323 and 324, respectively;
[0036] (28) SEQ ID NOs: 333, 334 and 335, respectively;
[0037] (29) SEQ ID NOs: 344, 345 and 346, respectively;
[0038] (30) SEQ ID NOs: 355, 356 and 357, respectively;
[0039] (31) SEQ ID NOs: 366, 367 and 368, respectively;
[0040] (32) SEQ ID NOs: 377, 378 and 379, respectively;
[0041] (33) SEQ ID NOs: 388, 389 and 390 respectively;
[0042] (34) SEQ ID NOs: 399, 400 and 401, respectively;
[0043] (35) SEQ ID NOs: 410, 411 and 412, respectively;
[0044] (36) SEQ ID NOs: 421, 422 and 423, respectively;
[0045] (37) SEQ ID NOs: 432, 433 and 434 respectively;
[0046] (38) SEQ ID NOs: 443, 444 and 445, respectively;
[0047] (39) SEQ ID NOs: 454, 455 and 456, respectively;
[0048] (40) SEQ ID NOs: 465, 466 and 467, respectively;
[0049] (41) SEQ ID NOs: 476, 477 and 478, respectively;
[0050] (42) SEQ ID NOs: 487, 488 and 489, respectively;
[0051] (43) SEQ ID NOs: 498, 499 and 500, respectively;
[0052] (44) SEQ ID NOs: 509, 510 and 511, respectively;
[0053] (45) SEQ ID NOs: 520, 521 and 522, respectively;
[0054] (46) SEQ ID NOs: 531, 530 and 531, respectively;
[0055] (47) SEQ ID NOs: 542, 543 and 544, respectively;
[0056] (48) SEQ ID NOs: 553, 554 and 555, respectively; or
[0057] (49) SEQ ID NOs: 564, 565 and 566, respectively.

[0058] In certain embodiments, the polypeptide comprises an amino acid sequence at least 80%, 85%, 90%, 95%, 98%, 99% or 100% identical to a sequence set forth in Table 3, e.g., any one of SEQ ID NO: 5, 20, 35, 50, 65, 80, 96, 112, 123, 134, 145, 156, 167, 178, 189, 200, 211, 222, 233, 244, 255, 266, 277, 288, 299, 310, 321, 332, 343, 354, 365, 376, 387, 398, 409, 420, 431, 442, 453, 464, 475, 486, 497, 508, 519, 530, 541, 552 and 563. In certain embodiments, the polypeptide comprises an amino acid sequence at least 80%, 85%, 90%, 95%, 98%, 99% or 100% identical to the non-BC, DE, and FG loop regions of SEQ ID NO: 5, 20, 35, 50, 65, 80, 96, 112, 123, 134, 145, 156, 167, 178, 189, 200, 211, 222, 233, 244, 255, 266, 277, 288, 299, 310, 321, 332, 343, 354, 365, 376, 387, 398, 409, 420, 431, 442, 453, 464, 475, 486, 497, 508, 519, 530, 541, 552 or 563. In certain embodiments, the polypeptide comprises an amino acid sequence at least 80%, 85%, 90%, 95%, 98%, 99% or 100% identical to an amino acid sequence selected from the group consisting of: SEQ ID NOs: 9-15, 24-30, 39-45, 54-60, 69-75, 84-91, 100-107, 116-122, 127-133, 138-144, 150-155, 160-166, 171-177, 182-188, 193-199, 204-210, 215-221, 227-232, 237-243, 248-254, 259-265, 271-276, 291-287, 292-298, 303-309, 314-320, 325-331, 337-342, 347-353, 358-364, 369-375, 380-386, 391-397, 402-408, 413-419, 424-430, 435-441, 446-452, 457-463, 468-474, 479-485, 490-496, 501-507, 512-518, 523-529, 534-540, 545-551, and 556-562. In certain embodiments, the polypeptide comprises an amino acid sequence at least 80%, 85%, 90%, 95%, 98%, 99% or 100% identical to the non-BC, DE, and FG loop regions of an amino acid sequence selected from the group consisting of: SEQ ID NOs: 9-15, 24-30, 39-45, 54-60, 69-75, 84-91, 100-107, 116-122, 127-133, 138-144, 150-155, 160-166, 171-177, 182-188, 193-199, 204-210, 215-221, 227-232, 237-243, 248-254, 259-265, 271-276, 291-287, 292-298, 303-309, 314-320, 325-331, 337-342, 347-353, 358-364, 369-375, 380-386, 391-397, 402-408, 413-419, 424-430, 435-441, 446-452, 457-463, 468-474, 479-485, 490-496, 501-507, 512-518, 523-529, 534-540, 545-551, and 556-562.

[0059] In certain embodiments, the polypeptide comprises an N-terminal leader selected from the group consisting of SEQ ID NOs: 574-583, and/or a C-terminal tail selected from the group consisting of SEQ ID NOs: 584-618 or PmCn, wherein P is proline, and wherein m is an integer that is at least 0 (e.g., 0, 1 or 2) and n is an integer of at least 1 (e.g., 1 or 2).

[0060] In certain embodiments, the polypeptide comprises one or more pharmacokinetic (PK) moieties selected from the group consisting of polyethylene glycol, sialic acid, Fc, Fc fragment, transferrin, serum albumin, a serum albumin binding protein, and a serum immunoglobulin binding protein. In certain embodiments, the PK moiety and the polypeptide are linked via at least one disulfide bond, a peptide bond, a polypeptide, a polymeric sugar or a polyethylene glycol moiety. In certain embodiments, the PK moiety and the polypeptide are linked via a linker with an amino acid sequence selected from the group consisting of SEQ ID NOs: 629-678.

[0061] Provided herein are nucleic acids encoding the polypeptides, as well as vectors and cells comprising the nucleic acids, described herein. In certain embodiments, the nucleic acid comprises a nucleotide sequence selected from the group consisting of SEQ ID NOs: 16-19, 31-34, 46-49, 61-64, 76-79, 92-95, and 108-111.

[0062] Provided herein are compositions comprising the polypeptides described herein, and a carrier. For example, the compositions described herein comprise a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 5, 9-15, 20, 24-30, 35, 39-45, 50, 54-60, 65, 69-75, 80, 84-91, 96, 100-107, 112, 116-122, 123, 127-133, 134, 138-144, 145, 150-155, 156, 160-166, 167, 171-177, 178, 182-188, 189, 193-199, 200, 204-210, 211, 215-221, 222, 227-232, 233, 237-243, 244, 248-254, 255, 259-265, 266, 271-276, 277, 291-287, 288, 292-298, 299, 303-309, 310, 314-320, 321, 325-331, 332, 337-342, 343, 347-353, 354, 358-364, 365, 369-375, 376, 380-386, 387, 391-397, 398, 402-408, 409, 413-419, 420, 424-430, 431, 435-441, 442, 446-452, 453, 457-463, 464, 468-474, 475, 479-485, 486, 490-496, 497, 501-507, 508, 512-518, 519, 523-529, 530, 534-540, 541, 545-551, 552, and 556-562, and a carrier.

[0063] Provided herein are imaging agents comprising the polypeptide disclosed herein. In certain embodiments, the imaging agent comprises a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 5, 9-15, 20, 24-30, 35, 39-45, 50, 54-60, 65, 69-75, 80, 84-91, 96, 100-107, 112, 116-122, 123, 127-133, 134, 138-144, 145, 150-155, 156, 160-166, 167, 171-177, 178, 182-188, 189, 193-199, 200, 204-210, 211, 215-221, 222, 227-232, 233, 237-243, 244, 248-254, 255, 259-265, 266, 271-276, 277, 291-287, 288, 292-298, 299, 303-309, 310, 314-320, 321, 325-331, 332, 337-342, 343, 347-353, 354, 358-364, 365, 369-375, 376, 380-386, 387, 391-397, 398, 402-408, 409, 413-419, 420, 424-430, 431, 435-441, 442, 446-452, 453, 457-463, 464, 468-474, 475, 479-485, 486, 490-496, 497, 501-507, 508, 512-518, 519, 523-529, 530, 534-540, 541, 545-551, 552, and 556-562.

[0064] In certain embodiments, the imaging agent comprises a detectable label. In certain embodiments, the imaging agent comprises a polypeptide disclosed herein, a chelating agent, and a detectable label. In certain embodiments, the imaging agent comprises a polypeptide disclosed herein, a bifunctional chelator or conjugating (BFC) moiety and a detectable label. In certain embodiments, the detectable label is a prosthetic group containing a radionuclide. In certain embodiments, the detectable label is detectable by positron emission tomography.

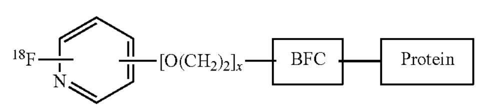
[0065] In certain embodiments, the chelating agent and/or bifunctional chelator or conjugating (BFC) moiety is selected from the group consisting of DFO, DOTA, CB-DO2A, 3p-C-DEPA, TCMC, DBCO, DIBO, BARAC, DIMAC, Oxo-DO3A, TE2A, CB-TE2A, CB-TElA1P, CB-TE2P, MM-TE2A, DM-TE2A, diamsar, NODASA, NODAGA, NOTA, NETA, TACN-TM, DTPA, 1B4M-DTPA, CHX-A"-DTPA, TRAP, NOPO, AAZTA, DATA, H_2dedpa, H_4octapa, H_2azapa, H_5decapa, H_6phospa, HBED, SHBED, BPCA, CP256, PCTA, HEHA, PEPA, EDTA, TETA, and TRITA.

[0066] In certain embodiments, the detectable label is a radionuclide, for example,

[0067] ^{64}Cu, ^{124}I, $^{76/77}$Br, ^{86}Y, ^{89}Zr, ^{68}Ga, ^{18}F, ^{11}C, ^{125}I, ^{124}I, ^{131}I, ^{123}I, ^{123}I, ^{131}I, ^{123}I, ^{32}Cl, ^{33}Cl, ^{34}Cl, ^{68}Ga, ^{74}Br, ^{75}Br, ^{76}Br, ^{77}Br, ^{78}Br, ^{89}Zr, ^{186}Re, ^{188}Re, ^{90}Y, ^{177}Lu, ^{99}Tc, or ^{153}Sm.

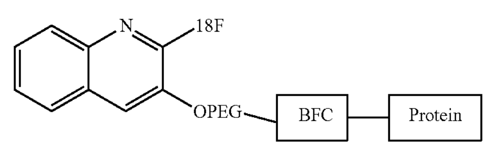
[0068] In certain embodiments, the chelating agent is NODAGA and the radionuclide is ^{64}Cu. In certain embodiments, the imaging agent comprises an anti-PD-L1 polypeptide (e.g., an anti-PD-L1 Adnectin described herein, e.g., an anti-PD-L1 Adnectin comprising the amino acid sequence set forth in SEQ ID NO: 80 or 96), the chelating agent NODAGA, and the radionuclide ^{64}Cu.

[0069] In certain embodiments, the imaging agent comprises an anti-PD-L1 polypeptide (e.g., an anti-PD-L1 Adnectin described herein, e.g., an anti-PD-L1 Adnectin comprising the amino acid sequence set forth in SEQ ID NO: 80 or 96), a bifunctional chelator or conjugating (BFC) moiety, and a prosthetic group comprising the radionuclide ^{18}F. In certain embodiments, the imaging agent has the following structure:



or a pharmaceutically acceptable salt thereof.

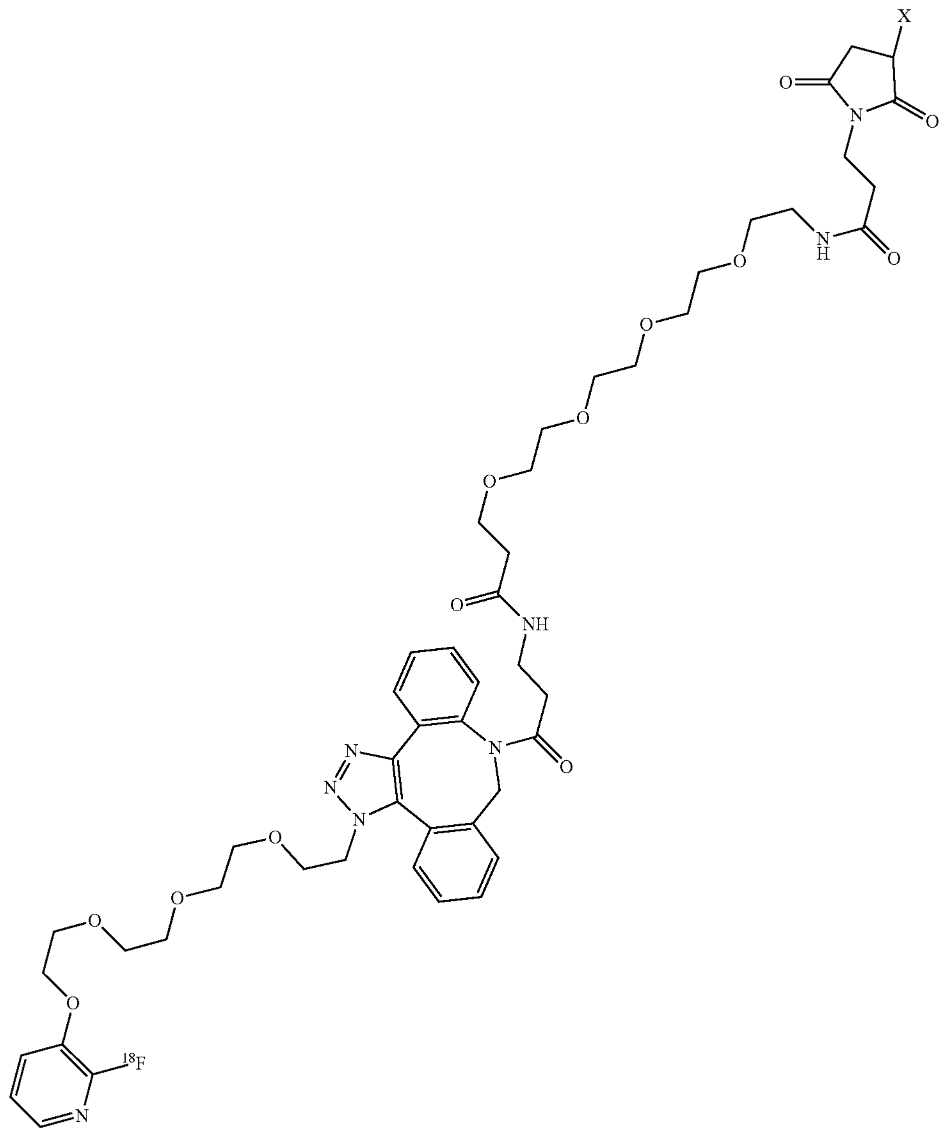
[0070] In certain embodiments, the imaging agent has the following structure:



[0071] In some embodiments, the BFC is a cyclooctyne comprising a reactive group that forms a covalent bond with an amine, carboxyl, carbonyl or thiol functional group on the protein. In some embodiments, the cyclooctyne is selected from the group consisting of dibenzocyclooctyne (DIBO), biarylazacyclooctynone (BARAC), dimethoxyazacyclooctyne (DIMAC) and dibenzocyclooctyne (DBCO). In some embodiments, the cyclooctyne is DBCO.

[0072] In some embodiments, the BFC is DBCO-PEG4-NHS-Ester, DBCO-Sulfo-NHS-Ester, DBCO-PEG4-Acid, DBCO-PEG4-Amine or DBCO-PEG4-Maleimide. In some embodiments, the BFC is DBCO-PEG4-Maleimide.

[0073] In certain embodiments, the imaging agent has the structure:



[0074] wherein X is a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs: 13, 28, 43, 58, 73, 88, 104, 120, 131, 142, 153, 164, 175, 186, 197, 208, 219, 230, 241, 252, 263, 274, 285, 296, 307, 318, 329, 340, 351, 362, 373, 384, 395, 406, 417, 428, 439, 450, 461, 472, 483, 494, 505, 516, 527, 538, 549, 560 and 571. In certain embodiments, the polypeptide comprises the amino acid sequence set forth in SEQ ID NO: 88. In certain embodiments, the polypeptide comprises the amino acid sequence set forth in SEQ ID NO: 104.

[0075] Provided herein are kits comprising an anti-PD-L1 Adnectin composition and/or imaging agent described herein, and instructions for use.

[0076] Provided herein is a method of detecting PD-L1 in a sample, the method comprising contacting the sample with an anti-PD-L1 Adnectin, and detecting PD-L1.

[0077] Provided herein is a method of detecting PD-L1 positive cells in a subject comprising administering to the subject an imaging agent comprising an anti-PD-L1 Adnectin, and detecting the imaging agent, the detected imaging agent defining the location of the PD-L1 positive cells in the subject.

[0078] Provided herein is a method of detecting PD-L1-expressing tumors in a subject comprising administering to the subject an imaging agent comprising an anti-PD-L1 Adnectin, and detecting the imaging agent, the detected imaging agent defining the location of the tumor in the subject. In certain embodiments, the imaging agent is detected by positron emission tomography.

[0079] Provided herein is a method of obtaining an image of an imaging agent comprising an anti-PD-L1 Adnectin, the method comprising,

[0080] a) administering the imaging agent to a subject; and

[0081] b) imaging in vivo the distribution of the imaging agent by positron emission tomography.

[0082] Provided herein is a method of obtaining a quantitative image of tissues or cells expressing PD-L1, the method comprising contacting the cells or tissue with an imaging agent comprising an anti-PD-L1 Adnectin, and detecting or quantifying the tissue expressing PD-L1 using positron emission tomography.

[0083] Provided herein is a method for detecting a PD-L1-expressing tumor comprising administering an imaging-effective amount of an imaging agent comprising an anti-PD-L1 Adnectin to a subject having a PD-L1-expressing tumor, and detecting the radioactive emissions of said imaging agent in the tumor using positron emission tomography, wherein the radioactive emissions are detected in the tumor.

[0084] Provided herein is a method of diagnosing the presence of a PD-L1-expressing tumor in a subject, the method comprising

[0085] (a) administering to a subject in need thereof an imaging agent comprising an anti PD-L1 Adnectin; and

[0086] (b) obtaining a radio-image of at least a portion of the subject to detect the presence or absence of the imaging agent;

wherein the presence and location of the imaging agent above background is indicative of the presence and location of a PD-L1 expressing tumor in the subject.

[0087] Provided herein is a method of treating a subject having cancer, comprising

[0088] (a) administering to a subject in need thereof an imaging agent comprising an anti-PD-L1 Adnectin, and obtaining an image of at least a portion of the subject to determine the presence of PD-L1 in one or more tumors; and, if PD-L1 is detected in one or more tumors, then,

[0089] (b) administering an anti-tumor therapy, e.g., an agent that inhibits the interaction between PD-1 and PD-L1 (a PD-1 or PD-L1 antagonist) to the subject.

[0090] Provided herein is a method of monitoring the progress of an anti-tumor therapy against PD-L1-expressing tumors in a subject, the method comprising

[0091] (a) administering to a subject in need thereof an imaging agent comprising an anti-PD-L1 Adnectin at a first time point and obtaining an image of at least a portion of the subject to determine the size of the tumor;

[0092] (b) administering an anti-tumor therapy to the subject;

[0093] (c) administering to the subject the imaging agent at one or more subsequent time points and obtaining an image of at least a portion of the subject at each time point; wherein the dimension and location of the tumor at each time point is indicative of the progress of the disease.

BRIEF DESCRIPTION OF THE DRAWINGS

[0094] FIG. **1** is a schematic of the core amino acid sequences of exemplary anti-PD-L1 Adnectins described herein. The BC, DE, and FG loops are underlined. Wildtype (WT) (SEQ ID NO: 2), ATI-968 (SEQ ID NO: 5), ATI-964 (SEQ ID NO: 20), ATI-967 (SEQ ID NO: 65), A02 (SEQ ID NO: 80), E01 (SEQ ID NO: 96), ATI-965 (SEQ ID NO: 35), and ATI-966 (SEQ ID NO: 50).

[0095] FIG. **2** is a schematic for the chemical synthesis of [^{18}F]-E01-4PEG-DBCO-FPPEGA. The E01 portion of the molecule has the sequence set forth in SEQ ID NO: 104.

[0096] FIG. **3** is a graph demonstrating discrimination of hPD-L1-positive L2987 cells from hPD-L1-negative HT-29 cells with the ^{64}Cu-E01 anti-PD-L1 Adnectin (with a NODAGA chelator). Specificity was confirmed by the reduction of cell-associated ^{64}Cu-E01 when co-incubated with excess cold (unlabeled) E01 Adnectin.

[0097] FIG. **4**A is a PET image depicting the discrimination of hPD-L1 (+) from hPD-L1 (−) tumors in bilateral xenograft mice with a NODAGA-^{64}Cu-labeled A02 anti-PD-L1 Adnectin. Shown are summed 0 to 2 hour images showing areas of probe residence. Bright areas are tissues of greatest occupancy during exposure.

[0098] FIG. **4**B is a graph depicting a time course of tumor labeling in hPD-L1 (+) [L2987] tumors. hPD-L1(−) [HT29] tumors and pulse chase experiment in hPD-L1(+) systems [L2987 block] show the specificity of the labelling.

[0099] FIG. **5** is a graph depicting tissue distribution of the ^{18}F-labeled A02 anti-PD-L1 Adnectin radiotracer in mice bearing bilateral hPD-L1(+) L2987 and hPD-L1(−) HT-29 xenografts as measured ex vivo by gamma counter.

[0100] FIG. **6** is a composite image of ^{18}F-labeled E01 anti-PD-L1 Adnectin distribution in cynomolgus monkey.

[0101] FIG. **7** is an image depicting in vitro autoradiography of xenograft and human lung tissues labelled with the 0.25 nM ^{18}F-DBCO-A02 anti-PD-L1 Adnectin co-incubated with the indicated concentrations of cold A02 Adnectin.

[0102] FIG. **8** depicts immunohistochemistry images of xenograft and human lung tumor specimens labelled with anti-PD-L1 Adnectins to demonstrate tumor expression of hPD-L1.

[0103] FIG. **9** shows a reaction scheme for synthesizing [^{18}F]-A02-4PEG-DBCO-FPPEGA. The same reaction scheme was used to label the E01 adnectin.

[0104] FIG. **10** is a schematic of the GE TRACERlab FX2 N Synthesis module for automated synthesis of [^{18}F]-FPPEGA.

[0105] FIG. **11** is a schematic of the Synthera Synthesis module (IBA) for automated synthesis of [^{18}F]-FPPEGA.

[0106] FIG. **12** depicts exemplary competition curves of anti-PD-L1 Adnectins.

DETAILED DESCRIPTION

Definitions

[0107] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by the skilled artisan. Although any methods and compositions similar or equivalent to those described herein can be used in practice or testing of the present invention, the preferred methods and compositions are described herein.

[0108] "Programmed Death Ligand-1 (PD-L1)" is one of two cell surface glycoprotein ligands for PD-1 (the other being PD-L2) that downregulate T cell activation and cytokine secretion upon binding to PD-1. The term "PD-L1" as used herein includes human PD-L1 (hPD-L1), variants, isoforms, and species homologs of hPD-L1, and analogs having at least one common epitope with hPD-L1. The complete hPD-L1 sequence can be found under GenBank Accession No. Q9NZQ7. PD-L1 is also referred to as CD274, B7-H, B7H1, PDCD1L1, and PDCD1LG1.

[0109] "Polypeptide" as used herein refers to any sequence of two or more amino acids, regardless of length, post-translation modification, or function. Polypeptides can include natural amino acids and non-natural amino acids such as those described in U.S. Pat. No. 6,559,126, incorporated herein by reference. Polypeptides can also be modified in any of a variety of standard chemical ways (e.g., an amino acid can be modified with a protecting group; the carboxy-terminal amino acid can be made into a terminal amide group; the amino-terminal residue can be modified with groups to, e.g., enhance lipophilicity; or the polypeptide can be chemically glycosylated or otherwise modified to increase stability or in vivo half-life). Polypeptide modifications can include the attachment of another structure such as a cyclic compound or other molecule to the polypeptide and can also include polypeptides that contain one or more amino acids in an altered configuration (i.e., R or S; or, L or D). The peptides described herein are proteins derived from the tenth type III domain of fibronectin that have been modified to bind specifically to human PD-L1 and are referred to herein as, "anti-PD-L1 Adnectin" or "PD-L1 Adnectin."

[0110] A "polypeptide chain," as used herein, refers to a polypeptide wherein each of the domains thereof is joined to other domain(s) by peptide bond(s), as opposed to non-covalent interactions or disulfide bonds.

[0111] An "isolated" polypeptide is one that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1) to greater than 95% by weight of polypeptide as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing condition using Coomassie blue or, preferably, silver stain. Isolated polypeptide includes the polypeptide in situ within recombinant cells since at least one component of the polypeptide's natural environment will not be present. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step.

[0112] A "region" of a ^{10}Fn3 domain as used herein refers to either a loop (AB, BC, CD, DE, EF and FG), a β-strand (A, B, C, D, E, F and G), the N-terminus (corresponding to amino acid residues 1-7 of SEQ ID NO: 1), or the C-terminus (corresponding to amino acid residues 93-94 of SEQ ID NO: 1) of the human ^{10}Fn3 domain.

[0113] A "scaffold region" refers to any non-loop region of a human ^{10}Fn3 domain. The scaffold region includes the A, B, C, D, E, F and G β-strands as well as the N-terminal region (amino acids corresponding to residues 1-7 of SEQ ID NO: 1) and the C-terminal region (amino acids corresponding to residues 93-94 of SEQ ID NO: 1 and optionally comprising the 7 amino acids constituting the natural linker between the 10^{th} and the 11^{th} repeat of the Fn3 domain in human fibronectin).

[0114] "Percent (%) amino acid sequence identity" herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in a selected sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN, ALIGN-2 or Megalign (DNASTAR™) software. Those skilled in the art can readily determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full-length of the sequences being compared. For example, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows: 100 times the fraction X/Y where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A.

[0115] As used herein, the term "Adnectin binding site" refers to the site or portion of a protein (e.g., PD-L1) that interacts or binds to a particular Adnectin. Adnectin binding sites can be formed from contiguous amino acids or non-contiguous amino acids juxtaposed by tertiary folding of a protein. Adnectin binding sites formed by contiguous amino acids are typically retained on exposure to denaturing solvents, whereas Adnectin binding sites formed by tertiary folding are typically lost on treatment of denaturing solvents.

[0116] An Adnectin binding site for an anti-PD-L1 Adnectin described herein may be determined by application of standard techniques typically used for epitope mapping of antibodies including, but not limited to protease mapping and mutational analysis. Alternatively, an Adnectin binding site can be determined by competition assay using a reference Adnectin or antibody which binds to the same polypeptide, e.g., PD-L1 (as further described infra in the section "Cross-Competing Adnectins and/or Adnectins that Bind to the Same Adnectin Binding Site." If the test Adnectin and reference molecule (e.g., another Adnectin or antibody) compete, then they bind to the same Adnectin binding site or to Adnectin binding sites sufficiently proximal such that binding of one molecule interferes with the other. An Adnectin binding site is defined by the method used to identify it. For example, an Adnectin may bind to a given binding site, as determined via HDX; an Adnectin may bind to a given binding site, as determined via crystallography; or an Adnectin may bind go to a given binding site as determined by directed mutational analysis.

[0117] The terms "specifically binds," "specific binding," "selective binding, and "selectively binds," as used interchangeably herein in the context of Adnectins binding to PD-L1 refers to an Adnectin that exhibits affinity for PD-L1, but does not significantly bind (e.g., less than about 10% binding) to a different polypeptides as measured by a technique available in the art such as, but not limited to, Scatchard analysis and/or competitive binding assays (e.g., competition ELISA, BIACORE assay). The term is also applicable where e.g., a binding domain of an Adnectin described herein is specific for PD-L1.

[0118] The term "preferentially binds" as used herein in the context of Adnectins binding to PD-L1 refers to the situation in which an Adnectin described herein binds PD-L1 at least about 20% greater than it binds a different polypeptide as measured by a technique available in the art such as, but not limited to, Scatchard analysis and/or competitive binding assays (e.g., competition ELISA, BIACORE assay).

[0119] As used herein in the context of Adnectins, the term "cross-reactivity" refers to an Adnectin which binds to more than one distinct protein having identical or very similar Adnectin binding sites.

[0120] The term "K_D," as used herein in the context of Adnectins binding to PD-L1, is intended to refer to the dissociation equilibrium constant of a particular Adnectin-protein (e.g., PD-L1) interaction or the affinity of an Adnectin for a protein (e.g., PD-L1), as measured using a surface plasmon resonance assay or a cell binding assay. A "desired K_D," as used herein, refers to a K_D of an Adnectin that is sufficient for the purposes contemplated. For example, a desired K_D may refer to the K_D of an Adnectin required to elicit a functional effect in an in vitro assay, e.g., a cell-based luciferase assay.

[0121] The term "k_a", as used herein in the context of Adnectins binding to a protein, is intended to refer to the association rate constant for the association of an Adnectin into the Adnectin/protein complex.

[0122] The term "k_d", as used herein in the context of Adnectins binding to a protein, is intended to refer to the dissociation rate constant for the dissociation of an Adnectin from the Adnectin/protein complex.

[0123] The term "IC_{50}", as used herein in the context of Adnectins, refers to the concentration of an Adnectin that inhibits a response, either in an in vitro or an in vivo assay, to a level that is 50% of the maximal inhibitory response, i.e., halfway between the maximal inhibitory response and the untreated response.

[0124] The term "PK" is an acronym for "pharmacokinetic" and encompasses properties of a compound including, by way of example, absorption, distribution, metabolism, and elimination by a subject. A "PK modulation protein" or "PK moiety" as used herein refers to any protein, peptide, or moiety that affects the pharmacokinetic properties of a biologically active molecule when fused to or administered together with the biologically active molecule.

[0125] Examples of a PK modulation protein or PK moiety include PEG, human serum albumin (HSA) binders (as disclosed in U.S. Publication Nos. 2005/0287153 and 2007/0003549, PCT Publication Nos. WO 2009/083804 and WO 2009/133208), human serum albumin and variants thereof, transferrin and variants thereof, Fc or Fc fragments and variants thereof, and sugars (e.g., sialic acid).

[0126] The "serum half-life" of a protein or compound is the time taken for the serum concentration of the polypeptide to be reduced by 50%, in vivo, for example due to degradation of the sequence or compound and/or clearance or sequestration of the sequence or compound by natural mechanisms. The half-life can be determined in any manner known per se, such as by pharmacokinetic analysis. Suitable techniques will be clear to the person skilled in the art, and may for example generally involve the steps of suitably administering to a subject a suitable dose of the amino acid sequence or compound described herein; collecting blood samples or other samples from the subject at regular intervals; determining the level or concentration of the amino acid sequence or compound described herein in said blood sample; and calculating, from (a plot of) the data thus obtained, the time until the level or concentration of the amino acid sequence or compound described herein has been reduced by 50% compared to the initial level upon dosing. Reference is, for example, made to the standard handbooks, such as Kenneth, A. et al., Chemical Stability of Pharmaceuticals: A Handbook for Pharmacists and in Peters et al., Pharmacokinete Analysis: A Practical Approach (1996). Reference is also made to Gibaldi, M. et al., Pharmacokinetics, 2nd Rev. Edition, Marcel Dekker (1982).

[0127] Half-life can be expressed using parameters such as the ti/2-alpha, ti/2-beta, HL_Lambda_z, and the area under the curve (AUC).

[0128] The term "detectable" refers to the ability to detect a signal over the background signal. The term "detectable signal" is a signal derived from non-invasive imaging techniques such as, but not limited to, positron emission tomography (PET). The detectable signal is detectable and distinguishable from other background signals that may be generated from the subject. In other words, there is a measurable and statistically significant difference (e.g., a statistically significant difference is enough of a difference to distinguish among the detectable signal and the background, such as about 0.1%, 1%, 3%, 5%, 10%, 15%, 20%, 25%, 30%, or 40% or more difference between the detectable signal and the background) between the detectable signal and the background. Standards and/or calibration curves can be used to determine the relative intensity of the detectable signal and/or the background.

[0129] A "detectably effective amount" of a composition comprising an imaging agent described herein is defined as an amount sufficient to yield an acceptable image using equipment that is available for clinical use. A detectably effective amount of an imaging agent provided herein may be administered in more than one injection. The detectably effective amount can vary according to factors such as the degree of susceptibility of the individual, the age, sex, and weight of the individual, idiosyncratic responses of the individual, and the like. Detectably effective amounts of imaging compositions can also vary according to instrument and methodologies used. Optimization of such factors is well within the level of skill in the art. In certain embodiments, a PD-L1 imaging agent, e.g., those described herein, provides a differentiation factor (i.e., specific signal to background signal) of 2 or more, e.g., 3, 4, 5 or more.

[0130] The term "bioorthogonal chemistry" refers to any chemical reaction that can occur inside of living systems without interfering with native biochemical processes. The term includes chemical reactions that are chemical reactions that occur in vitro at physiological pH in, or in the presence of water. To be considered bioorthogonol, the reactions are selective and avoid side-reactions with other functional groups found in the starting compounds. In addition, the resulting covalent bond between the reaction partners should be strong and chemically inert to biological reactions and should not affect the biological activity of the desired molecule.

[0131] The term "click chemistry" refers to a set of reliable and selective bioorthogonal reactions for the rapid synthesis of new compounds and combinatorial libraries. Properties of for click reactions include modularity, wideness in scope, high yielding, stereospecificity and simple product isolation (separation from inert by-products by non-chromatographic methods) to produce compounds that are stable under physiological conditions. In radiochemistry and radiopharmacy, click chemistry is a generic term for a set of labeling reactions which make use of selective and modular building blocks and enable chemoselective ligations to radiolabel biologically relevant compounds in the absence of catalysts. A "click reaction" can be with copper, or it can be a copper-free click reaction.

[0132] The term "prosthetic group" or "bifunctional labeling agent" refers to a small organic molecule containing a radionulide (e.g., ^{18}F) that is capable of being linked to peptides or proteins.

[0133] The term "chelator ligand" as used herein with respect to radiopharmaceutical chemistry refers to a bifunctional chelator or conjugating (BFC) moiety, which are used interchangeably herein, that covalently links a radiolabeled prosthetic group to a biologically active targeting molecule (e.g., peptide or protein). BFCs utilize functional groups such as carboxylic acids or activated esters for amide couplings, isothiocyanates for thiourea couplings and maleimides for thiol couplings.

[0134] The terms "individual," "subject," and "patient," used interchangeably herein, refer to a human.

[0135] A "cancer" refers a broad group of various diseases characterized by the uncontrolled growth of abnormal cells in the body. Unregulated cell division and growth divide and grow results in the formation of malignant tumors that invade neighboring tissues and may also metastasize to distant parts of the body through the lymphatic system or bloodstream.

[0136] An "immune response" refers to the action of a cell of the immune system (for example, T lymphocytes, B lymphocytes, natural killer (NK) cells, macrophages, eosinophils, mast cells, dendritic cells and neutrophils) and soluble macromolecules produced by any of these cells or the liver (including Abs, cytokines, and complement) that results in selective targeting, binding to, damage to, destruction of, and/or elimination from a vertebrate's body of invading pathogens, cells or tissues infected with pathogens, cancerous or other abnormal cells, or, in cases of autoimmunity or pathological inflammation, normal human cells or tissues.

[0137] An "immunoregulator" refers to a substance, an agent, a signaling pathway or a component thereof that regulates an immune response. "Regulating," "modifying" or "modulating" an immune response refers to any alteration in a cell of the immune system or in the activity of such cell. Such regulation includes stimulation or suppression of the immune system which may be manifested by an increase or decrease in the number of various cell types, an increase or decrease in the activity of these cells, or any other changes which can occur within the immune system. Both inhibitory and stimulatory immunoregulator have been identified, some of which may have enhanced function in the cancer microenvironment.

[0138] The term "immunotherapy" refers to the treatment of a subject afflicted with, or at risk of contracting or suffering a recurrence of, a disease by a method comprising inducing, enhancing, suppressing or otherwise modifying an immune response.

[0139] "Treatment" or "therapy" of a subject refers to any type of intervention or process performed on, or the administration of an active agent to, the subject with the objective of reversing, alleviating, ameliorating, inhibiting, slowing down or preventing the onset, progression, development, severity or recurrence of a symptom, complication, condition or biochemical indicia associated with a disease.

[0140] "Administration" or "administering," as used herein in the context of anti-PD-L1 Adnectins, refers to introducing a PD-L1 Adnectin or PD-L1 Adnectin-based probe or a labeled probe (also referred to as the "imaging agent") described herein into a subject. Any route of administration is suitable, such as intravenous, oral, topical, subcutaneous, peritoneal, intra-arterial, inhalation, vaginal, rectal, nasal, introduction into the cerebrospinal fluid, or instillation into body compartments can be used.

[0141] The term "therapeutically effective amount" refers to at least the minimal dose, but less than a toxic dose, of an agent which is necessary to impart a therapeutic benefit to a subject.

[0142] As used herein, an "effective amount" refers to at least an amount effective, at dosages and for periods of time necessary, to achieve the desired result.

[0143] As used herein, a "sufficient amount" refers to an amount sufficient to achieve the desired result.

[0144] As used herein, "positron emission tomography" or "PET" refers to a non-invasive, nuclear medicine technique that produces a three-dimensional image of tracer location in the body. The method detects pairs of gamma rays emitted indirectly by a positron-emitting radionuclide (tracer), which is introduced into the body on a biologically active molecule. PET imaging tools have a wide variety of uses and aid in drug development both preclinically and clinically. Exemplary applications include direct visualization of in vivo saturation of targets; monitoring uptake in normal tissues to anticipate toxicity or patient to patient variation; quantifying diseased tissue; tumor metastasis; and monitoring drug efficacy over time, or resistance over time.

Overview

[0145] Provided herein are polypeptides that bind to human PD-L1 and can be coupled to heterologous molecule (s), such as a radiolabel. Such polypeptides are useful, for example, for detecting PD-L1 in a sample or tissue, e.g., in a subject (e.g., a tissue, such as a cancer tissue that selectively expresses PD-L1), e.g., for diagnostic assays.

[0146] The invention is based on the development of a non-invasive clinical imaging agent that allows for whole body visualization of a patient's PD-L1 expression. In certain embodiments, single day "virtual biopsies" of a patient's whole body are performed to monitor and localize PD-L1 expression levels. PD-L1 imaging agents described herein may be used to provide a high contrast whole-body virtual biopsy in a single day.

I. FIBRONECTIN-BASED SCAFFOLDS

[0147] Fn3 refers to a type III domain from fibronectin. An Fn3 domain is small, monomeric, soluble, and stable. It lacks disulfide bonds and, therefore, is stable under reducing conditions. The overall structure of Fn3 resembles the immunoglobulin fold. Fn3 domains comprise, in order from N-terminus to C-terminus, a beta or beta-like strand, A; a loop, AB; a beta or beta-like strand, B; a loop, BC; a beta or beta-like strand, C; a loop, CD; a beta or beta-like strand, D; a loop, DE; a beta or beta-like strand, E; a loop, EF; a beta or beta-like strand, F; a loop, FG; and a beta or beta-like strand, G. The seven antiparallel β-strands are arranged as two beta sheets that form a stable core, while creating two "faces" composed of the loops that connect the beta or beta-like strands. Loops AB, CD, and EF are located at one face ("the south pole") and loops BC, DE, and FG are located on the opposing face ("the north pole"). There are at least 15 different Fn3 modules in human Fibronectin, and while the sequence homology between the modules is low, they all share a high similarity in tertiary structure.

[0148] Described herein are anti-PD-L1 Adnectins comprising an Fn3 domain in which one or more of the solvent accessible loops has been randomized or mutated. In certain embodiments, the Fn3 domain is an Fn3 domain derived from the wild-type tenth module of the human fibronectin type III domain (^{10}Fn3):

(SEQ ID NO: 1)
VSDVPRDLEVVAATPTSLLISW**DAPAVTVRY**YRITYGETGGNSPVQEFT
V**PGSKST**ATISGLKPGVDYTITVYA**VTGRGDSPASSKP**ISINYRT

(94 amino acids; AB, CD, and EF loops are underlined; the core ^{10}Fn3 domain begins with amino acid 9 ("E") and ends with amino acid 94 ("T") and corresponds to an 86 amino acid polypeptide). The core wild-type human ^{10}Fn3 domain is set forth in SEQ ID NO: 2.

[0149] Both variant and wild-type ^{10}Fn3 proteins are characterized by the same structure, namely seven beta-strand domain sequences designated A through G and six loop regions (AB loop, BC loop, CD loop, DE loop, EF loop, and FG loop) which connect the seven beta-strand domain sequences. The beta strands positioned closest to the N- and C-termini may adopt a beta-like conformation in solution. In SEQ ID NO: 1, the AB loop corresponds to residues 14-17, the BC loop corresponds to residues 23-31, the CD loop corresponds to residues 37-47, the DE loop corresponds to residues 51-56, the EF loop corresponds to residues 63-67, and the FG loop corresponds to residues 75-87.

[0150] Accordingly, in certain embodiments, the anti-PD-L1 Adnectin described herein is an ^{10}Fn3 polypeptide that is at least 40%, 50%, 60%, 65%, 70%, 75%, 80%, 85%, or 90% identical to the human ^{10}Fn3 domain, shown in SEQ ID NO: 1, or its core sequence, as shown in SEQ ID NO: 2. Much of the variability will generally occur in one or more of the loops or one or more of the beta strands or N- or C-terminal regions. Each of the beta or beta-like strands of a ^{10}Fn3 polypeptide may consist essentially of an amino acid sequence that is at least 80%, 85%, 90%, 95% or 100% identical to the sequence of a corresponding beta or beta-like strand of SEQ ID NO: 1 or 2, provided that such variation does not disrupt the stability of the polypeptide in physiological conditions.

[0151] In certain embodiments, the invention provides an anti-human PD-L1 Adnectin comprising a tenth fibronectin type III (^{10}Fn3) domain, wherein the ^{10}Fn3 domain comprises a loop, AB; a loop, BC; a loop, CD; a loop, DE; a loop EF; and a loop FG; and has at least one loop selected from loop BC, DE, and FG with an altered amino acid sequence relative to the sequence of the corresponding loop of the human ^{10}Fn3 domain. An "Adnectin" is a modified human ^{10}Fn3 domain that binds to a target that is not bound by the unmodified human ^{10}Fn3 domain. In some embodiments, the anti-PD-L1 Adnectins described herein comprise a ^{10}Fn3 domain comprising an amino acid sequence at least 80%, 85%, 90%, 95%, 98%, 99% or 100% identical to the non-loop regions of SEQ ID NO: 1 or 2, wherein at least one loop selected from BC, DE, and FG is altered. In certain embodiments, the BC and FG loops are altered, in certain embodiments, the BC and DE loops are altered, in certain embodiments, the DE and FG loops are altered, and in certain embodiments, the BC, DE, and FG loops are altered, i.e., the ^{10}Fn3 domains comprise non-naturally occurring loops. In certain embodiments, the AB, CD and/or the EF loops are altered. By "altered" is meant one or more amino acid sequence alterations relative to a template sequence (corresponding human fibronectin domain) and includes amino acid additions, deletions, substitutions or a combination thereof. Altering an amino acid sequence may be accomplished through intentional, blind, or spontaneous sequence variation, generally of a nucleic acid coding sequence, and may occur by any technique, for example, PCR, error-prone PCR, or chemical DNA synthesis.

[0152] In certain embodiments, one or more loops selected from BC, DE, and FG may be extended or shortened in length relative to the corresponding human fibronectin loop. In some embodiments, the length of the loop may be extended by 2-25 amino acids. In some embodiments, the length of the loop may be decreased by 1-11 amino acids. To optimize antigen binding, therefore, the length of a loop of ^{10}Fn3 may be altered in length as well as in sequence to obtain the greatest possible flexibility and affinity in antigen binding.

[0153] In certain embodiments, the polypeptide comprises a Fn3 domain that comprises an amino acid sequence of the non-loop regions that is at least 80, 85, 90, 95, 98, 99, or 100% identical to the non-loop regions of SEQ ID NO: 1 or 2, wherein at least one loop selected from BC, DE, and FG is altered. In some embodiments, the altered BC loop has up to 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acid substitutions, up to 1, 2, 3, or 4 amino acid deletions, up to 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acid insertions, or a combination thereof.

[0154] In some embodiments, one or more residues of the integrin-binding motif "arginine-glycine-aspartic acid" (RGD) (amino acids 78-80 of SEQ ID NO: 1) may be substituted so as to disrupt integrin binding. In some embodiments, the FG loop of the polypeptides provided herein does not contain an RGD integrin binding site. In one embodiment, the RGD sequence is replaced by a polar amino acid-neutral amino acid-acidic amino acid sequence (in the N-terminal to C-terminal direction). In some embodiments, the RGD sequence is replaced with SGE. In one embodiment, the RGD sequence is replaced with RGE.

[0155] In certain embodiments, the fibronectin based scaffold protein comprises a ^{10}Fn3 domain that is defined generally by following the sequence:

(SEQ ID NO: 3)
EVVAA(Z)$_a$LLISW(Z)$_x$YRITY(Z)$_b$FTV(Z)$_y$ATISGL(Z)$_c$YTITVYA
(Z)$_z$ISINYRT

wherein the AB loop is represented by $(Z)_a$, the CD loop is represented by $(Z)_b$, the EF loop is represented by $(Z)_c$, the BC loop is represented by $(Z)_x$, the DE loop is represented by $(Z)_y$, and the FG loop is represented by $(Z)_z$. Z represents any amino acid and the subscript following the Z represents an integer of the number of amino acids. In particular, a may be anywhere from 1-15, 2-15, 1-10, 2-10, 1-8, 2-8, 1-5, 2-5, 1-4, 2-4, 1-3, 2-3, or 1-2 amino acids; and b, c, x, y and z may each independently be anywhere from 2-20, 2-15, 2-10, 2-8, 5-20, 5-15, 5-10, 5-8, 6-20, 6-15, 6-10, 6-8, 2-7, 5-7, or 6-7 amino acids. The sequences of the beta strands may have anywhere from 0 to 10, from 0 to 8, from 0 to 6, from 0 to 5, from 0 to 4, from 0 to 3, from 0 to 2, or from 0 to 1 substitutions, deletions or additions across all 7 scaffold regions relative to the corresponding amino acids shown in SEQ ID NO: 1 or 2. In certain embodiments, the sequences of the beta strands may have anywhere from 0 to 10, from 0 to 8, from 0 to 6, from 0 to 5, from 0 to 4, from 0 to 3, from 0 to 2, or from 0 to 1 conservative substitutions across all 7 scaffold regions relative to the corresponding amino acids shown in SEQ ID NO: 1 or 2. In certain embodiments, the core amino acid residues are fixed and any substitutions, conservative substitutions, deletions or additions occur at residues other than the core amino acid residues.

[0156] In certain embodiments, the anti-PD-L1 Adnectins described herein are based on a ^{10}Fn3 scaffold and are defined generally by the sequence:

(SEQ ID NO: 4)
EVVAATPTSLLISW$(Z)_x$YRITYGETGGNSPVQEFTV$(Z)_y$ATISGLKP GVDYTITVYA$(Z)_z$ISINYRT.

wherein the BC loop is represented by $(Z)_x$, the DE loop is represented by $(Z)_y$, and the FG loop is represented by $(Z)_z$. Z represents any amino acid and the subscript following the Z represents an integer of the number of amino acids. In particular, x, y and z may each independently be anywhere from 2-20, 2-15, 2-10, 2-8, 5-20, 5-15, 5-10, 5-8, 6-20, 6-15, 6-10, 6-8, 2-7, 5-7, or 6-7 amino acids. In preferred embodiments, x is 11 amino acids, y is 6 amino acids, and z is 12 amino acids. The sequences of the beta strands may have anywhere from 0 to 10, from 0 to 8, from 0 to 6, from 0 to 5, from 0 to 4, from 0 to 3, from 0 to 2, or from 0 to 1 substitutions, deletions or additions across all 7 scaffold regions relative to the corresponding amino acids shown in SEQ ID NO: 1 or 2. In certain embodiments, the sequences of the beta strands may have anywhere from 0 to 10, from 0 to 8, from 0 to 6, from 0 to 5, from 0 to 4, from 0 to 3, from 0 to 2, or from 0 to 1 conservative substitutions across all 7 scaffold regions relative to the corresponding amino acids shown in SEQ ID NO: 1 or 2. In certain embodiments, the core amino acid residues, e.g., outside one or more loops, are fixed and any substitutions, conservative substitutions, deletions or additions occur at residues other than the core amino acid residues.

[0157] In certain embodiments, an anti-PD-L1 Adnectin may comprise the sequence as set forth in SEQ ID NO: 3 or 4, wherein at least one of BC, DE, and FG loops as represented by $(Z)_x$, $(Z)_y$, and $(Z)_z$, respectively, are altered. As described above, amino acid residues corresponding to residues 23-31, 51-56, and 75-87 of SEQ ID NO: 1 define the BC, DE, and FG loops, respectively. However, it should be understood that not every residue within the loop region needs to be modified in order to achieve a ^{10}Fn3 binder having strong affinity for a desired target (e.g., PD-L1).

[0158] In certain embodiments, an anti-PD-L1 Adnectin comprises the sequence set forth in SEQ ID NO: 3 or 4, wherein BC, DE and FG loops as represented by $(Z)_x$, $(Z)_y$, and $(Z)_z$, respectively, have amino acid sequences at least 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identical to the BC, DE or FG loop sequences set forth in SEQ ID NOs: 21, 22, and 23, respectively.

[0159] In certain embodiments, an anti-PD-L1 Adnectin comprises the sequence set forth in SEQ ID NO: 3 or 4, wherein BC, DE and FG loops as represented by $(Z)_x$, $(Z)_y$, and $(Z)_z$, respectively, comprise BC, DE, and FG loops having the amino acid sequences of SEQ ID NOs: 21, 22, and 23, respectively.

[0160] In certain embodiments, an anti-PD-L1 Adnectin comprises the sequence set forth in SEQ ID NO: 3 or 4, wherein BC, DE and FG loops as represented by $(Z)_x$, $(Z)_y$, and $(Z)_z$, respectively, have amino acid sequences at least 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identical to the BC, DE or FG loop sequences set forth in SEQ ID NOs: 36, 37, and 38, respectively.

[0161] In certain embodiments, an anti-PD-L1 Adnectin comprises the sequence set forth in SEQ ID NO: 3 or 4, wherein BC, DE and FG loops as represented by $(Z)_x$, $(Z)_y$, and $(Z)_z$, respectively, comprise BC, DE, and FG loops having the amino acid sequences of SEQ ID NOs: 36, 37, and 38, respectively.

[0162] In certain embodiments, an anti-PD-L1 Adnectin comprises the sequence set forth in SEQ ID NO: 3 or 4, wherein BC, DE and FG loops as represented by $(Z)_x$, $(Z)_y$, and $(Z)_z$, respectively, have amino acid sequences at least 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identical to the BC, DE or FG loop sequences set forth in SEQ ID NOs: 51, 52, and 53, respectively.

[0163] In certain embodiments, an anti-PD-L1 Adnectin comprises the sequence set forth in SEQ ID NO: 3 or 4, wherein BC, DE and FG loops as represented by $(Z)_x$, $(Z)_y$, and $(Z)_z$, respectively, comprise BC, DE, and FG loops having the amino acid sequences of SEQ ID NOs: 51, 52, and 53, respectively.

[0164] In certain embodiments, an anti-PD-L1 Adnectin comprises the sequence set forth in SEQ ID NO: 3 or 4, wherein BC, DE and FG loops as represented by $(Z)_x$, $(Z)_y$, and $(Z)_z$, respectively, have amino acid sequences at least 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identical to the BC, DE or FG loop sequences set forth in SEQ ID NOs: 66, 67, and 68, respectively.

[0165] In certain embodiments, an anti-PD-L1 Adnectin comprises the sequence set forth in SEQ ID NO: 3 or 4, wherein BC, DE and FG loops as represented by $(Z)_x$, $(Z)_y$, and $(Z)_z$, respectively, comprise BC, DE, and FG loops having the amino acid sequences of SEQ ID NOs: 66, 67, and 68, respectively.

[0166] In certain embodiments, an anti-PD-L1 Adnectin comprises the sequence set forth in SEQ ID NO: 3 or 4, wherein BC, DE and FG loops as represented by $(Z)_x$, $(Z)_y$, and $(Z)_z$, respectively, have amino acid sequences at least 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identical to the BC, DE or FG loop sequences set forth in SEQ ID NOs: 6, 7, and 8, respectively.

[0167] In certain embodiments, an anti-PD-L1 Adnectin comprises the sequence set forth in SEQ ID NO: 3 or 4, wherein BC, DE and FG loops as represented by $(Z)_x$, $(Z)_y$, and $(Z)_z$, respectively, comprise BC, DE, and FG loops having the amino acid sequences of SEQ ID NOs: 6, 7, and 8, respectively.

[0168] In certain embodiments, an anti-PD-L1 Adnectin comprises the sequence set forth in SEQ ID NO: 3 or 4, wherein BC, DE and FG loops as represented by $(Z)_x$, $(Z)_y$, and $(Z)_z$, respectively, have amino acid sequences at least 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identical to the BC, DE or FG loop sequences set forth in SEQ ID NOs: 81, 82, and 83, respectively.

[0169] In certain embodiments, an anti-PD-L1 Adnectin comprises the sequence set forth in SEQ ID NO: 3 or 4, wherein BC, DE and FG loops as represented by $(Z)_x$, $(Z)_y$, and $(Z)_z$, respectively, comprise BC, DE, and FG loops having the amino acid sequences of SEQ ID NOs: 81, 82, and 83, respectively.

[0170] In certain embodiments, an anti-PD-L1 Adnectin comprises the sequence set forth in SEQ ID NO: 3 or 4, wherein BC, DE and FG loops as represented by $(Z)_x$, $(Z)_y$, and $(Z)_z$, respectively, have amino acid sequences at least 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identical to the BC, DE or FG loop sequences set forth in SEQ ID NOs: 97, 98, and 99, respectively. In certain embodiments, an anti-PD-L1 Adnectin comprises the sequence set forth in SEQ ID NO: 3 or 4, wherein BC, DE and FG loops as represented by $(Z)_x$, $(Z)_y$, and $(Z)_z$, respectively, comprise BC, DE, and FG loops having the amino acid sequences of SEQ ID NOs: 97, 98, and 99, respectively.

[0171] In certain embodiments, an anti-PD-L1 Adnectin comprises the sequence set forth in SEQ ID NO: 3 or 4, wherein BC, DE and FG loops as represented by $(Z)_x$, $(Z)_y$, and $(Z)_z$, respectively, comprise BC, DE, and FG loops having the amino acid sequences of SEQ ID NOs: 113, 114, and 115, respectively; SEQ ID NOs: 124, 125 and 126, respectively; SEQ ID NOs: 135, 136 and 137, respectively; SEQ ID NOs: 146, 147 and 148, respectively; SEQ ID NOs: 157, 158 and 159, respectively; SEQ ID NOs: 168, 169 and 170, respectively; SEQ ID NOs: 179, 180 and 181, respectively; SEQ ID NOs: 190, 191 and 192, respectively; SEQ ID NOs: 201, 202 and 203, respectively; SEQ ID NOs: 212, 213 and 214, respectively; SEQ ID NOs: 223, 224 and 225, respectively; SEQ ID NOs: 234, 235, and 236, respectively; SEQ ID NOs: 245, 246 and 247, respectively; SEQ ID NOs: 256, 257 and 258, respectively; SEQ ID NOs: 267, 268 and 269, respectively; SEQ ID NOs: 278, 279 and 280, respectively; SEQ ID NOs: 289, 290 and 291, respectively; SEQ ID NOs: 300, 301 and 302, respectively; SEQ ID NOs: 311, 312 and 313, respectively; SEQ ID NOs: 322, 323 and 324, respectively; SEQ ID NOs: 333, 334 and 335, respectively; SEQ ID NOs: 344, 345 and 346, respectively; SEQ ID NOs: 355, 356 and 357, respectively; SEQ ID NOs: 366, 367 and 368, respectively; SEQ ID NOs: 377, 378 and 379, respectively; SEQ ID NOs: 388, 389 and 390 respectively; SEQ ID NOs: 399, 400 and 401, respectively; SEQ ID NOs: 410, 411 and 412, respectively; SEQ ID NOs: 421, 422 and 423, respectively; SEQ ID NOs: 432, 433 and 434 respectively; SEQ ID NOs: 443, 444 and 445, respectively; SEQ ID NOs: 454, 455 and 456, respectively; SEQ ID NOs: 465, 466 and 467, respectively; SEQ ID NOs: 476, 477 and 478, respectively; SEQ ID NOs: 487, 488 and 489, respectively; SEQ ID NOs: 498, 499 and 500, respectively; SEQ ID NOs: 509, 510 and 511, respectively; SEQ ID NOs: 520, 521 and 522, respectively; SEQ ID NOs: 531, 530 and 531, respectively; SEQ ID NOs: 542, 543 and 544, respectively; SEQ ID NOs: 553, 554 and 555, respectively; or SEQ ID NOs: 564, 565 and 566, respectively. The scaffold regions of such anti-PD-L1 Adnectins may comprise anywhere from 0 to 20, from 0 to 15, from 0 to 10, from 0 to 8, from 0 to 6, from 0 to 5, from 0 to 4, from 0 to 3, from 0 to 2, or from 0 to 1 substitutions, conservative substitutions, deletions or additions relative to the scaffold amino acids residues of SEQ ID NO: 4. Such scaffold modifications may be made, so long as the anti-PD-L1 Adnectin is capable of binding PD-L1 with a desired K_D.

[0172] In certain embodiments, the BC loop of the anti-PD-L1 Adnectin comprises an amino acid sequence selected from the group consisting of: 6, 21, 36, 51, 66, 81, and 97.

[0173] In certain embodiments, the DE loop of the anti-PD-L1 Adnectin comprises an amino acid sequence selected from the group consisting of: 7, 22, 37, 52, 67, 82, and 98.

[0174] In certain embodiments, the FG loop of the anti-PD-L1 Adnectin comprises an amino acid sequence selected from the group consisting of: 8, 23, 38, 53, 68, 83, and 99.

[0175] In certain embodiments, the anti-PD-L1 Adnectin comprises a BC, DE and FG loop amino acid sequence at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, 99% or 100% identical to any one of SEQ ID NOs: 6, 21, 36, 51, 66, 81, and 97; 7, 22, 37, 52, 67, 82, and 98; and 8, 23, 38, 53, 68, 83, and 99, respectively.

[0176] In certain embodiments, the anti-PD-L1 Adnectin comprises an amino acid sequence at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, 99%, or 100% identical to any one of SEQ ID NOs: 5, 20, 35, 50, 65, 80, 96, 112, 123, 134, 145, 156, 167, 178, 189, 200, 211, 222, 233, 244, 255, 266, 277, 288, 299, 310, 321, 332, 343, 354, 365, 376, 387, 398, 409, 420, 431, 442, 453, 464, 475, 486, 497, 508, 519, 530, 541, 552 and 563.

[0177] In certain embodiments, the anti-PD-L1 Adnectins described herein comprise an amino acid sequence at least 80%, 85%, 90%, 95%, 98%, 99% or 100% identical to the non-BC, DE, and FG loop regions of SEQ ID NOs: 5, 20, 35, 50, 65, 80, or 96.

[0178] In certain embodiments, the anti-PD-L1 Adnectin comprises an amino acid sequence at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, 99% or 100% identical to any one of SEQ ID NOs: 9-15, 24-30, 39-45, 54-60, 6975, 84-91, 100-107, 116-122, 127-133, 138-144, 150-155, 160-166, 171-177, 182-188, 193-199, 204-210, 215-221, 227-232, 237-243, 248-254, 259-265, 271-276, 291-287, 292-298, 303-309, 314-320, 325-331, 337-342, 347-353, 358-364, 369-375, 380-386, 391-397, 402-408, 413-419, 424-430, 435-441, 446-452, 457-463, 468-474, 479-485, 490-496, 501-507, 512-518, 523-529, 534-540, 545-551, and 556-562. In certain embodiments, the anti-PD-L1 Adnectins described herein comprise an amino acid sequence at least 80%, 85%, 90%, 95%, 98%, 99% or 100% identical to the non-BC, DE, and FG loop regions of any one of SEQ ID NOs: 9-15, 24-30, 39-45, 54-60, 6975, 84-91, and 100-107.

[0179] In certain embodiments, the anti-PD-L1 Adnectin comprises BC, DE, and FG loops as set forth in SEQ ID NOs: 6, 7, and 8, respectively.

[0180] In certain embodiments, the anti-PD-L1 Adnectin comprises BC, DE, and FG loops as set forth in SEQ ID NOs: 21, 22, and 23, respectively.

[0181] In certain embodiments, the anti-PD-L1 Adnectin comprises BC, DE, and FG loops as set forth in SEQ ID NOs: 36, 37, and 38, respectively.

[0182] In certain embodiments, the anti-PD-L1 Adnectin comprises BC, DE, and FG loops as set forth in SEQ ID NOs: 51, 52, and 53, respectively.

[0183] In certain embodiments, the anti-PD-L1 Adnectin comprises BC, DE, and FG loops as set forth in SEQ ID NOs: 66, 67, and 68, respectively.

[0184] In certain embodiments, the anti-PD-L1 Adnectin comprises BC, DE, and FG loops as set forth in SEQ ID NOs: 81, 82, and 83, respectively.

[0185] In certain embodiments, the anti-PD-L1 Adnectin comprises BC, DE, and FG loops as set forth in SEQ ID NOs: 97, 98, and 99, respectively.

[0186] In certain embodiments, BC, DE and/or FG loop amino acid sequences described herein (e.g., SEQ ID NOs: 6, 21, 36, 51, 66, 81, and 97; 7, 22, 37, 52, 67, 82, and 98; and 8, 23, 38, 53, 68, 83, and 99, respectively) are grafted into non-^{10}Fn3 domain protein scaffolds. For instance, one or more loop amino acid sequences is exchanged for or inserted into one or more CDR loops of an antibody heavy or light chain or fragment thereof. In some embodiments, the protein domain into which one or more amino acid loop sequences are exchanged or inserted includes, but is not limited to, consensus Fn3 domains (Centocor, US), ankyrin repeat proteins (Molecular Partners AG, Zurich Switzerland), domain antibodies (Domantis, Ltd, Cambridge, Mass.), single domain camelid nanobodies (Ablynx, Belgium), lipocalins (e.g., anticalins; Pieris Proteolab AG, Freising, Germany), Avimers (Amgen, Calif.), affibodies (Affibody AG, Sweden), ubiquitin (e.g., affilins; Scil Proteins GmbH, Halle, Germany), protein epitope mimetics (Polyphor Ltd, Allschwil, Switzerland), helical bundle scaffolds (e.g. alphabodies, Complix, Belgium), Fyn SH3 domains (Covagen AG, Switzerland), or atrimers (Anaphor, Inc., CA).

[0187] In certain embodiments, the amino acid sequences of the N-terminal and/or C-terminal regions of the polypeptides provided herein may be modified by deletion, substitution or insertion relative to the amino acid sequences of the corresponding regions of the wild-type human ^{10}Fn3 domain (SEQ ID NO: 1 or 2). The ^{10}Fn3 domains generally begin with amino acid number 1 of SEQ ID NO: 1. However, domains with amino acid deletions are also encompassed by the invention. Additional sequences may also be added to the N- or C-terminus of a ^{10}Fn3 domain having the amino acid sequence of SEQ ID NO: 1 or 2. For example, in some embodiments, the N-terminal extension consists of an amino acid sequence selected from the group consisting of: M, MG, and G. In certain embodiments, an MG sequence may be placed at the N-terminus of the ^{10}Fn3 defined by SEQ ID NO: 1. The M will usually be cleaved off, leaving a G at the N-terminus. In addition, an M, G or MG may also be placed N-terminal to any of the N-terminal extensions shown in Table 3.

[0188] In exemplary embodiments, an alternative N-terminal region having from 1-20, 1-15, 1-10, 1-8, 1-5, 1-4, 1-3, 1-2, or 1 amino acids in length can be added to the N-terminal region of SEQ ID NO: 1 or 2 or any adnectin set forth in Table 3. Exemplary alternative N-terminal regions include (represented by the single letter amino acid code) M, MG, G, MGVSDVPRDL (SEQ ID NO: 574) and GVSDVPRDL (SEQ ID NO: 575). Other suitable alternative N-terminal regions, which may be linked, e.g., to the N-terminus of an adnectin core sequence, include, for example, X_nSDVPRDL (SEQ ID NO: 576), X_nDVPRDL (SEQ ID NO: 577), X_nVPRDL (SEQ ID NO: 578), X_nPRDL (SEQ ID NO: 579) X_nRDL (SEQ ID NO: 580), X_nDL (SEQ ID NO: 581), or X_nL, wherein n=0, 1 or 2 amino acids, wherein when n=1, X is Met or Gly, and when n=2, X is Met-Gly. When a Met-Gly sequence is added to the N-terminus of a ^{10}Fn3 domain, the M will usually be cleaved off, leaving a G at the N-terminus. In some embodiments, the alternative N-terminal region comprises the amino acid sequence MASTSG (SEQ ID NO: 582).

[0189] In exemplary embodiments, an alternative C-terminal region having from 1-20, 1-15, 1-10, 1-8, 1-5, 1-4, 1-3, 1-2, or 1 amino acids in length can be added to the C-terminal region of SEQ ID NO: 1 or 2 or any adnectin set forth in Table 3. Specific examples of alternative C-terminal region sequences include, for example, polypeptides comprising, consisting essentially of, or consisting of, EIEK (SEQ ID NO: 584), EGSGC (SEQ ID NO: 585), EIEKPCQ (SEQ ID NO: 586), EIEKPSQ (SEQ ID NO: 587), EIEKP (SEQ ID NO: 588), EIEKPS (SEQ ID NO: 589), or EIEKPC (SEQ ID NO: 590). In some embodiments, the alternative C-terminal region comprises EIDK (SEQ ID NO: 591), and in particular embodiments, the alternative C-terminal region is either EIDKPCQ (SEQ ID NO: 592) or EIDKPSQ (SEQ ID NO: 593). Additional suitable alternative C-terminal regions are set forth in SEQ ID NOs: 594-618.

[0190] In certain embodiments, an Adnectin is linked to a C-terminal extension sequence that comprises E and D residues, and may be between 8 and 50, 10 and 30, 10 and 20, 5 and 10, and 2 and 4 amino acids in length. In some embodiments, tail sequences include ED-based linkers in which the sequence comprises tandem repeats of ED. In exemplary embodiments, the tail sequence comprises 2-10, 2-7, 2-5, 3-10, 3-7, 3-5, 3, 4 or 5 ED repeats. In certain embodiments, the ED-based tail sequences may also include additional amino acid residues, such as, for example: EI, EID, ES, EC, EGS, and EGC. Such sequences are based, in part, on known Adnectin tail sequences, such as EIDKPSQ (SEQ ID NO: 593), in which residues D and K have been removed. In exemplary embodiments, the ED-based tail comprises an E, I or E1 residues before the ED repeats.

[0191] In certain embodiments, the N- or C-terminal extension sequences are linked to the anti-PD-L1 Adnectin sequences with known linker sequences (e.g., SEQ ID NOs: 629-678 in Table 3). In some embodiments, sequences may be placed at the C-terminus of the ^{10}Fn3 domain to facilitate attachment of a pharmacokinetic moiety. For example, a cysteine containing linker such as GSGC (SEQ ID NO: 638) may be added to the C-terminus to facilitate site directed PEGylation on the cysteine residue.

[0192] In certain embodiments, an alternative C-terminal moiety, which can be linked to the C-terminal amino acids RT (i.e., amino acid 94) comprises the amino acids P_mX_n, wherein P is proline, X is any amino acid, m is an integer that is at least 1 and n is 0 or an interger that is at least 1. In certain embodiments, the alternative C-terminal moiety comprises the amino acids PC. In certain embodiments, the alternative C-terminal moiety comprises the amino acids PI, PC, PID, PIE, PIDK (SEQ ID NO: 605), PIEK (SEQ ID NO: 606), PIDKP (SEQ ID NO: 607), PIEKP (SEQ ID NO: 608), PIDKPS (SEQ ID NO: 609), PIEKPS (SEQ ID NO: 610), PIDKPC (SEQ ID NO: 611), PIEKPC (SEQ ID NO: 612), PIDKPSQ (SEQ ID NO: 613), PIEKPSQ (SEQ ID NO: 614), PIDKPCQ (SEQ ID NO: 615), PIEKPCQ (SEQ ID NO: 616), PHHHHHH (SEQ ID NO: 617), and PCHHHHHH (SEQ ID NO: 618). Exemplary anti-PD-L1 Adnectins having PC at their C-terminus are provided in the Examples and Table 3.

[0193] In certain embodiments, the Adnectins described herein have a 6× his tail (SEQ ID NO: 619).

[0194] In certain embodiments, the fibronectin based scaffold proteins comprise a ^{10}Fn3 domain having both an alternative N-terminal region sequence and an alternative C-terminal region sequence, and optionally a 6× his tail.

II. BIOLOGICAL PROPERTIES OF ANTI-PD-L1 ADNECTINS

[0195] Provided herein are adnectins that bind to human PD-L1 with a KD of 10 nM, 1 nM, 0.5 nM, 0.1 nM or less, as determined, e.g., by SPR (Biacore) and exhibit one or more of the following properties:

[0196] 1. Inhibition of the interaction between human PD-L1 and human PD-1 by at least 50%, 70%, 80%, 90% or more, as determined, e.g., by flow cytometry, e.g., using a human PD-1Fc protein and human PD-L1 positive cells, such as L2987 cells;

[0197] 2. Inhibition of the binding of human CD80 (B7-1) to human PD-L1 by at least 50%, 70%, 80%, 90% or more, as determined, e.g., in an ELISA assay or by SPR (Biacore);

[0198] 3. Inhibition of the binding of the anti-PD-L1 antibody 12A4 (described, e.g., in U.S. Pat. No. 7,943,743) to human PD-L1 by at least 50%, 70%, 80%, 90% or more, as determined, e.g., in an ELISA assay or by SPR (Biacore); and

[0199] 4. Inhibit cell proliferation in a mixed lymphocyte reaction (MLR).

[0200] In certain embodiments, an anti-PD-L1 adnectin binds to human PD-L1 with a KD of 1 nM or less and exhibits each one of properties 1-4. In certain embodiments, an anti-PD-L1 adnectin binds to human PD-L1 with a KD of 0.1 nM or less and exhibits each one of properties 1-4.

[0201] Provided herein are adnectins that comprise an amino acid sequence that is at least 70%, 80%, 90%, 95%, 97%, 98% or 99% identical to an anti-PD-L1 adnectin described herein or a portion thereof (e.g., the BC, DE and FG loops), bind to human PD-L1 with a KD of 10 nM, 1 nM, 0.5 nM, 0.1 nM or less, as determined, e.g., by SPR (Biacore) and exhibit one or more of the following properties:

[0202] 1. Inhibition of the interaction between human PD-L1 and human PD-1 by at least 50%, 70%, 80%, 90% or more, as determined, e.g., by flow cytometry, e.g., using a human PD-1Fc protein and human PD-L1 positive cells, such as L2987 cells;

[0203] 2. Inhibition of the binding of human CD80 (B7-1) to human PD-L1 by at least 50%, 70%, 80%, 90% or more, as determined, e.g., in an ELISA assay or by SPR (Biacore);

[0204] 3. Inhibition of the binding of the anti-PD-L1 antibody 12A4 to human PD-L1 by at least 50%, 70%, 80%, 90% or more, as determined, e.g., in an ELISA assay or by SPR (Biacore); and

[0205] 4. Inhibit cell proliferation in a mixed lymphocyte reaction (MLR).

[0206] In certain embodiments, an anti-PD-L1 adnectin comprises an amino acid sequence that is at least 70%, 80%, 90%, 95%, 97%, 98% or 99% identical to an anti-PD-L1 adnectin described herein or a portion thereof (e.g., the BC, DE and FG loops), binds to human PD-L1 with a KD of 1 nM or less and exhibits each one of properties 1-4. In certain embodiments, an anti-PD-L1 adnectin comprises an amino acid sequence that is at least 70%, 80%, 90%, 95%, 97%, 98% or 99% identical to an anti-PD-L1 adnectin described herein or a portion thereof (e.g., the BC, DE and FG loops), binds to human PD-L1 with a KD of 0.1 nM or less and exhibits each one of properties 1-4.

[0207] In certain embodiments, the anti-PD-L1 Adnectins compete (e.g., cross-compete) for binding to PD-L1 with the particular anti-PD-L1 Adnectins described herein. Such competing Adnectins can be identified based on their ability to competitively inhibit binding to PD-L1 of Adnectins described herein in standard PD-L1 binding assays. For example, standard ELISA assays can be used in which a recombinant PD-L1 protein is immobilized on the plate, one of the Adnectins is fluorescently labeled and the ability of non-labeled Adnectins to compete off the binding of the labeled Adnectin is evaluated.

[0208] In certain embodiments, a competitive ELISA format can be performed to determine whether two anti-PD-L1 Adnectins bind overlapping Adnectin binding sites on PD-L1. In one format, Adnectin #1 is coated on a plate, which is then blocked and washed. To this plate is added either PD-L1 alone, or PD-L1 pre-incubated with a saturating concentration of Adnectin #2. After a suitable incubation period, the plate is washed and probed with a polyclonal anti-PD-L1 antibody, such as a biotinylated anti-PD-L1 polyclonal antibody, followed by detection with streptavidin-HRP conjugate and standard tetramethylbenzidine development procedures. If the OD signal is the same with or without preincubation with Adnectin #2, then the two Adnectins bind independently of one another, and their Adnectin binding sites do not overlap. If, however, the OD signal for wells that received PD-L1/Adnectin #2 mixtures is lower than for those that received PD-L1 alone, then binding of Adnectin #2 is confirmed to block binding of Adnectin #1 to PD-L1.

[0209] Alternatively, a similar experiment is conducted by surface plasmon resonance (SPR, e.g., BIAcore). Adnectin #1 is immobilized on an SPR chip surface, followed by injections of either PD-L1 alone or PD-L1 pre-incubated with a saturating concentration of Adnectin #2. If the binding signal for PD-L1/Adnectin #2 mixtures is the same or higher than that of PD-L1 alone, then the two Adnectins bind independently of one another, and their Adnectin binding sites do not overlap. If, however, the binding signal for PD-L1/Adnectin #2 mixtures is lower than the binding signal for PD-L1 alone, then binding of Adnectin #2 is confirmed to block binding of Adnectin #1 to PD-L1. A feature of these experiments is the use of saturating concentrations of Adnectin #2. If PD-L1 is not saturated with Adnectin #2, then the conclusions above do not hold. Similar experiments can be used to determine if any two PD-L1 binding proteins bind to overlapping Adnectin binding sites.

[0210] Both assays exemplified above may also be performed in the reverse order where Adnectin #2 is immobilized and PD-L1-Adnectin #1 are added to the plate. Alternatively, Adnectin #1 and/or #2 can be replaced with a monoclonal antibody and/or soluble receptor-Fc fusion protein.

[0211] In certain embodiments, competition can be determined using a HTRF sandwich assay.

[0212] In certain embodiments, the competing Adnectin is an Adnectin that binds to the same Adnectin binding site on PD-L1 as a particular anti-PD-L1 Adnectin described herein. Standard mapping techniques, such as protease mapping, mutational analysis, HDX-MS, x-ray crystallography and

2-dimensional nuclear magnetic resonance, can be used to determine whether an Adnectin binds to the same Adnectin binding site or epitope as a reference Adnectin (see, e.g., *Epitope Mapping Protocols in Methods in Molecular Biology*, Vol. 66, G. E. Morris, Ed. (1996)). An epitope is defined by the method used to locate it. For example, in certain embodiments, a PD-L1 adnectin or antibody binds to the same epitope as that of one of the PD-L1 adnectins described herein, as determined by HDX-MS or as determined by X-ray crystallography.

[0213] Candidate competing anti-PD-L1 Adnectins can inhibit the binding of anti-PD-L1 Adnectins described herein to PD-L1 by at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 98%, or at least 99% and/or their binding is inhibited by at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 98%, or at least 99% by anti-PD-L1 Adnectins. The % competition can be determined using the methods described above.

[0214] Provided herein are adnectins that bind to human PD-L1 with a KD of 10 nM, 1 nM, 0.5 nM, 0.1 nM or less, as determined, e.g., by SPR (Biacore) and exhibit one or more of the following properties:

[0215] 1. Inhibition of the interaction between human PD-L1 and human PD-1 by at least 50%, 70%, 80%, 90% or more, as determined, e.g., by flow cytometry, e.g., using a human PD-1Fc protein and human PD-L1 positive cells, such as L2987 cells;

[0216] 2. Inhibition of the binding of human CD80 (B7-1) to human PD-L1 by at least 50%, 70%, 80%, 90% or more, as determined, e.g., in an ELISA assay or by SPR (Biacore);

[0217] 3. Inhibition of the binding of the anti-PD-L1 antibody 12A4 to human PD-L1 by at least 50%, 70%, 80%, 90% or more, as determined, e.g., in an ELISA assay or by SPR (Biacore);

[0218] 4. Inhibit cell proliferation in a mixed lymphocyte reaction (MLR); and

[0219] 5. Compete with an anti-PD-L1 antibody described herein for binding to human PD-L1.

[0220] In certain embodiments, an anti-PD-L1 adnectin binds to human PD-L1 with a KD of 1 nM or less and exhibits each one of properties 1-5. In certain embodiments, an anti-PD-L1 adnectin binds to human PD-L1 with a KD of 0.1 nM or less and exhibits each one of properties 1-5.

[0221] Provided herein are adnectins that comprise an amino acid sequence that is at least 70%, 80%, 90%, 95%, 97%, 98% or 99% identical to an anti-PD-L1 adnectin described herein or a portion thereof (e.g., the BC, DE and FG loops), bind to human PD-L1 with a KD of 10 nM, 1 nM, 0.5 nM, 0.1 nM or less, as determined, e.g., by SPR (Biacore) and exhibit one or more of the following properties:

[0222] 1. Inhibition of the interaction between human PD-L1 and human PD-1 by at least 50%, 70%, 80%, 90% or more, as determined, e.g., by flow cytometry, e.g., using a human PD-1Fc protein and human PD-L1 positive cells, such as L2987 cells;

[0223] 2. Inhibition of the binding of human CD80 (B7-1) to human PD-L1 by at least 50%, 70%, 80%, 90% or more, as determined, e.g., in an ELISA assay or by SPR (Biacore);

[0224] 3. Inhibition of the binding of the anti-PD-L1 antibody 12A4 to human PD-L1 by at least 50%, 70%, 80%, 90% or more, as determined, e.g., in an ELISA assay or by SPR (Biacore);

[0225] 4. Inhibit cell proliferation in a mixed lymphocyte reaction (MLR); and

[0226] 5. Compete with an anti-PD-L1 antibody described herein for binding to human PD-L1.

[0227] In certain embodiments, an anti-PD-L1 adnectin comprises an amino acid sequence that is at least 70%, 80%, 90%, 95%, 97%, 98% or 99% identical to an anti-PD-L1 adnectin described herein or a portion thereof (e.g., the BC, DE and FG loops), binds to human PD-L1 with a KD of 1 nM or less and exhibits each one of properties 1-5. In certain embodiments, an anti-PD-L1 adnectin comprises an amino acid sequence that is at least 70%, 80%, 90%, 95%, 97%, 98% or 99% identical to an anti-PD-L1 adnectin described herein or a portion thereof (e.g., the BC, DE and FG loops), binds to human PD-L1 with a KD of 0.1 nM or less and exhibits each one of properties 1-5.

III. FUSIONS, INCLUDING PHARMACOKINETIC MOIETIES

[0228] In certain embodiments, the anti-PD-L1 Adnectins desirably have a short half-life, for example, when used in PET imaging. In certain embodiments, an anti-PD-L1 adnectin has a half-life in blood or serum of 30 minutes to 3 hours, 30 minutes to 120 minutes, 60 minutes to 120 minutes, or 80 minutes to 100 minutes. In certain embodiments, the half-life of a PD-L1 Adnectin is similar to that of the label that is attached to it, e.g., ^{18}F.

[0229] The anti-PD-L1 Adnectins described herein may comprise a pharmacokinetic (PK) moiety. Improved pharmacokinetics may be assessed according to the perceived therapeutic need. The anti-PD-L1 Adnectin may be attached to a moiety that reduces the clearance rate of the polypeptide in a human by greater than two-fold, greater than three-fold, greater than four-fold or greater than five-fold relative to the unmodified anti-PD-L1 Adnectin. Other measures of improved pharmacokinetics may include serum half-life, which is often divided into an alpha phase and a beta phase. Either or both phases may be improved significantly by addition of an appropriate moiety. For example, the PK moiety may increase the serum half-life of the polypeptide by more than 10%, 20%, 50%, 2 fold, 3 fold or 5 fold relative to the Fn3 domain (or Adnectin) alone.

[0230] Moieties that slow clearance of a protein from the blood, herein referred to as "PK moieties", include polyoxyalkylene moieties (e.g., polyethylene glycol), sugars (e.g., sialic acid), and well-tolerated protein moieties (e.g., Fc and fragments and variants thereof, transferrin, or serum albumin). Other PK moieties that can be used in the invention include those described in Kontermann et al., (*Current Opinion in Biotechnology* 2011; 22:868-76), herein incorporated by reference. Such PK moieties include, but are not limited to PAS fusions (i.e., recombinant PEG mimetics based on the three amino acids proline, alanine, and serine), carbohydrate conjugates (e.g., hydroxyethyl starch (HES)), glycosylation, polysialic acid conjugates, and fatty acid conjugates.

IV. NUCLEIC ACID-PROTEIN FUSION TECHNOLOGY

[0231] In one aspect, the invention provides an Adnectin comprising fibronectin type III domains that binds PD-L1.

One way to rapidly make and test Fn3 domains with specific binding properties is the nucleic acid-protein fusion technology of Adnexus, a Bristol-Myers Squibb R&D Company. This disclosure utilizes the in vitro expression and tagging technology, termed 'PROfusion' which exploits nucleic acid-protein fusions (RNA- and DNA-protein fusions) to identify novel polypeptides and amino acid motifs that are important for binding to proteins. Nucleic acid-protein fusion technology is a technology that covalently couples a protein to its encoding genetic information. For a detailed description of the RNA-protein fusion technology and fibronectin-based scaffold protein library screening methods see Szostak et al., U.S. Pat. Nos. 6,258,558, 6,261,804, 6,214,553, 6,281,344, 6,207,446, 6,518,018 and 6,818,418; Roberts et al., *Proc. Natl. Acad. Sci.,* 1997; 94:12297-12302; and Kurz et al., *Molecules,* 2000; 5:1259-64, all of which are herein incorporated by reference.

V. VECTORS AND POLYNUCLEOTIDES

[0232] Also included in the present disclosure are nucleic acid sequences encoding any of the proteins described herein. As appreciated by those skilled in the art, because of third base degeneracy, almost every amino acid can be represented by more than one triplet codon in a coding nucleotide sequence. In addition, minor base pair changes may result in a conservative substitution in the amino acid sequence encoded but are not expected to substantially alter the biological activity of the gene product. Therefore, a nucleic acid sequence encoding a protein described herein may be modified slightly in sequence and yet still encode its respective gene product. Certain exemplary nucleic acids encoding the anti-PD-L1 Adnectins and their fusions described herein include nucleic acids having the sequences set forth in SEQ ID NOs: 16-19, 31-34, 46-49, 61-64, 76-79, 92-95, and 108-111.

[0233] Also contemplated are nucleic acid sequences that are at least 50%, such as at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to SEQ ID NOs: 16-19, 31-34, 46-49, 61-64, 76-79, 92-95, and 108-111, and encode a protein that binds to PD-L1. In some embodiments, nucleotide substitutions are introduced so as not to alter the resulting translated amino acid sequence.

[0234] Nucleic acids encoding any of the various proteins or polypeptides described herein may be synthesized chemically. Codon usage may be selected so as to improve expression in a cell. Such codon usage will depend on the cell type selected. Specialized codon usage patterns have been developed for *E. coli* and other bacteria, as well as mammalian cells, plant cells, yeast cells and insect cells. See for example: Mayfield et al., *Proc. Natl. Acad. Sci. USA,* 100(2):438-442 (Jan. 21, 2003); Sinclair et al., *Protein Expr. Purif.,* 26(I):96-105 (October 2002); Connell, N. D., *Curr. Opin. Biotechnol.,* 12(5):446-449 (October 2001); Makrides et al., *Microbiol. Rev.,* 60(3):512-538 (September 1996); and Sharp et al., *Yeast,* 7(7):657-678 (October 1991).

[0235] General techniques for nucleic acid manipulation are described in, for example, Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Edition, Vols. 1-3, Cold Spring Harbor Laboratory Press (1989), or Ausubel, F. et al., Current Protocols in Molecular Biology, Green Publishing and Wiley-Interscience, New York (1987) and periodic updates, herein incorporated by reference. Generally, the DNA encoding the polypeptide is operably linked to suitable transcriptional or translational regulatory elements derived from mammalian, viral, or insect genes. Such regulatory elements include a transcriptional promoter, an optional operator sequence to control transcription, a sequence encoding suitable mRNA ribosomal binding site, and sequences that control the termination of transcription and translation. The ability to replicate in a host, usually conferred by an origin of replication, and a selection gene to facilitate recognition of transformants is additionally incorporated.

[0236] The proteins described herein may be produced recombinantly not only directly, but also as a fusion polypeptide with a heterologous polypeptide, which is preferably a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. The heterologous signal sequence selected preferably is one that is recognized and processed (i.e., cleaved by a signal peptidase) by the host cell. An exemplary N-terminal leader sequence for production of polypeptides in a mammalian system is: METDTLLLWVLLLWVPGSTG (SEQ ID NO: 583), which is removed by the host cell following expression.

[0237] For prokaryotic host cells that do not recognize and process a native signal sequence, the signal sequence is substituted by a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase, 1 pp, or heat-stable enterotoxin II leaders.

[0238] For yeast secretion the native signal sequence may be substituted by, e.g., a yeast invertase leader, a factor leader (including *Saccharomyces* and *Kluyveromyces* alpha-factor leaders), or acid phosphatase leader, the *C. albicans* glucoamylase leader, or the signal sequence described in U.S. Pat. No. 5,631,144. In mammalian cell expression, mammalian signal sequences as well as viral secretory leaders, for example, the herpes simplex gD signal, are available. The DNA for such precursor regions may be ligated in reading frame to DNA encoding the protein.

[0239] Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Generally, in cloning vectors this sequence is one that enables the vector to replicate independently of the host chromosomal DNA, and includes origins of replication or autonomously replicating sequences. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the 2 micron plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for cloning vectors in mammalian cells. Generally, the origin of replication component is not needed for mammalian expression vectors (the SV40 origin may typically be used only because it contains the early promoter).

[0240] Expression and cloning vectors may contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, e.g., the gene encoding D-alanine racemase for Bacilli.

[0241] Expression and cloning vectors usually contain a promoter that is recognized by the host organism and is operably linked to the nucleic acid encoding the protein described herein, e.g., a fibronectin-based scaffold protein. Promoters suitable for use with prokaryotic hosts include the phoA promoter, beta-lactamase and lactose promoter systems, alkaline phosphatase, a tryptophan (trp) promoter system, and hybrid promoters such as the tan promoter. However, other known bacterial promoters are suitable. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding the protein described herein. Promoter sequences are known for eukaryotes. Virtually all eukaryotic genes have an AT-rich region located approximately 25 to 30 bases upstream from the site where transcription is initiated. Another sequence found 70 to 80 bases upstream from the start of transcription of many genes is a CNCAAT region where N may be any nucleotide. At the 3' end of most eukaryotic genes is an AATAAA sequence that may be the signal for addition of the poly A tail to the 3' end of the coding sequence. All of these sequences are suitably inserted into eukaryotic expression vectors.

[0242] Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase or other glycolytic enzymes, such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

[0243] Transcription from vectors in mammalian host cells can be controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus, adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and most preferably Simian Virus 40 (SV40), from heterologous mammalian promoters, e.g., the actin promoter or an immunoglobulin promoter, from heat-shock promoters, provided such promoters are compatible with the host cell systems.

[0244] Transcription of a DNA encoding protein described herein by higher eukaryotes is often increased by inserting an enhancer sequence into the vector. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, α-fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. See also Yaniv, Nature, 297:17-18 (1982) on enhancing elements for activation of eukaryotic promoters. The enhancer may be spliced into the vector at a position 5' or 3' to the peptide-encoding sequence, but is preferably located at a site 5' from the promoter.

[0245] Expression vectors used in eukaryotic host cells (e.g., yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of mRNA encoding the protein described herein. One useful transcription termination component is the bovine growth hormone polyadenylation region. See WO 94/11026 and the expression vector disclosed therein.

[0246] The recombinant DNA can also include any type of protein tag sequence that may be useful for purifying the protein. Examples of protein tags include, but are not limited to, a histidine tag, a FLAG tag, a myc tag, an HA tag, or a GST tag. Appropriate cloning and expression vectors for use with bacterial, fungal, yeast, and mammalian cellular hosts can be found in Cloning Vectors: A Laboratory Manual, (Elsevier, New York (1985)), the relevant disclosure of which is hereby incorporated by reference.

[0247] The expression construct is introduced into the host cell using a method appropriate to the host cell, as will be apparent to one of skill in the art. A variety of methods for introducing nucleic acids into host cells are known in the art, including, but not limited to, electroporation; transfection employing calcium chloride, rubidium chloride, calcium phosphate, DEAE-dextran, or other substances; microprojectile bombardment; lipofection; and infection (where the vector is an infectious agent).

[0248] Suitable host cells include prokaryotes, yeast, mammalian cells, or bacterial cells. Suitable bacteria include gram negative or gram positive organisms, for example, *E. coli* or *Bacillus* spp. Yeast, preferably from the *Saccharomyces* species, such as *S. cerevisiae*, may also be used for production of polypeptides. Various mammalian or insect cell culture systems can also be employed to express recombinant proteins. Baculovirus systems for production of heterologous proteins in insect cells are reviewed by Luckow et al. (Bio/Technology, 6:47 (1988)). Examples of suitable mammalian host cell lines include endothelial cells, COS-7 monkey kidney cells, CV-1, L cells, C127, 3T3, Chinese hamster ovary (CHO), human embryonic kidney cells, HeLa, 293, 293T, and BHK cell lines. Purified polypeptides are prepared by culturing suitable host/vector systems to express the recombinant proteins. For many applications, the small size of many of the polypeptides described herein would make expression in *E. coli* as the preferred method for expression. The protein is then purified from culture media or cell extracts.

VI. PROTEIN PRODUCTION

[0249] Also described herein are cell lines that express an anti-PD-L1 Adnectin or fusion polypeptide thereof. Creation and isolation of cell lines producing an anti-PD-L1 Adnectin can be accomplished using standard techniques known in the art, such as those described herein.

[0250] Host cells are transformed with the herein-described expression or cloning vectors for protein production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences.

[0251] Adnectins of the present invention can also be obtained in aglycosylated form by producing the Adnectins in, e.g., prokaryotic cells (e.g., *E. coli*). Notably, aglycosylated forms of the Adnectins described herein exhibit the same affinity, potency, and mechanism of action as glycosylated Adnectins when tested in vitro.

[0252] The host cells used to produce the proteins of this invention may be cultured in a variety of media. Commercially available media such as Ham's F10 (Sigma), Minimal Essential Medium ((MEM), (Sigma), RPMI-1640 (Sigma), and Dulbecco's Modified Eagle's Medium ((DMEM), Sigma)) are suitable for culturing the host cells. In addition, many of the media described in Ham et al., Meth. Enzymol., 58:44 (1979), Barites et al., Anal. Biochem., 102:255 (1980), U.S. Pat. Nos. 4,767,704, 4,657,866, 4,927,762, 4,560,655, 5,122,469, 6,048,728, 5,672,502, or U.S. Pat. No. RE 30,985 may be used as culture media for the host cells. Any of these media may be supplemented as necessary with hormones and/or other growth factors (such as insulin, transferrin, or epidermal growth factor), salts (such as sodium chloride, calcium, magnesium, and phosphate), buffers (such as HEPES), nucleotides (such as adenosine and thymidine), antibiotics (such as Gentamycin drug), trace elements (defined as inorganic compounds usually present at final concentrations in the micromolar range), and glucose or an equivalent energy source. Any other necessary supplements may also be included at appropriate concentrations that would be known to those skilled in the art. The culture conditions, such as temperature, pH, and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

[0253] Proteins described herein can also be produced using cell-free translation systems. For such purposes the nucleic acids encoding the polypeptide must be modified to allow in vitro transcription to produce mRNA and to allow cell-free translation of the mRNA in the particular cell-free system being utilized (eukaryotic such as a mammalian or yeast cell-free translation system or prokaryotic such as a bacterial cell-free translation system).

[0254] Proteins described herein can also be produced by chemical synthesis (e.g., by the methods described in Solid Phase Peptide Synthesis, 2nd Edition, The Pierce Chemical Co., Rockford, Ill. (1984)). Modifications to the protein can also be produced by chemical synthesis.

[0255] The proteins of the present invention can be purified by isolation/purification methods for proteins generally known in the field of protein chemistry. Non-limiting examples include extraction, recrystallization, salting out (e.g., with ammonium sulfate or sodium sulfate), centrifugation, dialysis, ultrafiltration, adsorption chromatography, ion exchange chromatography, hydrophobic chromatography, normal phase chromatography, reversed-phase chromatography, get filtration, gel permeation chromatography, affinity chromatography, electrophoresis, countercurrent distribution or any combinations of these. After purification, polypeptides may be exchanged into different buffers and/or concentrated by any of a variety of methods known to the art, including, but not limited to, filtration and dialysis.

[0256] The purified polypeptide is preferably at least 85% pure, or preferably at least 95% pure, and most preferably at least 98% pure. Regardless of the exact numerical value of the purity, the polypeptide is sufficiently pure for use as a pharmaceutical product.

High Throughput Protein Production (HTPP)

[0257] Selected binders cloned into the PET9d vector upstream of a HIS_6tag and are transformed into *E. coli* BL21 DE3 plysS cells and inoculated in 5 ml LB medium containing 50 µg/mL kanamycin in a 24-well format and grown at 37° C. overnight. Fresh 5 ml LB medium (50 µg/mL kanamycin) cultures are prepared for inducible expression by aspiration of 200 µl from the overnight culture and dispensing it into the appropriate well. The cultures are grown at 37° C. until A_{600} 0.6-0.9. After induction with 1 mM isopropyl-β-thiogalactoside (IPTG), the culture is expressed for 6 hours at 30° C. and harvested by centrifugation for 10 minutes at 2750 g at 4° C.

[0258] Cell pellets (in 24-well format) are lysed by resuspension in 450 µl of Lysis buffer (50 mM NaH_2PO_4, 0.5 M NaCl, 1× Complete™ Protease Inhibitor Cocktail-EDTA free (Roche), 1 mM PMSF, 10 mM CHAPS, 40 mM imidazole, 1 mg/ml lysozyme, 30 µg/ml DNAse, 2 µg/ml aprotonin, pH 8.0) and shaken at room temperature for 1-3 hours. Lysates are cleared and re-racked into a 96-well format by transfer into a 96-well Whatman GF/D Unifilter fitted with a 96-well, 1.2 ml catch plate and filtered by positive pressure. The cleared lysates are transferred to a 96-well Nickel or Cobalt-Chelating Plate that had been equilibrated with equilibration buffer (50 mM NaH_2PO_4, 0.5 M NaCl, 40 mM imidazole, pH 8.0) and are incubated for 5 min. Unbound material is removed by positive pressure. The resin is washed twice with 0.3 ml/well with Wash buffer #1 (50 mM NaH_2PO_4, 0.5 M NaCl, 5 mM CHAPS, 40 mM imidazole, pH 8.0). Each wash is removed by positive pressure. Prior to elution, each well is washed with 50 µl Elution buffer (PBS+20 mM EDTA), incubated for 5 min, and this wash is discarded by positive pressure. Protein is eluted by applying an additional 100 µl of Elution buffer to each well. After a 30 minute incubation at room temperature, the plate(s) are centrifuged for 5 minutes at 200 g and eluted protein collected in 96-well catch plates containing 5 µl of 0.5 M $MgCl_2$ added to the bottom of elution catch plate prior to elution. Eluted protein is quantified using a total protein assay with wild-type ^{10}Fn3 domain as the protein standard.

Midscale Expression and Purification of Insoluble Fibronectin-Based Scaffold Protein Binders

[0259] For expression of insoluble clones, the clone(s), followed by the HIS_6tag, are cloned into a pET9d (EMD Bioscience, San Diego, Calif.) vector and are expressed in *E. coli* HMS174 cells. Twenty ml of an inoculum culture (generated from a single plated colony) is used to inoculate 1 liter of LB medium containing 50 µg/ml carbenicillin and 34 µg/ml chloramphenicol. The culture is grown at 37° C. until A_{600} 0.6-1.0. After induction with 1 mM isopropyl-β-thiogalactoside (IPTG) the culture is grown for 4 hours at 30° C. and is harvested by centrifugation for 30 minutes at >10,000 g at 4° C. Cell pellets are frozen at −80° C. The cell pellet is resuspended in 25 ml of lysis buffer (20 mM $aH2P0_4$, 0.5 M NaCl, 1× Complete Protease Inhibitor Cocktail-EDTA free (Roche), ImM PMSF, pH 7.4) using an ULTRA-TURRAX® homogenizer (IKA works) on ice. Cell lysis is achieved by high pressure homogenization (>18,000 psi) using a Model M-1 10S MICROFLUIDIZER® (Microfluidics). The insoluble fraction is separated by centrifugation for 30 minutes at 23,300 g at 4° C. The insoluble pellet recovered from centrifugation of the lysate is washed with 20 mM sodiumphosphate/500 mM NaCl, pH7.4. The pellet is resolubilized in 6.0 M guanidine hydrochloride in 20 mM sodium phosphate/500M NaCl pH 7.4 with sonication followed by incubation at 37 degrees for 1-2 hours. The resolubilized pellet is filtered to 0.45 m and loaded onto a Histrap column equilibrated with the 20 mM sodium phosphate/500 M NaCl/6.0 M guanidine pH 7.4 buffer. After loading, the column is washed for an additional 25 CV with the same buffer. Bound protein is eluted with 50 mM Imidazole in 20 mM sodium phosphate/500 mM NaCl/6.0

M guan-HCl pH7.4. The purified protein is refolded by dialysis against 50 mM sodium acetate/150 mM NaCl pH 4.5.

Midscale Expression and Purification of Soluble Fibronectin-Base Scaffold Protein Binders

[0260] For expression of soluble clones, the clone(s), followed by the HIS_6tag, are cloned into a pET9d (EMD Bioscience, San Diego, Calif.) vector and expressed in *E. coli* HMS174 cells. Twenty ml of an inoculum culture (generated from a single plated colony) is used to inoculate 1 liter of LB medium containing 50 μg/ml carbenicillin and 34 μg/ml chloramphenicol. The culture is grown at 37° C. until A_{600} 0.6-1.0. After induction with 1 mM isopropyl-β-thiogalactoside (IPTG), the culture is grown for 4 hours at 30° C. and harvested by centrifugation for 30 minutes at >10,000 g at 4° C. Cell pellets are frozen at −80° C. The cell pellet is resuspended in 25 ml of lysis buffer (20 mM NaH_2PO_4, 0.5 M NaCl, 1× Complete Protease Inhibitor Cocktail-EDTA free (Roche), 1 mM PMSF, pH 7.4) using an ULTRA-TURRAX® homogenizer (IKA works) on ice. Cell lysis is achieved by high pressure homogenization (>18,000 psi) using a Model M-1 10S MICROFLUIDIZER® (Microfluidics). The soluble fraction is separated by centrifugation for 30 minutes at 23,300 g at 4° C. The supernatant is clarified via 0.45 m filter. The clarified lysate is loaded onto a Histrap column (GE) pre-equilibrated with the 20 mM sodium phosphate/500M NaCl pH 7.4. The column is then washed with 25 column volumes of the same buffer, followed by 20 column volumes of 20 mM sodium phosphate/500 M NaCl/25 mM Imidazole, pH 7.4 and then 35 column volumes of 20 mM sodium phosphate/500 M NaCl/40 mM Imidazole, pH 7.4. Protein is eluted with 15 column volumes of 20 mM sodium phosphate/500 M NaCl/500 mM Imidazole, pH 7.4, fractions are pooled based on absorbance at A_2so and dialyzed against 1×PBS, 50 mM Tris, 150 mM NaCl; pH 8.5 or 50 mM NaOAc; 150 mM NaCl; pH4.5. Any precipitate is removed by filtering at 0.22 m.

VII. COMPOSITIONS

[0261] The present invention further provides compositions, such as pharmaceutical compositions and radiopharmaceutical compositions, comprising an anti-PD-L1 Adnectin or fusion proteins thereof described herein, wherein the composition is essentially endotoxin free, or at least contain no more than acceptable levels of endotoxins as determined by the appropriate regulatory agency (e.g., FDA).

[0262] Methods well known in the art for making compositions are found, for example, in "Remington: The Science and Practice of Pharmacy" (20th ed., ed. A. R. Gennaro A R., 2000, Lippincott Williams & Wilkins, Philadelphia, Pa.). Compositions for parenteral administration may, for example, contain excipients, sterile water, saline, polyalkylene glycols such as polyethylene glycol, oils of vegetable origin, or hydrogenated napthalenes. Biocompatible, biodegradable lactide polymer, lactide/glycolide copolymer, or polyoxyethylene-polyoxypropylene copolymers may be used to control the release of the compounds. Nanoparticulate compositions (e.g., biodegradable nanoparticles, solid lipid nanoparticles, liposomes) may be used to control the biodistribution of the compounds. Other potentially useful parenteral delivery systems include ethylene-vinyl acetate copolymer particles, osmotic pumps, implantable infusion systems, and liposomes. The concentration of the compound in the composition varies depending upon a number of factors, including the dosage of the drug to be administered, the route of administration, and the purpose of the composition (e.g., prophylactic, therapeutic, diagnostic).

[0263] Acceptable carriers, excipients, or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid and methionine; preservatives (such as octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride, benzethonium chloride; phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium; metal complexes (e.g., Zn-protein complexes); and/or non-ionic surfactants such as Tween, PLURONIC™ or polyethylene glycol (PEG).

[0264] The polypeptides of the present invention may be optionally administered as a pharmaceutically acceptable salt, such as non-toxic acid addition salts or metal complexes that are commonly used in the pharmaceutical industry. Examples of acid addition salts include organic acids such as acetic, lactic, pamoic, maleic, citric, malic, ascorbic, succinic, benzoic, palmitic, suberic, salicylic, tartaric, methanesulfonic, toluenesulfonic, or trifluoroacetic acids or the like; polymeric acids such as tannic acid, carboxymethyl cellulose, or the like; and inorganic acid such as hydrochloric acid, hydrobromic acid, sulfuric acid phosphoric acid, or the like. Metal complexes include zinc, iron, and the like. In one example, the polypeptide is formulated in the presence of sodium acetate to increase thermal stability.

[0265] The active ingredients may also be entrapped in a microcapsule prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsule and poly-(methylmethacylate) microcapsule, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles and nanocapsules) or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. (1980).

[0266] The pharmaceutical composition to be used for in vivo administration typically must be sterile. This may be accomplished by filtration through sterile filtration membranes. Where the composition is lyophilized, sterilization using this method may be conducted either prior to or following lyophilization and reconstitution. The composition for parenteral administration may be stored in lyophilized form or in solution. In addition, parenteral compositions generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

[0267] Once the pharmaceutical composition has been formulated, it may be stored in sterile vials as a solution, suspension, gel, emulsion, solid, or a dehydrated or lyophilized powder. Such formulations may be stored either in a ready-to-use form or in a form (e.g., lyophilized) requiring reconstitution prior to administration.

VII. BIOPHYSICAL AND BIOCHEMICAL CHARACTERIZATION

[0268] Binding of an anti-PD-L1 Adnectin described herein to PD-L1, e.g., human PD-L1, may be assessed in terms of equilibrium constants (e.g., dissociation. K_D) and in terms of kinetic constants (e.g., on-rate constant, k_{on} and off-rate constant, k_{off}). An Adnectin will generally bind to a target molecule with a K_D of less than 500 nM, 100 nM, 10 nM, I nM, 500 pM, 200 pM, or 100 pM, although higher K_D values may be tolerated where the k_{off} is sufficiently low or the k_{on}, is sufficiently high.

In Vitro Assays for Binding Affinity

[0269] An Anti-PD-L1 Adnectin that binds to and antagonizes PD-L1 can be identified using various in vitro assays. In certain embodiments, the assays are high-throughput assays that allow for screening multiple candidate Adnectins simultaneously.

[0270] Exemplary assays for determining the binding affinity of an anti-PD-L1 Adnectin includes, but is not limited to, solution phase methods such as the kinetic exclusion assay (KinExA) (Blake et al., *JBC* 1996; 271: 27677-85; Drake et al., *Anal Biochen* 2004; 328:35-43), surface plasmon resonance (SPR) with the Biacore system (Uppsala, Sweden) (Welford et al., *Opt. Quant. Elect* 1991; 23:1; Morton and Myszka, *Methods in Enzymology* 1998; 295:268) and homogeneous tine resolved fluorescence (HTRF) assays (Newton et al., *J. Biomol Screen* 2008; 13:674-82; Patel et al., *Assay Drug Dev Technol* 2008; 6:55-68).

[0271] In certain embodiments, biomolecular interactions can be monitored in real time with the Bilacore system, which uses SPR to detect changes in the resonance angle of light at the surface of a thin gold film on a glass support due to changes in the refractive index of the surface up to 300 nm away. Biacore analysis generates association rate constants, dissociation rate constants, equilibrium dissociation constants, and affinity constants. Binding affinity is obtained by assessing the association and dissociation rate constants using a Biacore surface plasmon resonance system (Biacore. Inc.). A biosensor chip is activated for covalent coupling of the target. The target is then diluted and injected over the chip to obtain a signal in response units of immobilized material. Since the signal in resonance units (RU) is proportional to the mass of immobilized material, this represents a range of immobilized target densities on the matrix. Association and dissociation data are fit simultaneously in a global analysis to solve the net rate expression for a 1:1 bimolecular interaction, yielding best fit values for k_{on}, k_{off} and R_{max} (maximal response at saturation). Equilibrium dissociation constants for binding, K_D's are calculated from SPR measurements as k_{off}/k_{on}.

[0272] In some embodiments, the anti-PD-L1 Adnectins described herein exhibit a K_D of binding to human PD-L1 in the SPR affinity assay described in Example 2 of 500 nM or less, 400 nM or less, 300 nM or less, 200 nM or less, 150 nM or less, 100 nM or less, 90 nM or less, 80 nM or less, 70 n M or less, 60 nM or less, 50 nM or less, 40 n M or less, 30 nM or less, 20 nM or less, 15 nM or less, 10 nM or less, 5 nM or less, or 1 nM or less.

[0273] It should be understood that the assays described herein above are exemplary, and that any method known in the art for determining the binding affinity between proteins (e.g., fluorescence based-transfer (FRET), enzyme-linked immunosorbent assay, and competitive binding assays (e.g., radioimmunoassays)) can be used to assess the binding affinities of the anti-PD-L1 Adnectins described herein.

IX. IN VIVO IMAGING WITH ANTI-PD-L1 ADNECTINS

Imaging Agents

[0274] The anti-PD-L1 Adnectins described herein also are useful in a variety of diagnostic and imaging applications. In certain embodiments, an anti-PD-L1 Adnectin is labelled with a moiety that is detectable in vivo and such labelled Adnectins may be used as in vivo imaging agents, e.g., for whole body imaging. For example, in one embodiment, a method for detecting a PD-L1 positive tumor in a subject comprises administering to the subject an anti-PD-L1 Adnectin linked to a detectable label, and following an appropriate time, detecting the label in the subject.

[0275] An anti-PD-L1 Adnectin imaging agent may be used to diagnose a disorder or disease associated with increased levels of PD-L1, for example, a cancer in which a tumor selectively overexpresses PD-L1. In a similar manner, an anti-PD-L1 Adnectin can be used to monitor PD-L1 levels in a subject, e.g., a subject that is being treated to reduce PD-L1 levels and/or PD-L1 positive cells (e.g., tumor cells or tumor infiltrating lymphocytes (TILs)) or a subject treated with an immunotherapy, e.g., a PD-1 antagonist. The anti-PD-L1 Adnectin imaging agent may be used to determine whether a subject is likely to respond to a therapy that requires the presence of PD-L1, e.g., an immunotherapy, such as a PD-1 or PD-L1 antagonist treatment. The anti-PD-L1 Adnectins may be used with or without modification, and may be labeled by covalent or non-covalent attachment of a detectable moiety.

[0276] Detectable moieties that may be used include radioactive agents, such as: radioactive heavy metals such as iron chelates, radioactive chelates of gadolinium or manganese, positron emitters of oxygen, nitrogen, iron, carbon, or gallium, ^{18}F, ^{60}Cu, ^{61}Cu, ^{62}Cu, ^{64}Cu, ^{124}I, ^{86}Y, ^{89}Zr, ^{66}Ga, ^{67}Ga, ^{68}Ga, ^{44}Sc, ^{47}Sc, ^{11}C, 111In, ^{114m}In, ^{114}In, ^{125}I, ^{124}I, ^{131}I, ^{123}I, ^{131}I, ^{123}I, ^{32}Cl, ^{33}Cl, ^{34}Cl, ^{74}Br, ^{76}Br, ^{77}Br, ^{77}Br, ^{78}Br, ^{89}Zr, ^{186}Re, ^{188}Re, ^{86}Y, ^{90}Y, ^{177}Lu, ^{99}Tc, ^{212}Bi, ^{213}Bi, ^{212}Pb, ^{225}Ac, or ^{153}Sn.

[0277] In certain embodiments, the radioactive agent is conjugated to the Adnectin at one or more amino acid residues. In certain embodiments, one or more, such as two or more, three or more, four or more, or a greater number of radionuclides can be present in the labelled probe. In certain embodiments, the radionuclide is attached directly to the Adnectin by a chelating agent (e.g., see U.S. Pat. No. 8,808,665). In certain embodiments, the radionuclide is present in a prosthetic group conjugated to the Adnectin by a bifunctional chelator or conjugating (BFC) moieity. In certain embodiments, the radionuclide chelating agent and/or conjugating moiety is DFO, DOTA and its derivatives (CB-DO2A, 3p-C-DEPA, TCMC, Oxo-1DO3A), DBCO, TE2A, CB-TE2A, CB-TE1A1P, CB-TE2P, MM-TE2A, DM-TE2A, diamsar and derivatives, NODASA, NODAGA, NOTA, NETA, TACN-TM, DTPA, 1B4M-DTPA, CHX-A"-DTPA, TRAP (PRP9), NOPO, AAZTA and derivatives (DATA), H_2dedpa, H_4octapa, H_2azapa, H_5decapa, H_6phospa, HBED, SHBED, BPCA, CP256, PCTA, HEHA, PEPA, EDTA, TETA, and TRITA based chelating agents, and close analogs and derivatives thereof.

[0278] In certain embodiments, the radionuclide chelating or conjugating (BFC) moiety is maleamide-NODAGA or maleamide-DBCO, which can be attached covalently to a polypeptide via cysteine residues near the C-terminus of the polypeptide. In certain embodiments, an anti-PD-L1 Adnectin is modified at its C-terminus by the addition of a cysteine. For example, PxCy may be linked C-terminal to the amino acid residues NYRT, wherein P is proline, C is cysteine, and x and y are integrers that are at least 1. Exemplary anti-PD-L1 Adnectins having the amino acid residues PC at their C-terminus are set forth in the Examples. Maleimide-NODAGA or maleimide-DBCO can be reacted with the cysteine, to yield Adnectin-NODAGA or Adnectin-DBCO, respectively.

[0279] In certain embodiments, the radionuclide chelating agent is DFO, which can be attached, e.g., at random surface lysines.

[0280] In certain embodiments, the chelator for ^{64}Cu is DOTA, NOTA, EDTA, Df, DTPA, or TETA. Suitable combinations of chelating agents and radionuclides are extensively reviewed in Price et al., *Chem Soc Rev* 2014; 43:260-90.

[0281] In certain embodiments, an anti-PD-L1 Adnectin is labelled with the PET tracer ^{18}F. ^{18}F is an attractive PET radionuclide with a 1.8 hour radioactive half life, which provides a same day imaging tool, where the PET radionuclide better matches the Adnectin 's biological half-life, resulting in excellent images with less radiation exposure to the patient. A PD-L1 Adnectin may be labelled with a prosthetic group, such as [^{18}F]-3-(2-(2-(2-(2-azidoethoxy) ethoxy)ethoxy)ethoxy)-2-fluoropyridine ([^{18}F]-FFPEGA), as further described in the Examples and in FIGS. **2** and **9**. As further shown in the Examples, an ^{18}F-labelled anti-PD-L1 Adnectin specifically and efficiently labelled human PD-L1 positive tumors in mice, PD-L1 positive human lung cancer tissue, and PD-L1 positive tumors in cynomolgus monkeys. Specific details on the labelling method is provided below and in the Examples.

[0282] In certain embodiments, a PD-L1 imaging agent is an anti-PD-L1 Adnectin that is labelled with ^{64}Cu, e.g., as described in the Examples. ^{64}Cu may be linked to an Adnectin with a chelating agent, such as NODAGA. As further shown in the Examples, a ^{64}Cu-labelled anti-PD-L1 Adnectin specifically and efficiently labelled human PD-L1 positive tumors in mice and PD-L1 positive tumors in cyno.

[0283] Other art-recognized methods for labelling polypeptides with radionuclides such as ^{64}Cu and ^{18}F for synthesizing the anti-PD-L1 Adnectin-based imaging agents described herein and in PCT applications PCT/US15/62485 and PCT/US15/62502 may also be used. See, e.g., US2014/0271467; Gill et al., *Nature Protocols* 2011; 6:1718-25; Berndt et al. *Nuclear Medicine and Biology* 2007; 34:5-15, Inkster et al., *Bioorganic & Medicinal Chemistry Letters* 2013; 23:3920-6, the contents of which are herein incorporated by reference in their entirety.

[0284] In certain embodiments, a PD-L1 imaging agent comprises a PEG molecule (e.g., 5 KDa PEG, 6 KDa PEG, 7 KDa PEG, 8 KDa PEG, 9 KDa PEG, or 10 KDa PEG) to increase the blood PK of the imaging agent by small increments to enhance the imaging contrast or increase avidity of the anti-PD-L1 Adnectin based imaging agent.

Administration and Imaging

[0285] In certain embodiments, the labeled anti-PD-L1 Adnectins can be used to image PD-L1-positive cells or tissues, e.g., PD-L1 expressing tumors. For example, the labeled anti-PD-L1 Adnectin is administered to a subject in an amount sufficient to uptake the labeled Adnectin into the tissue of interest (e.g., the PD-L1-expressing tumor). The subject is then imaged using an imaging system such as PET for an amount of time appropriate for the particular radionuclide being used. The labeled anti-PD-L1 Adnectin-bound PD-L1-expressing cells or tissues, e.g., PD-L1-expressing tumors, are then detected by the imaging system.

[0286] PET imaging with a PD-L1 imaging agent may be used to qualitatively or quantitatively detect PD-L1. A PD-L1 imaging agent may be used as a biomarker, and the presence or absence of a PD-L1 positive signal in a subject may be indicative that, e.g., the subject would be responsive to a given therapy, e.g., a cancer therapy, or that the subject is responding or not to a therapy.

[0287] In certain embodiments, the progression or regression of disease (e.g., tumor) can be imaged as a function of time or treatment. For instance, the size of the tumor can be monitored in a subject undergoing cancer therapy (e.g., chemotherapy, radiotherapy) and the extent of regression of the tumor can be monitored in real-time based on detection of the labeled anti-PD-L1 Adnectin. The distribution of PD-L1 within one or more tumors or healthy cells may also be visualized, and monitored prior and/or during a treatment and/or a disease.

[0288] The amount effective to result in uptake of the imaging agent (e.g., ^{18}F-Adnectin imaging agent, ^{64}Cu-Adnectin imaging agent) into the cells or tissue of interest (e.g., tumors) may depend upon a variety of factors, including for example, the age, body weight, general health, sex, and diet of the host; the time of administration; the route of administration; the rate of excretion of the specific probe employed; the duration of the treatment; the existence of other drugs used in combination or coincidental with the specific composition employed; and other factors.

[0289] In certain embodiments, imaging of tissues expressing PD-L1 is effected before, during, and after administration of the labeled anti-PD-L1 Adnectin to a subject.

[0290] In certain embodiments, the subject receiving a PD-L1 imaging agent is a mammal, for example, a human, dog, cat, ape, monkey, rat, or mouse.

[0291] In certain embodiments, the anti-PD-L1 Adnectins described herein are useful for PET imaging of lungs, heart, kidneys, liver, and skin, and other organs, or tumors associated with these organs which express PD-L1.

[0292] In certain embodiments, the anti-PD-L1 imaging agents provide a contrast of at least 50%, 75%, 2, 3, 4, 5 or more. The Examples show that all anti-PD-L1 Adnectins that were used provided a PET contrast of 2 or more, and that the affinity of the Adnectins was not important.

[0293] When used for imaging (e.g., PET) with short half-life radionuclides (e.g., ^{18}F), the radiolabeled anti-PD-L1 Adnectins are preferably administered intravenously, e.g., as a bolus injection. Other routes of administration are also suitable and depend on the half-life of the radionuclides used.

[0294] In certain embodiments, the anti-PD-L1 imaging agents described herein are used to detect PD-L1 positive cells in a subject by administering to the subject an anti-PD-L1 imaging agent disclosed herein, and detecting the imaging agent, the detected imaging agent defining the location of the PD-L1 positive cells in the subject. In certain embodiments, the imaging agent is detected by positron emission tomography.

[0295] In certain embodiments, the anti-PD-L1 imaging agents described herein are used to detect PD-L1 expressing tumors in a subject by administering to the subject an anti-PD-L1 imaging agent disclosed herein, and detecting the imaging agent, the detected imaging agent defining the location of the tumor in the subject. In certain embodiments, the imaging agent is detected by positron emission tomography.

[0296] In certain embodiments, an image of an anti-PD-L1 imaging agent described herein is obtained by administering the imaging agent to a subject and imaging in vivo the distribution of the imaging agent by positron emission tomography.

[0297] Disclosed herein are methods of obtaining a quantitative image of tissues or cells expressing PD-L1, the method comprising contacting the cells or tissue with an anti-PD-L1 imaging agent described herein and detecting or quantifying the tissue expressing PD-L1 using positron emission tomography.

[0298] Also disclosed herein are methods of detecting a PD-L1-expressing tumor comprising administering an imaging-effective amount of an anti-PD-L1 imaging agent described herein to a subject, e.g., a subject having or suspected of having a PD-L1-expressing tumor, and detecting the radioactive emissions of said imaging agent in the tumor using positron emission tomography, wherein the radioactive emissions are detected in the tumor.

[0299] Also disclosed herein are methods of diagnosing the presence of a PD-L1-expressing tumor in a subject, the method comprising

- **[0300]** (a) administering to a subject in need thereof an anti-PD-L1 imaging agent described herein; and
- **[0301]** (b) obtaining an radio-image of at least a portion of the subject to detect the presence or absence of the imaging agent;

wherein the presence and location of the imaging agent above background is indicative of the presence and location of PD-L1 or PD-L1 expressing tumors.

[0302] Also provided herein are methods for determining whether a subject having cancer is likely to respond to an immunotherapy, e.g., with a PD-1 or PD-L1 antagonist, the method comprising (a) administering to the subject having cancer a PD-L1 imaging agent, e.g., described herein; and (b) obtaining an image (static or dynamic) of at least a portion of the subject after step (a), and if the subject has a level of PD-L1 in one tumor or across several tumors that is equal to or above that required for treatment with a PD-1 or PD-L1 antagonist (e.g., OPDIVO™, KEYTRUDA™ or TECENTRIQ™), then treating the subject with an anti-tumor therapy, e.g., a PD-1 or PD-L1 antagonist e.g., OPDIVO™, KEYTRUDA™ or TECENTRIQ™.

[0303] Also provided herein is a method of treating a subject having cancer, comprising (a) administering to a subject in need thereof an imaging agent comprising a PD-L1 imaging agent, e.g., described herein, and obtaining an image (static or dynamic) of at least a portion of the subject to determine the presence of PD-L1 in one or more tumors; and if the subject has a level of PD-L1 in one tumor or across several tumors that is equal to or above that required for treatment with a PD-1 or PD-L1 antagonist (e.g., OPDIVO™ KEYTRUDA™ or TECENTRIQ™), then, (a) administering to the subject an anti-tumor therapy, e.g., an agent that inhibits the interaction between PD-1 and PD-L1 (a PD-1 or PD-L1 antagonist), e.g., OPDIVO™, KEYTRUDA™ or TECENTRIQ™, to the subject. Also disclosed herein are methods of monitoring the progress of an anti-tumor therapy against PD-L1-expressing tumors in a subject, the method comprising

- **[0304]** (a) administering to a subject in need thereof an anti-PD-L1 imaging agent described herein at a first time point and obtaining an image of at least a portion of the subject to determine the size of the tumor;
- **[0305]** (b) administering an anti-tumor therapy to the subject;
- **[0306]** (c) administering to the subject the imaging agent at one or more subsequent time points and obtaining an image of at least a portion of the subject at each time point;

wherein the dimension and location of the tumor at each time point is indicative of the progress of the disease.

PET Imaging

[0307] Typically, for PET imaging purposes it is desirable to provide the recipient with a dosage of Adnectin that is in the range of from about 0.1 mg to 200 mg as a single intravenous infusion, although a lower or higher dosage also may be administered as circumstances dictate. It may be desirable to provide the recipient with a dosage that is in the range of from about 0.1 mg to 10 mg per square meter of body surface area of the protein or peptide for the typical adult, although a lower or higher dosage also may be administered as circumstances dictate. Examples of dosages of proteins or peptides that may be administered to a human subject for imaging purposes are 10 μg to 1000 μg, 100 μg to 1000 μg, 100 μg to 500 μg, 200 μg to 500 μg, and 300 μg to 400 μg, although higher or lower doses may be used. For example, an ^{18}F labeled anti-PD-L1 Adnectin, e.g., [^{18}F]-A02-4PEG-DBCO-FPPEGA or [^{18}F]-E01-4PEG-DBCO-FPPEGA imaging agents may be administered in an amount, e.g., as a bolus injection, to a human ranging from 10 μg to 1000 μg, 100 μg to 1000 μg, 100 μg to 500 μg, 200 μg to 500 μg, and 300 μg to 400 μg. In certain embodiments, an ^{18}F labeled anti-PD-L1 Adnectin, e.g., [^{18}F]-A02-4PEG-DBCO-FPPEGA or [^{18}F]-E01-4PEG-DBCO-FPPEGA imaging agent is administered to a human subject in a n amount of about 350 μg, which corresponds to about 4.4 μg/kg for an 80 kg subject.

[0308] In certain embodiments, administration occurs in an amount of radiolabeled Adnectin, e.g., anti-PD-L1 Adnectin, of between 0.005 μg/kg of body weight to 50 μg/kg of body weight per day, e.g., between 0.02 μg/kg of body weight to 10 μg/kg, e.g., per day, between 0.1 μg/kg of body weight to 10 μg/kg of body weight, e.g., per day, between 1 μg/kg of body weight to 10 μg/kg of body weight, e.g., per day, between 2 μg/kg of body weight to 6 μg/kg of body weight, e.g., per day or between 4 μg/kg of body weight to 5 μg/kg of body weight, e.g., per day. The mass associated with a PET tracer is in the form of the natural isotope (e.g., ^{19}F for a ^{18}F PET tracer). In certain embodiments, an ^{18}F labeled anti-PD-L1 Adnectin, e.g., [^{18}F]-A02-4PEG-DBCO-FPPEGA or [^{18}F]-E01-4PEG-DBCO-FPPEGA imaging agent is administered to a human subject in an amount between 0.1 μg/kg of body weight to 10 μg/kg of body weight, e.g., per day, between 1 μg/kg of body weight to 10 μg/kg of body weight, e.g., per day, between 2 μg/kg of body weight to 6 μg/kg of body weight, e.g., per day or between 4 μg/kg of body weight to 5 μg/kg of body weight, e.g., per day.

[0309] Dosage regimens are adjusted to provide the optimum detectable amount for obtaining a clear image of the tissue or cells which uptake the radiolabeled Adnectin. It is especially advantageous to formulate parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subjects to which the radiolabeled Adnectin is to be administered. The specification for the dosage unit forms described herein are dictated by and directly dependent on (a) the unique characteristics of the targeting portion of the radiolabeled Adnectin; (b) the tissue or cells to be targeted; (c) the limitations inherent in the imaging technology used.

[0310] For administration of the radiolabeled Adnectin, the dosage used will depend upon the disease type, targeting compound used, the age, physical condition, and gender of the subject, the degree of the disease, the site to be examined, and others. In particular, sufficient care has to be taken about exposure doses to a subject. A saturating dose of radiolabel (e.g., ^{18}F or ^{64}Cu) may be administered to the patient. For example, the amount of radioactivity of ^{18}F-labeled Adnectin may range from 3.7 megabecquerels (MBq) to 3.7 gigabecquerels (GBq), from 18 MBq to 740 MBq, from 100 MBq to 500 MBq, from 100 MBq to 400 MBq, from 100 MBq to 333 MBq, from 100 MBq to 250 MBq, from 150 MBq to 250 MBq, from 200 MBq to 250 MBq or from 200 MBq to 225 MBq. Alternatively, the dosage may be measured in millicuries, for example. In some embodiments, the amount of ^{18}F imaging agent administered for imaging studies is 1 to 10 mCi, 3 to 10 mCi, 3 to 8 mCi, 4 to 7 mCi or 5 to 6 mCi. In some embodiments, an effective amount will be the amount of compound sufficient to produce emissions in the range of from 1 to 10 mCi, 3 to 10 mCi, 3 to 8 mCi, 4 to 7 mCi or 5 to 6 mCi. In certain embodiments, an ^{18}F labeled anti-PD-L1 Adnectin, e.g., [^{18}F]-A02-4PEG-DBCO-FPPEGA or [^{18}F]-E01-4PEG-DBCO-FPPEGA imaging agent is administered to a human subject in an amount of 1 to 10 mCi, 3 to 10 mCi, 3 to 8 mCi, 4 to 7 mCi or 5 to 6 mCi.

[0311] In certain embodiments, an ^{18}F labeled anti-PD-L1 Adnectin, e.g., [^{18}F]-A02-4PEG-DBCO-FPPEGA or [^{18}F]-E01-4PEG-DBCO-FPPEGA imaging agent, is administered as a composition comprising 1-5% of the ^{18}F labeled anti-PD-L1 Adnectin, e.g., [^{18}F]-A02-4PEG-DBCO-FPPEGA or [^{18}F]-E01-4PEG-DBCO-FPPEGA, and 95-99%, respectively, of the non-radiolabeled Adnectin precursor, e.g., PD-L1 Adnectin-4PEG-DBCO. In certain embodiments, the ratio is 2% of the ^{18}F labeled anti-PD-L1 Adnectin, e.g., [^{18}F]-A02-4PEG-DBCO-FPPEGA or [^{18}F]-E01-4PEG-DBCO-FPPEGA, and 98%, of the non-radiolabeled Adnectin precursor, e.g., PD-L1 Adnectin-4PEG-DBCO. The ratio may vary, provided that, preferably, the total amount of protein administered to the subject for imaging remains a microdose, i.e., ≤30 nM.

[0312] Actual dosage levels of the active ingredients in the pharmaceutical compositions described herein may be varied so as to obtain an amount of the active ingredient which is effective to achieve the desired uptake of the radiolabeled Adnectin in the cells or tissues of a particular patient, composition, and mode of administration, without being toxic to the patient. It will be understood, however, that the total daily usage of the radiolabeled Adnectin of the present disclosure will be decided by the attending physician or other attending professional within the scope of sound medical judgment. The specific effective dose level for any particular subject will depend upon a variety of factors, including for example, the activity of the specific composition employed; the specific composition employed; the age, body weight, general health, sex, and diet of the host; the time of administration; the route of administration; the rate of excretion of the specific compound employed; the duration of the treatment; other drugs, compounds and/or materials used in combination with the particular compositions employed, the age, sex, weight, condition, general health and prior medical history of the patient being treated, and like factors well known in the medical arts. In certain embodiments, the amount of radiolabeled Adnectin administered into a human subject required for imaging will be determined by the prescribing physician with the dosage generally varying according to the quantity of emission from the radionuclide.

[0313] In certain embodiments, the radiolabeled Adnectin described herein can be formulated to ensure proper distribution in vivo. For example, the blood-brain barrier (BBB) excludes many highly hydrophilic compounds. Agents may cross the BBB by formulating them, for example, in liposomes. For methods of manufacturing liposomes, see, e.g., U.S. Pat. Nos. 4,522,811; 5,374,548; and 5,399,331. The liposomes may comprise one or more moieties which are selectively transported into specific cells or organs, thus enhance targeted drug delivery (see, e.g., V. V. Ranade (1989) *J. Clin. Pharmacol.* 29:685). Exemplary targeting moieties include folate or biotin (see, e.g., U.S. Pat. No. 5,416,016 to Low et al.); mannosides (Umezawa et al., (1988) *Biochem. Biophys. Res. Commun.* 153:1038); antibodies (P. G. Bloeman et al. (1995) *FEBS Lett.* 357:140; M. Owais et al. (1995) *Antimicrob. Agents Chemother.* 39:180); surfactant protein A receptor (Briscoe et al. (1995) *Am. J. Physiol.* 1233:134); p120 (Schreier et al. (1994) *J. Biol. Chem.* 269:9090); see also K. Keinanen; M. L. Laukkanen (1994) *FEBS Lett.* 346:123; J. J. Killion; I. J. Fidler (1994).

Exemplary PET Procedure

[0314] The following illustrative procedure may be utilized when performing PET imaging studies on patients in the clinic. A venous catheter, e.g., a 20 G two-inch venous catheter, is inserted into the contralateral ulnar vein for radiotracer administration. Administration of the PET tracer is often timed to coincide with time of maximum (T max) or minimum (T min) of the anti-PD-L1 Adnectin concentration in the blood.

[0315] The patient is positioned in the PET camera and a tracer dose of the PET tracer of radiolabeled anti-PD-L1 Adnectin such as [18F]-A02-4PEG-DBCO-FPPEGA or [18F]-E01-4PEG-DBCO-FPPEGA (<20 mCi) is administered via i.v. catheter. A subject may, prior to administration of the PET tracer, drink a liter of water to promote the renal clearance of unbound tracer from the circulation in order to enhance signal to background ratio and/or empty his bladder. Either arterial or venous blood samples may be taken at 15 appropriate time intervals throughout the PET scan in order to, e.g., analyze and quantitate the fraction of unmetabolized PET tracer in plasma. Images may be acquired for up to 120 min. Within ten minutes of the injection of radiotracer and at the end of the imaging session, 1 ml blood samples may be obtained, e.g., for determining the plasma concentration of any labeled or unlabeled anti-PD-L1 Adnectin.

[0316] Two types of PET procedures may be used. One type involves obtaining single time point estimates of tracer uptake or static imaging that provides a spatial map of regional tracer concentration. With static imaging, only an average value is measured (e.g. Standardized Uptake Value, SUV). The second type is referred to as dynamic tracer imaging, which can provide considerably more information about in vivo biology by delineating both the temporal and spatial pattern of tracer uptake. See, e.g., Muzi et al. Magn Reson Imaging. 2012 30(9): 1203-1215. PD-L1 Adnectin imaging agents, such as such as [^{18}F]-A02-4PEG-DBCO-FPPEGA and [^{18}F]-E01-4PEG-DBCO-FPPEGA, may be used in either static tracer imaging or dynamic tracer imaging.

[0317] For quantification of tracer uptake, the clinician may visually identify tumor lesions on a PET or CT scan and determine a region-of-interest (ROI) around these lesions. [^{18}F]PD-L1-uptake in these ROI's may be corrected for body weight and injected dose and quantified as standardized uptake value (SUVmax and SUVmean).

[0318] Tomographic images are obtained through image reconstruction. For determining the distribution of radiotracer, ROIs may be drawn on the reconstructed image including, but not limited to, the lungs, liver, heart, kidney, skin, or other organs and tissue (e.g., cancer tissue). Radiotracer uptakes over time in these regions are used to generate time activity curves (TAC) obtained in the absence of any intervention or in the presence of the unlabeled anti-PD-L1 Adnectin at the various dosing paradigms examined. Data may be expressed as radioactivity per unit time per unit volume (pci/cc/mCi injected dose).

[0319] PET may be accompanied by a low-dose or diagnostic CT-scan for anatomic reference purposes.

IX EXEMPLARY PET PROCEDURES WITH ^{18}F LABELED ANTI-PD-L1 ADNECTINS

[0320] By labeling a PD-L1 binding agent with Fluoride-18 (^{18}F), serial [^{18}F]PD-L1-PET scanning can be used to assess whole body distribution, pharmacokinetics (PK) and pharmacodynamics (PD) and to relate findings to treatment effects. This could help in patient selection and possibly serve as an (early) biomarker for response to PD1/PD-L1 checkpoint inhibitors in the future.

[0321] Exemplary PET procedures with ^{18}F labeled imaging agents, such as ^{18}F labeled anti-PD-L1 Adnectin imaging agents, e.g., [^{18}F]-A02-4PEG-DBCO-FPPEGA or [^{18}F]-E01-4PEG-DBCO-FPPEGA, are as follows.

[0322] In one embodiment, a method comprises (a) administering to a subject, e.g., a human, a PD-L1 imaging agent, e.g., an ^{18}F labeled PD-L1 Adnectin imaging agent, at a dose of about 3-10 mCi (100-333 MBq); and (b) conducting a PET scan of the subject about 1-120 minutes (such as 30-120, 30-60 or 60-120 minutes) after step (a). The PET scan maybe a static PET scan or a dynamic PET scan. If the PET scan is a static PET scan, the PET scan may occur 30-120, 30-60 or 60-120 minutes after administration of the PD-L1 imaging agent, and if the PET scan is a dynamic PET scan, it may occur 1-120, 30-120, 30-60 or 60-120 minutes after administration of the PD-L1 imaging agent, such as 1, 35, 70 and 105 minutes post injection. A dynamic PET scan may take a total duration of 30 to 120 minutes, such as 30 to 60 minutes, e.g., 30 minutes or 60 minutes, with variable frame lengths. The scan may be a whole body scan or a partial body scan, e.g., a scan of a single tumor. For example, a dynamic PET scan may be a scan of a single tumor and a static PET scan may be a whole body scan. In certain embodiments, the dose administered is about 200-225 MBq (i.e., ±10%) or about 6 mCi (i.e., ±10%).

[0323] In certain embodiments, a subject is a subject with cancer, and the method comprises (a) administering to the subject a PD-L1 imaging agent, e.g., an ^{18}F labeled PD-L1 Adnectin imaging agent, at a dose of about 3-10 mCi (100-333 MBq); and (b) conducting a PET scan of the subject about 1-120 minutes (such as 30-120, 30-60 or 60-120 minutes) after step (a), wherein steps (a) and (b) are conducted prior to the initiation of a cancer treatment. In certain embodiments, a subject is a subject with cancer, and the method comprises (a) administering to the subject a PD-L1 imaging agent, e.g., an ^{18}F labeled PD-L1 Adnectin imaging agent, at a dose of about 3-10 mCi (100-333 MBq); and (b) conducting a PET scan of the subject about 1-120 minutes (such as 30-120, 30-60 or 60-120 minutes) after step (a), wherein steps (a) and (b) are conducted at at least 2 time points, e.g., one of which is prior to the initiation of a cancer treatment, and one of which is during the cancer treatment, or wherein both time points are during the cancer treatment. The two time points may be separated by, e.g., a time of 1-10 weeks, such as 2-8 weeks, such as 5-7 weeks, such as 6 weeks. In certain embodiments, steps (a) and (b) are conducted at at least 3, 4, 5 or more time points, wherein the successive time points are separated by, e.g., a time of 1-10 weeks, such as 2-8 weeks, such as 5-7 weeks, such as 6 weeks.

[0324] In certain embodiments, a subject is a subject with cancer and the subject is being treated with an immunotherapy, e.g., a PD-1 antagonist and/or a PD-L1 antagonist, and the method comprises (a) administering to the subject a PD-L1 imaging agent, e.g., an ^{18}F labeled PD-L1 Adnectin imaging agent, at a dose of about 3-10 mCi (100-333 MBq); and (b) conducting a PET scan of the subject about 1-120 minutes (such as 30-120, 30-60 or 60-120 minutes) after step (a), wherein steps (a) and (b) are conducted at at least 2, 3, 4 or 5 time points, e.g., one of which is prior to the initiation of the immunotherapy treatment, and one of which is during the immunotherapy treatment, or wherein both time points are during the immunotherapy treatment.

[0325] In certain embodiments, a subject is a subject with cancer and the subject is being treated with an immunotherapy, e.g., a PD-1 antagonist and/or a PD-L1 antagonist, and the method comprises (a) administering to the subject a PD-L1 imaging agent, e.g., an ^{18}F labeled PD-L1 Adnectin imaging agent, at a dose of about 3-10 mCi (100-333 MBq); and (b) conducting a PET scan of the subject about 1-120 minutes (such as 30-120, 30-60 or 60-120 minutes) after step (a), wherein steps (a) and (b) are conducted at at least 1, 2, 3, 4 or 5 time points, e.g., one of which is prior to the initiation of the immunotherapy treatment, and if there are more than one iteration of steps (a) and (b), one of which is during the immunotherapy treatment, or wherein all time points are during the immunotherapy treatment, and wherein the results of the PET scan are informative for further treatment of the subject. For example, the results of the PET scan may indicate that the tumors of the subject are not reduced in size during the treatment, which suggests that the treatment may not be successful and should be changed or stopped.

[0326] Alternatively, a first scan, prior to treatment, may indicate that the subject does not express PD-L1 in a majority of tumors, and that a treatment with a PD-1 antagonist and/or a PD-L1 antagonist, would not be successful. Accordingly, provided herein is a method of treating a subject having cancer, comprising

[0327] (a) administering to a subject in need thereof an imaging agent comprising an anti-PD-L1 Adnectin, and obtaining an image (static or dynamic) of at least a portion of the subject to determine the presence of PD-L1 in one or more tumors; and, if PD-L1 is detected in one or more tumors, then,

[0328] (b) administering to the subject an anti-tumor therapy, e.g., an agent that inhibits the interaction between PD-1 and PD-L1 (a PD-1 or PD-L1 antagonist), e.g., OPDIVO™, KEYTRUDA™ or TECENTRIQ™.

[0329] Also provided is a method of predicting whether a subject having cancer is likely to respond to a therapy with a PD-1 or PD-L1 antagonist, comprising (a) administering to a subject in need thereof an imaging agent comprising an anti-PD-L1 Adnectin, and obtaining an image (static or dynamic) of at least a portion of the subject to determine the presence of PD-L1 in one or more tumors; and, if PD-L1 is detected in one or more tumors, then, the subject is likely to respond to a therapy with a PD-1 or PD-L1 antagonist.

[0330] The methods may comprise administering an anti-tumor therapy when at least 1%, 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 95% of the cells in a tumor specimen are PD-L1 positive, or on average across several tumors. In certain embodiments, an anti-tumor therapy, e.g., a PD-1 or PD-L1 antagonist, is not administered to the subject, unless the subject is PD-L1 positive in at least 1%, 5%, 10%, 20%, 30%, 40%, 50%. 60%, 70%, 80%, 90%, or 95% of the cells in a tumor specimen, or on average across several tumors. In certain embodiments, an anti-tumor therapy is administered if the level of PD-L1 detected in one or more tumors is at least equal to the level of PD-L1 that is necessary for receiving treatment with an a PD-1 or PD-L1 antagonist therapeutic.

[0331] Methods in which more than one iteration of steps (a) and (b) are used may comprise comparing a PET scan conducted at a first time point with a PET scan conducted at a second time point, and/or later time point. Such comparison may inform on a patient's evolution of the disease, a patient's response to a treatment, a patient's potential adverse reaction or other.

[0332] In certain embodiments, a subject is a subject with cancer and the subject is being treated with an immunotherapy, e.g., a PD-1 antagonist and/or a PD-L1 antagonist, and the method comprises (a) administering to the subject a PD-L1 imaging agent, e.g., an ^{18} labeled PD-L1 Adnectin imaging agent, at a dose of about 3-10 mCi (100-333 MBq); and (b) conducting a PET scan of the subject about 1-120 minutes (such as 30-120, 30-60 or 60-120 minutes) after step (a), wherein steps (a) and (b) are conducted at at least 1, 2, 3, 4 or 5 time points, e.g., one of which is prior to the initiation of the immunotherapy treatment, and if there are more than one iteration of steps (a) and (b), one of which is during the immunotherapy treatment, or wherein all time points are during the immunotherapy treatment, wherein the ^{18}F labeled PD-L1 Adnectin imaging agent comprises one of the following:

[0333] the modified loops BC, DE and FG of the A02 Adnectin (i.e., SEQ ID NOs: 81, 82 and 83); or wherein one of these loops differs in one amino acid deletion, addition or substitution relative to the corresponding loop in the A02 Adnectin; wherein two of these loops each differ in one amino acid deletion, addition or substitution (e.g., conservative amino acid substitution) relative to the corresponding loops in the A02 Adnectin; or wherein three of these loops each differ in one amino acid deletion, addition or substitution relative to the corresponding loops in the A02 Adnectin, and wherein the Adnectin binds specifically to human PD-L1 as determined by Biacore; the modified loops BC, DE and FG of the E01 Adnectin (i.e., SEQ ID NOs: 97, 98 and 99); or wherein one of these loops differs in one amino acid deletion, addition or substitution relative to the corresponding loop in the E01 Adnectin; wherein two of these loops each differ in one amino acid deletion, addition or substitution (e.g., conservative amino acid substitution) relative to the corresponding loops in the E01 Adnectin; or wherein three of these loops each differ in one amino acid deletion, addition or substitution relative to the corresponding loops in the E01 Adnectin, and wherein the Adnectin binds specifically to human PD-L1 as determined by Biacore; an amino acid sequence that is at least 95%, 96%, 97%, 98%, 99% or 100% identical to an amino acid sequence of the A02 Adnectin (e.g., any one of SEQ ID NOs: 80, and 84-91) or the E01 Adnectin (e.g., any one of SEQ ID NOs: 96, 100-107), wherein a substitution may be a conservative substitution, and wherein the Adnectin binds specifically to human PD-L1 as determined by Biacore; and/or

[0334] an amino acid sequence that differs from the amino acid sequence of the A02 Adnectin, comprising, e.g., any one of SEQ ID NOs: 80, and 84-91 or the E01 Adnectin comprising, e.g., any one of SEQ ID NOs: 96, 100-107, in 1-10 amino acid deletions, additions or substitutions (e.g., conservative substitutions), wherein a substitution may be a conservative substitution, and wherein the Adnectin binds specifically to human PD-L1 as determined by Biacore.

[0335] In certain embodiments, a subject is a subject with cancer and the subject is being treated with an immunotherapy, e.g., a PD-1 antagonist and/or a PD-L1 antagonist, and the method comprises (a) administering to the subject a PD-L1 imaging agent, e.g., an ^{18}F labeled PD-L1 Adnectin imaging agent, at a dose of about 3-10 mCi (100-333 MBq); and (b) conducting a PET scan of the subject about 1-120 minutes (such as 30-120, 30-60 or 60-120 minutes) after step (a), wherein steps (a) and (b) are conducted at at least 1, 2, 3, 4 or 5 time points, e.g., one of which is prior to the initiation of the immunotherapy treatment, and if there are more than one iteration of steps (a) and (b), one of which is during the immunotherapy treatment, or wherein all time points are during the immunotherapy treatment, wherein the ^{18}F labeled PD-L1 Adnectin imaging agent is [^{18}F]-A02-4PEG-DBCO-FPPEGA, wherein the A02 Adnectin comprises any one of SEQ ID NOs: 80 and 84-91, or [^{18}F]-E01-4PEG-DBCO-FPPEGA, wherein the E01 Adnectin comprises any one of SEQ ID NOs: 96 and 100-107, and the structure of 4PEG-DBCO-FPPEGA is the structure provided in FIG. **2** or **9**. The composition that is administered to a subject may be a composition wherein 2% of the molecules are [^{18}F]-A02-4PEG-DBCO-FPPEGA or [18F]-E01-4PEG-DBCO-FPPEGA and 98% of the molecules are A02-4PEG-DBCO or E01-4PEG-DBCO, respectively, and where, preferably, equal or less than 30 nM of total protein is administered to the subject in one tracer administration.

[0336] Also provided herein are methods for determining whether a subject having cancer is likely to respond to an immunotherapy, e.g., with a PD-1 or PD-L1 antagonist, the method comprising (a) administering to the subject having cancer a PD-L1 imaging agent, e.g., an ^{18}F labeled PD-L1 Adnectin imaging agent, at a dose of about 3-10 mCi (100-333 MBq); and (b) conducting a PET scan of the subject about 1-120 minutes (such as 30-120, 30-60 or 60-120 minutes) after step (a), and if the subject has a level of PD-L1 in one tumor or across several tumors that is equal to or above that required for treatment with a PD-1 or PD-L1 antagonist (e.g., OPDIVO™, KEYTRUDA™ or TECENTRIQ™), then the subject is likely to respond to an anti-tumor therapy, e.g., a PD-1 or PD-L1 antagonist e.g., OPDIVO™, KEYTRUDA™ or TECENTRIQ™, wherein the ^{18}F labeled PD-L1 Adnectin imaging agent comprises one of the following:

[0337] the modified loops BC, DE and FG of the A02 Adnectin (i.e., SEQ ID NOs: 81, 82 and 83); or wherein one of these loops differs in one amino acid deletion, addition or substitution relative to the corresponding loop in the A02 Adnectin; wherein two of these loops each differ in one amino acid deletion, addition or substitution (e.g., conservative amino acid substitution) relative to the corresponding loops in the A02 Adnectin; or wherein three of these loops each differ in one amino acid deletion, addition or substitution relative to the corresponding loops in the A02 Adnectin, and wherein the Adnectin binds specifically to human PD-L1 as determined by Biacore; the modified loops BC, DE and FG of the E01 Adnectin (i.e., SEQ ID NOs: 97, 98 and 99); or wherein one of these loops differs in one amino acid deletion, addition or substitution relative to the corresponding loop in the E01 Adnectin; wherein two of these loops each differ in one amino acid deletion, addition or substitution (e.g., conservative amino acid substitution) relative to the corresponding loops in the E01 Adnectin; or wherein three of these loops each differ in one amino acid deletion, addition or substitution relative to the corresponding loops in the E01 Adnectin, and wherein the Adnectin binds specifically to human PD-L1 as determined by Biacore; an amino acid sequence that is at least 95%, 96%, 97%, 98%, 99% or 100% identical to an amino acid sequence of the A02 Adnectin (e.g., any one of SEQ ID NOs: 80, and 84-91) or the E01 Adnectin (e.g., any one of SEQ ID NOs: 96, 100-107), wherein a substitution may be a conservative substitution, and wherein the Adnectin binds specifically to human PD-L1 as determined by Biacore; and/or

[0338] an amino acid sequence that differs from the amino acid sequence of the A02 Adnectin, comprising, e.g., any one of SEQ ID NOs: 80, and 84-91 or the E01 Adnectin comprising, e.g., any one of SEQ ID NOs: 96, 100-107, in 1-10 amino acid deletions, additions or substitutions (e.g., conservative substitutions), wherein a substitution may be a conservative substitution, and wherein the Adnectin binds specifically to human PD-L1 as determined by Biacore.

[0339] Provided herein is a method of treating a subject having cancer, comprising (a) administering to the subject a PD-L1 imaging agent, e.g., an ^{18}F labeled PD-L1 Adnectin imaging agent, at a dose of about 3-10 mCi (100-333 MBq); and (b) conducting a PET scan of the subject about 1-120 minutes (such as 30-120, 30-60 or 60-120 minutes) after step (a), and if the subject has a level of PD-L1 in one tumor or across several tumors that is equal to or above that required for treatment with a PD-1 or PD-L1 antagonist (e.g., OPDIVO™ KEYTRUDA™ or TECENTRIQ™), then administering to the subject an anti-tumor therapy, e.g., a PD-1 or PD-L1 antagonist e.g., OPDIVO™, KEYTRUDA™ or TECENTRIQ™ wherein the ^{18}F labeled PD-L1 Adnectin imaging agent comprises one of the following:

[0340] the modified loops BC, DE and FG of the A02 Adnectin (i.e., SEQ ID NOs: 81, 82 and 83); or wherein one of these loops differs in one amino acid deletion, addition or substitution relative to the corresponding loop in the A02 Adnectin; wherein two of these loops each differ in one amino acid deletion, addition or substitution (e.g., conservative amino acid substitution) relative to the corresponding loops in the A02 Adnectin; or wherein three of these loops each differ in one amino acid deletion, addition or substitution relative to the corresponding loops in the A02 Adnectin, and wherein the Adnectin binds specifically to human PD-L1 as determined by Biacore; the modified loops BC, DE and FG of the E01 Adnectin (i.e., SEQ ID NOs: 97, 98 and 99); or wherein one of these loops differs in one amino acid deletion, addition or substitution relative to the corresponding loop in the E01 Adnectin; wherein two of these loops each differ in one amino acid deletion, addition or substitution (e.g., conservative amino acid substitution) relative to the corresponding loops in the E01 Adnectin; or wherein three of these loops each differ in one amino acid deletion, addition or substitution relative to the corresponding loops in the E01 Adnectin, and wherein the Adnectin binds specifically to human PD-L1 as determined by Biacore;

[0341] an amino acid sequence that is at least 95%, 96%, 97%, 98%, 99% or 100% identical to an amino acid sequence of the A02 Adnectin (e.g., any one of SEQ ID NOs: 80, and 84-91) or the E01 Adnectin (e.g., any one of SEQ ID NOs: 96, 100-107), wherein a substitution may be a conservative substitution, and wherein the Adnectin binds specifically to human PD-L1 as determined by Biacore; and/or

[0342] an amino acid sequence that differs from the amino acid sequence of the A02 Adnectin, comprising, e.g., any one of SEQ ID NOs: 80, and 84-91 or the E01 Adnectin comprising, e.g., any one of SEQ ID NOs: 96, 100-107, in 1-10 amino acid deletions, additions or substitutions (e.g., conservative substitutions), wherein a substitution may be a conservative substitution, and wherein the Adnectin binds specifically to human PD-L1 as determined by Biacore.

[0343] Provided herein is a method of treating a subject having cancer, comprising (a) administering to the subject a PD-L1 imaging agent, e.g., an ^{18}F labeled PD-L1 Adnectin imaging agent, at a dose of about 3-10 mCi (100-333 MBq); and (b) conducting a PET scan of the subject about 1-120 minutes (such as 30-120, 30-60 or 60-120 minutes) after step (a), and if the subject has a level of PD-L1 in one tumor or across several tumors that is equal to or above that required for treatment with a PD-1 or PD-L1 antagonist (e.g., OPDIVO™ KEYTRUDA™ or TECENTRIQ™), then administering to the subject an anti-tumor therapy, e.g., a PD-1 or PD-L1 antagonist e.g., OPDIVO™, KEYTRUDA™ or TECENTRIQ™, to the subject, the ^{18}F labeled PD-L1 Adnectin imaging agent is [^{18}F]-A02-4PEG-DBCO-FPPEGA, wherein the A02 Adnectin comprises any one of SEQ ID NOs: 80 and 84-91, or [18F]-E01-4PEG-DBCO-FPPEGA, wherein the E01 Adnectin comprises any one of SEQ ID NOs: 96 and 100-107, and the structure of 4PEG-DBCO-FPPEGA is the structure provided in FIG. **2** or **9**. The composition that is administered to a subject may be a composition wherein 2% of the molecules are [^{18}F]-A02-4PEG-DBCO-FPPEGA or [^{18}F]-E01-4PEG-DBCO-FPPEGA and 98% of the molecules are A02-4PEG-DBCO or E01-4PEG-DBCO, respectively, and where, preferably, equal or less than 30 nM of total protein is administered to the subject in one tracer administration.

X. DETECTION OF PD-L1 WITH ANTI-PD-L1 ADNECTINS

[0344] In addition to detecting PD-L1 in vivo, anti-PDL1 Adnectins, such as those described herein, may be used for detecting a target molecule in a sample. A method may comprise contacting the sample with an anti-PD-L1 Adnectins described herein, wherein said contacting is carried out under conditions that allow anti-PD-L1 Adnectin-target complex formation; and detecting said complex, thereby detecting said target in said sample. Detection may be carried out using any art-recognized technique, such as, e.g., radiography, immunological assay, fluorescence detection, mass spectroscopy, or surface plasmon resonance. The sample may be from a human or other mammal. For diagnostic purposes, appropriate agents are detectable labels that include radioisotopes, for whole body imaging, and radioisotopes, enzymes, fluorescent labels and other suitable antibody tags for sample testing.

[0345] The detectable labels can be any of the various types used currently in the field of in vitro diagnostics, including particulate labels including metal sols such as colloidal gold, isotopes such as I^{125} or Tc^{99} presented for instance with a peptidic chelating agent of the N_2S_2, N_3S or N_4 type, chromophores including fluorescent markers, biotin, luminescent markers, phosphorescent markers and the like, as well as enzyme labels that convert a given substrate to a detectable marker, and polynucleotide tags that are revealed following amplification such as by polymerase chain reaction. A biotinylated antibody would then be detectable by avidin or streptavidin binding. Suitable enzyme labels include horseradish peroxidase, alkaline phosphatase and the like. For instance, the label can be the enzyme alkaline phosphatase, detected by measuring the presence or formation of chemiluminescence following conversion of 1,2 dioxetane substrates such as adamantyl methoxy phosphoryloxy phenyl dioxetane (AMPPD), disodium 3-(4-(methoxyspiro{1,2-dioxetane-3,2'-(5'-chloro)tricyclo{3.3.1.1 3,7}decan}-4-yl) phenyl phosphate (CSPD), as well as CDP and CDP-Star® or other luminescent substrates well-known to those in the art, for example the chelates of suitable lanthanides such as Terbium(III) and Europium(III). Other labels include those set forth above in the imaging section. The detection means is determined by the chosen label. Appearance of the label or its reaction products can be achieved using the naked eye, in the case where the label is particulate and accumulates at appropriate levels, or using instruments such as a spectrophotometer, a luminometer, a fluorimeter, and the like, all in accordance with standard practice.

[0346] In certain embodiments, conjugation methods result in linkages which are substantially (or nearly) non-immunogenic, e.g., peptide- (i.e. amide-), sulfide-, (sterically hindered), disulfide-, hydrazone-, and ether linkages. These linkages are nearly non-immunogenic and show reasonable stability within serum (see e.g. Senter, P. D., Curr. Opin. Chem. Biol. 13 (2009) 235-244; WO 2009/059278; WO 95/17886).

[0347] Depending on the biochemical nature of the moiety and Adnectin, different conjugation strategies can be employed. In case the moiety is naturally occurring or recombinant polypeptide of between 50 to 500 amino acids, there are standard procedures in textbooks describing the chemistry for synthesis of protein conjugates, which can be easily followed by the skilled artisan (see e.g. Hackenberger, C. P. R., and Schwarzer, D., Angew. Chem. Int. Ed. Engl. 47 (2008) 10030-10074). In one embodiment the reaction of a maleinimido moiety with a cysteine residue within the Adnectin or the moiety is used. Alternatively, coupling to the C-terminal end of the Adnectin is performed. C-terminal modification of a protein can be performed as described in, e.g., Sunbul, M. and Yin, J., Org. Biomol. Chem. 7 (2009) 3361-3371). When the moiety is a peptide or polypeptide, the Adnectin and moiety can be fused by standard genetic fusion, optionally with a linker disclosed herein.

[0348] In general, site specific reaction and covalent coupling is based on transforming a natural amino acid into an amino acid with a reactivity which is orthogonal to the reactivity of the other functional groups present. For example, a specific cysteine within a rare sequence context can be enzymatically converted in an aldehyde (see Frese, M. A., and Dierks, T., ChemBioChem. 10 (2009) 425-427). It is also possible to obtain a desired amino acid modification by utilizing the specific enzymatic reactivity of certain enzymes with a natural amino acid in a given sequence context (see, e.g., Taki, M. et al., Prot. Eng. Des. Sel. 17 (2004) 119-126; Gautier, A. et al. Chem. Biol. 15 (2008) 128-136. Protease-catalyzed formation of C—N bonds is described at Bordusa, F., Highlights in Bioorganic Chemistry (2004) 389-403.

[0349] Site specific reaction and covalent coupling can also be achieved by the selective reaction of terminal amino acids with appropriate modifying reagents. The reactivity of an N-terminal cysteine with benzonitrils (see Ren, H. et al., Angew. Chem. Int. Ed. Engl. 48 (2009) 9658-9662) can be used to achieve a site-specific covalent coupling. Native chemical ligation can also rely on C-terminal cysteine residues (Taylor, E. Vogel; Imperiali, B, Nucleic Acids and Molecular Biology (2009), 22 (Protein Engineering), 65-96). EP 1 074 563 describes a conjugation method which is based on the faster reaction of a cysteine within a stretch of negatively charged amino acids than a cysteine located in a stretch of positively charged amino acids.

[0350] The moiety may also be a synthetic peptide or peptide mimic. In case a polypeptide is chemically synthesized, amino acids with orthogonal chemical reactivity can be incorporated during such synthesis (see e.g. de Graaf, A. J. et al., Bioconjug. Chem. 20 (2009) 1281-1295). Since a great variety of orthogonal functional groups is at stake and can be introduced into a synthetic peptide, conjugation of such peptide to a linker is standard chemistry.

[0351] In order to obtain a mono-labeled polypeptide the conjugate with 1:1 stoichiometry may be separated by chromatography from other conjugation side-products. This procedure can be facilitated by using a dye labeled binding pair member and a charged linker. By using this kind of labeled and highly negatively charged binding pair member, mono conjugated polypeptides are easily separated from non-labeled polypeptides and polypeptides which carry more than one linker, since the difference in charge and molecular weight can be used for separation. The fluorescent dye can be useful for purifying the complex from un-bound components, like a labeled monovalent binder.

XI. SYNTHESIS OF ^{18}F-LABELED ANTI-PD-L1 ADNECTINS

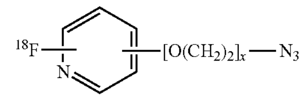
[0352] ^{18}F-labeled anti-PD-L1 Adnectins may be synthesized by first preparing an ^{18}F radiolabeled prosthetic group, linking an Adnectin to a bifunctional chelating agent, and then combining these two reagents (see, e.g., FIG. **9**).

^{18}F Radiolabeled Prosthetic Groups

[0353] In one aspect, provided herein is an ^{18}F-radiolabeled compound containing a prosthetic group for use in a bioorthogonal reaction involving 1,3-dipolar cycloaddition between an azide and a cyclooctyne which proceeds selectively under water tolerant conditions. The ^{18}F-radiolabeled prosthetic groups disclosed herein are soluble in 100% aqueous, and there is no need for an organic phase to link the prosthetic groups to the anti-PD-L1 Adnectins disclosed herein. This feature is particularly advantageous as there is no need for an organic phase to link the prosthetic group to the anti-PD-L1 Adnectins, which cannot withstand even small amounts of organic solvents, given degradation and aggregation issues.

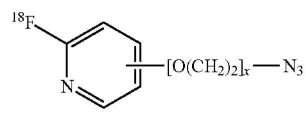
[0354] Additionally, unlike aliphatic prosthetic groups, the ^{18}F fluorination reaction can be monitored with UV, and the ^{18}F-radiolabeled prosthetic groups described herein are not volatile. Moreover, the ^{18}F-radiolabeled prosthetic groups can be incorporated into the anti-PD-L1 Adnectins using a copper free click chemistry, e.g., as described in the Examples, thus avoiding the stability issues observed in some biologics when copper mediated click chemistry is used.

[0355] In one aspect, provided herein is a PEGylated ^{18}F-pyridine covalently bound to an azide with the following structure,



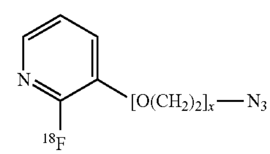
wherein x is an integer from 1 to 8. In certain embodiments, x is an integer from 2 to 6. In some embodiments x is an integer from 3 to 5. In certain embodiments, x is 4. In certain embodiments, ^{18}F is attached to the pyridine ortho to the N atom. In certain embodiments, the $[O(CH_2)_2]_x$ moiety is present in the 1-3 configuration relative to the nitrogen on the pyridine ring. In certain embodiments, the $[O(CH_2)_2]_x$ moiety is present in the 1-2 configuration relative to the nitrogen on the pyridine ring. In certain embodiments, the $[O(CH_2)_2]_x$ moiety is present in the 1-4 configuration relative to the nitrogen on the pyridine ring.

[0356] In certain embodiments, the ^{18}F-radiolabeled compound has the structure



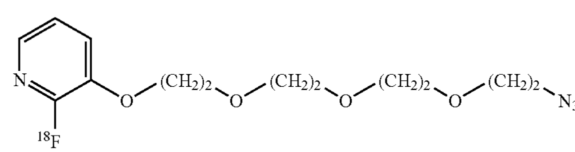
wherein x is an integer from 1 to 8. In certain embodiments, x is an integer from 2 to 6. In some embodiments x is an integer from 3 to 5. In certain embodiments, x is 4.

[0357] In certain embodiments, the ^{18}F-radiolabeled compound has the structure



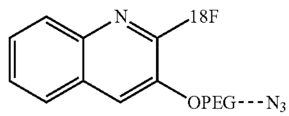
wherein x is an integer from 1 to 8. In certain embodiments, x is an integer from 2 to 6. In certain embodiments x is an integer from 3 to 5. In certain embodiments, x is 4.

[0358] In certain embodiments, the ^{18}F-radiolabeled compound is [^{18}F]-3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-fluoropyridine (^{18}F-FPPEGA) and has the structure



[0359] In certain embodiments, the ^{18}F-radiolabeled prosthetic group may contain additional groups on the pyridine ring which do not interfere with the fluorination reaction. In certain embodiments, additions to the pyridine ring include C_{1-6} alkyl groups, for example methyl, ethyl and propyl.

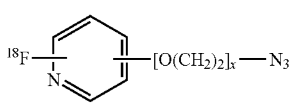
[0360] In certain embodiments, the ^{18}F-radiolabeled prosthetic group is a fused ring system with the following structure:



wherein "OPEG" is $[O(CH_2)_2]_x$, and x is an integer from 1 to 8. In certain embodiments, x is an integer from 2 to 6. In certain embodiments x is an integer from 3 to 5. In certain embodiments, x is 4.

[0361] The ^{18}F-radiolabeled prosthetic groups described herein may be produced using chemical reactions described in the Examples herein.

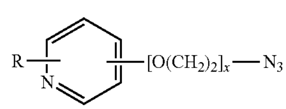
[0362] Also provided herein is a method of preparing a PEGylated ^{18}F-pyridine covalently bound to an azide with the following structure,



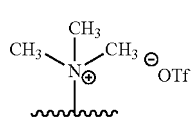
wherein x is an integer from 1 to 8, the method comprising the steps of

[0363] (a) providing a solution of a compound a with the following structure:

a



wherein x is an integer from 1 to 8, and R is NO_2, Br, F or



and is ortho to the N atom of the pyridine ring;

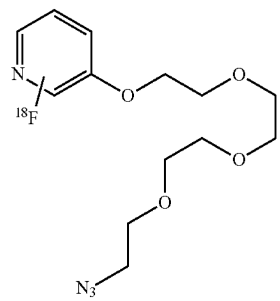
[0364] (b) providing a mixture of ^{18}F in ^{18}Owater, 4,7,13,16,21,24-hexaoxa-1,10-diazabicyclo[8.8.8]hexacosane and a weak base;

[0365] (c) drying the mixture from step b) to form a solid; and

[0366] (d) reacting the solution from step a) with the solid from step c) to form the ^{18}F-labeled compound.

[0367] In certain embodiments, the method produces a ^{18}F-pyridine prosthetic group with the following structure b

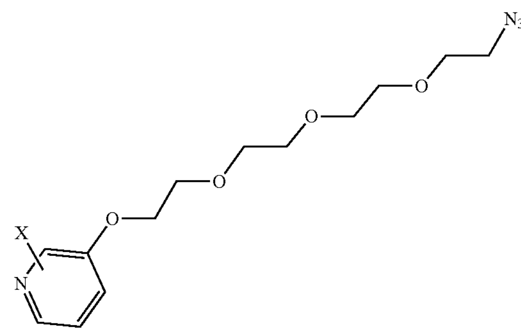
b



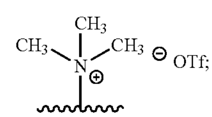
(where ^{18}F is ortho to the N atom), and includes the steps of

[0368] (a) providing a solution of the compound of the structure

c



(where X is ortho to the N atom) where X is NO_2, Br or

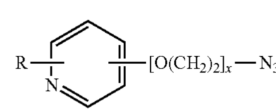


[0369] (b) providing a mixture of ^{18}F in ^{18}Owater, 4,7,13,16,21,24-hexaoxa-1,10-diazabicyclo[8.8.8]hexacosane and weak base, such as K_2CO_3;

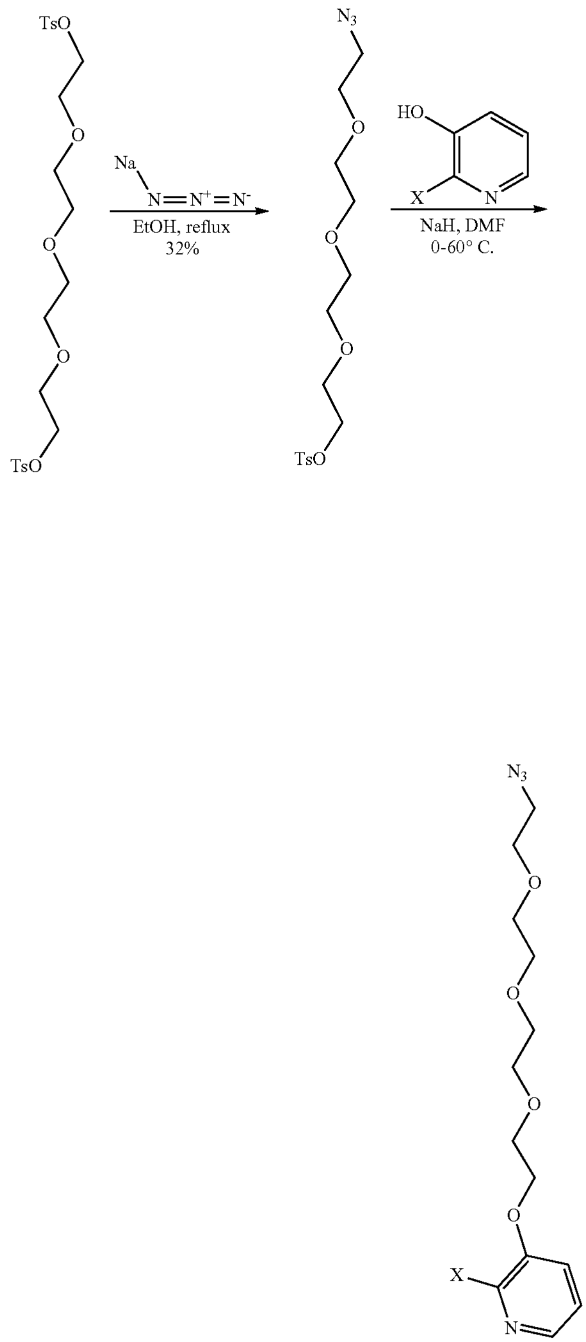
[0370] (c) drying the mixture from step b) to form a solid; and

[0371] (d) reacting the solution from step a) with the solid from step c) to form the ^{18}F-labeled compound.

[0372] In certain embodiments, the method further comprises the step of producing a compound with the following structure a

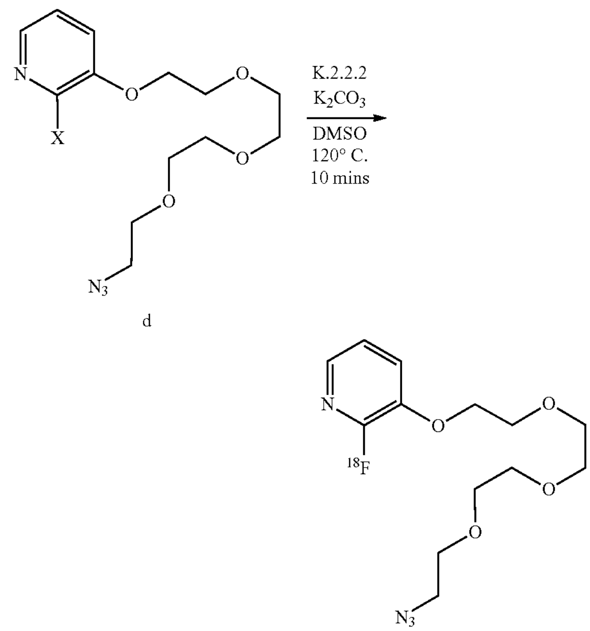


according to the Scheme I shown below:



X = Br, NO_2, F

[0373] In certain embodiments, the method comprises producing ^{18}F-pyridine prosthetic group is [^{18}F]-3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-fluoropyridine (^{18}F-FPPEGA), e, from d according to the following reaction conditions:



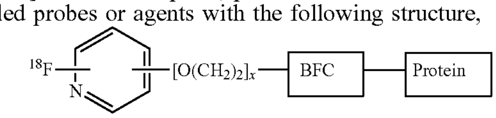
d

e

([^{18}F]-FPPEGA)

^{18}F-Radiolabeled PD-L1 Adnectins

[0374] In some aspects, provided herein are ^{18}F-radiolabeled probes or agents with the following structure,



wherein the Protein is a PD-L1 Adnectin and x is an integer from 1 to 8. In certain embodiments, x is an integer from 2 to 6. In certain embodiments x is an integer from 3 to 5. In some embodiments, x is 4.

BFC

[0375] Bifunctional chelating or conjugating (BFC) moieties, which can be used in the ^{18}F-radiolabeled compositions disclosed herein are commercially available (e.g., Sigma Aldrich; Click Chemistry Tools), or may be synthesized according to well-known chemical reactions.

[0376] In certain embodiments, the BFC is selected from cyclooctyne based chelating agents (e.g., DBCO, DIBO), DFO, DOTA and its derivatives (CB-DO2A, 3p-C-DEPA, TCMC, Oxo-DO3A), TE2A, CB-TE2A, CB-TE1A1P, CB-TE2P, MM-TE2A, DM-TE2A, diamsar and derivatives, NODASA, NODAGA, NOTA, NETA, TACN-TM, DTPA, 1B4M-DTPA, CHX-A"-DTPA, TRAP (PRP9), NOPO, AAZTA and derivatives (DATA), H_2dedpa, H_4octapa, H_2azapa, H_5decapa, H_6phospa, HBED, SHBED, BPCA, CP256, PCTA, HEHA, PEPA, EDTA, TETA, and TRITA based chelating agents, and close analogs and derivatives thereof. Suitable combinations of chelating agents and radionuclides are extensively described in Price et al., *Chem Soc Rev* 2014; 43:260-90.

[0377] In certain embodiments, the BFC is a cyclooctyne comprising a reactive group that forms a covalent bond with an amine, carboxyl, carbonyl or thiol functional group on the targeting protein or peptide. Reactive groups on the cyclooctyne include esters, acids, hydroxyl groups, aminooxy groups, malaiemides, α-halogenketones and α-halogenacetamides.

[0378] In certain embodiments, the BFC is a cyclooctyne is dibenzocyclooctyne (DIBO), biarylazacyclooctynone (BARAC), dimethoxyazacyclooctyne (DIMAC) and dibenzocyclooctyne (DBCO). In certain embodiments, the cyclootyne is DBCO.

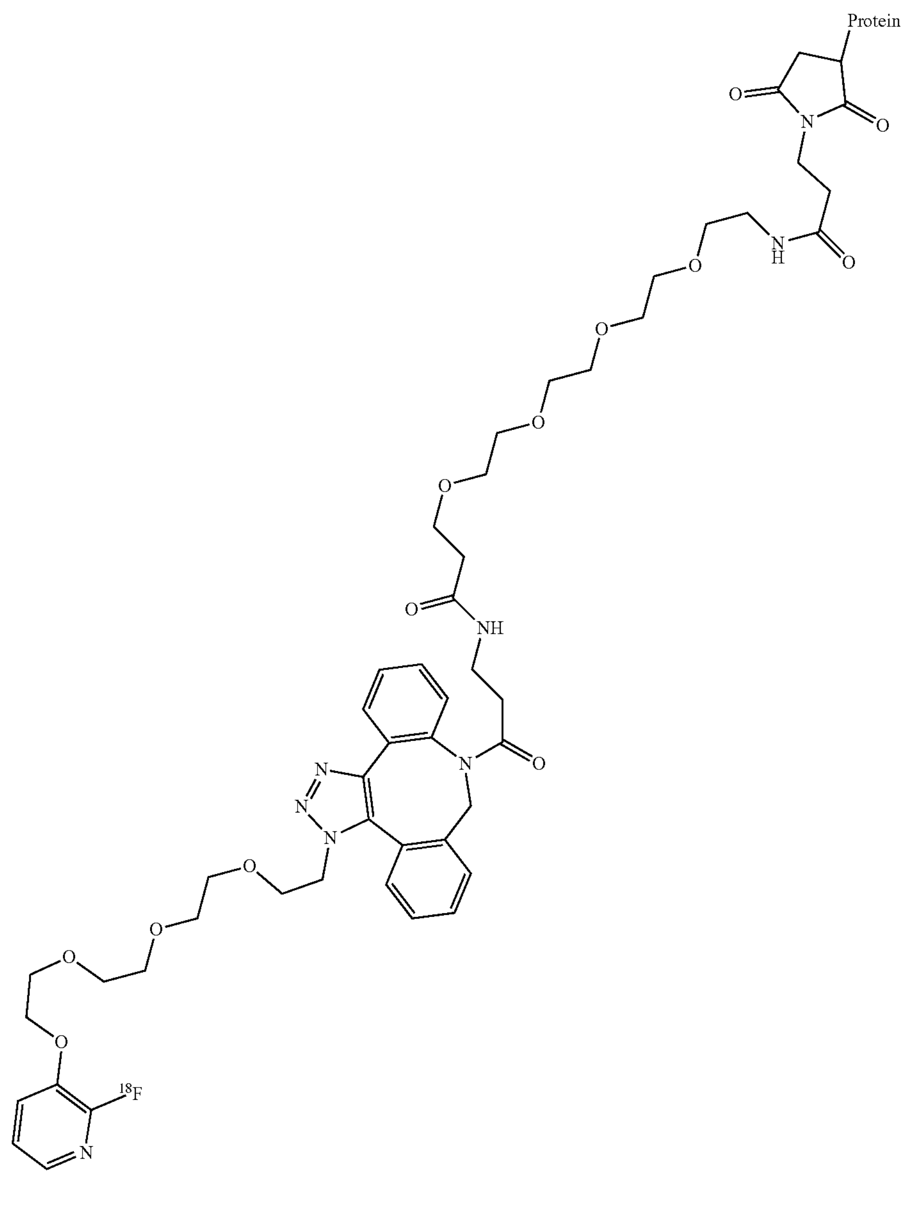
[0379] In certain embodiments, the cyclooctyne comprises a hydrophilic polyethylene glycol $(PEG)_y$ spacer arm, wherein y is an integer from 1 to 8. In certain embodiments, y is an integer from 2 to 6. In certain embodiments, y is 4 or 5.

[0380] In certain embodiments, the BFC is DBCO-PEG4-NHS-Ester or DBCO-Sulfo-NHS-Ester which react specifically and efficiently with a primary amine (e.g., side chain of lysine residues or aminosilane-coated surfaces). In certain embodiments, the BFC is DBCO-PEG4-Acid with terminal carboxylic acid (—COOH) that can be reacted with primary or secondary amine groups in the presence activators (e.g. EDC) forming a stable amide bond. In certain embodiments, the BFC is DBCO-PEG4-Amine which reacts with carboxyl groups in the presence of activators (e.g. EDC, or DCC) or with activated esters (e.g. NHS esters) forming stable amide bonds.

[0381] In certain embodiments, the BFC is DBCO-PEG4-Maleimide which reacts with sulfhydryl groups on cysteine residues, e.g., at or near the C-terminus of the polypeptide.

[0382] In certain embodiments, the polypeptide is modified at its C-terminus by the addition of a cysteine. For example, P_mC_n may be linked to the C-terminal amino acid residue of the polypeptide, wherein P is proline, C is cysteine, m is an integer that at least 0 and n is an integer that is at least 1. Methods for making such modifications are well-known in the art.

[0383] In certain embodiments, the ^{18}F-radiolabeled probe or agent has the following structure a,



wherein the BFC is conjugated to the protein (e.g., an anti-PD-L1 Adnectin) at a cysteine residue.

[0384] The ^{18}F-radiolabeled targeting agents described herein are produced using bioorthogonal, metal free click chemistry in medium suitable for direct use in vivo (e.g., saline) according to the procedures described herein.

XIII. KITS AND ARTICLES OF MANUFACTURE

[0385] The anti-PD-L1 Adnectins described herein can be provided in a kit, a packaged combination of reagents in predetermined amounts with instructions for use in the methods described herein.

[0386] For example, in certain embodiments, an article of manufacture containing materials useful for the treatment or prevention of the disorders or conditions described herein, or for use in the methods of detection described herein, are provided. The article of manufacture comprises a container and a label. Suitable containers include, for example, bottles, vials, syringes, and test tubes. The containers may be formed from a variety of materials such as glass or plastic. The container may hold a composition described herein for in vivo imaging, and may have a sterile access port (for example the container may be an intravenous solution bag or a vial having a stopper pierceable by a hypodermic injection needle). The active agent in the composition is an anti-PD-L1 Adnectin or derivative or precursor thereof, e.g., as described herein. The article of manufacture may further comprise a second container comprising a pharmaceutically-acceptable buffer, such as phosphate-buffered saline, Ringer's solution and dextrose solution. It may further include other materials desirable from a commercial and user standpoint, including other buffers, diluents, filters, needles, syringes, and package inserts with instructions for use.

[0387] In certain embodiments, a kit comprises one or more reagents necessary for forming an ^{18}F labelled anti-PD-L1 Adnectin in vivo imaging agent, such as a [^{18}F]-PD-L1 Adnectin-4-PEG-DBCO-FPPEGA, as further described herein. For example, a kit may comprise a first vial comprising a PD-L1 Adnectin-4-PEG-DBCO and a second vial comprising [^{18}F]FPPEGA. A kit may comprise a first vial comprising a PD-L1 Adnectin-4-PEG-DBCO, a second vial comprising a non-radiolabeled precursor of [^{18}F]FPPEGA, e.g., 4-PEG-tosyl-azide, and optionally, a third vial comprising ^{18}F (e.g., in O^{18} water). The kits may further comprise vials, solutions and optionally additional reagents necessary for the manufacture of a [^{18}F]-PD-L1 Adnectin-4-PEG-DBCO-FPPEGA. The kits may contain instructions to complete the synthesis of the [^{18}F]-PD-L1 Adnectin-4-PEG-DBCO-FPPEGA, per the methods described in the Examples.

[0388] Similarly, kits may comprise the reagents necessary for forming a ^{64}Cu labelled anti-PD-L1 Adnectin, such as the reagents described herein.

XIV. EXEMPLARY EMBODIMENTS

[0389] 1. A polypeptide comprising a fibronectin type III tenth domain (^{10}Fn3), wherein (a) the ^{10}Fn3 domain comprises AB, BC, CD, DE, EF, and FG loops, (b) the ^{10}Fn3 has at least one loop selected from loop BC, DE, and FG with an altered amino acid sequence relative to the sequence of the corresponding loop of the human ^{10}Fn3 domain (SEQ ID NO: 1), and (c) the polypeptide specifically binds to PD-L1.

2. The polypeptide of embodiment 1, wherein the polypeptide binds to PD-L1 with a K_D of 500 mM or less.

3. The polypeptide of embodiment 2, wherein the polypeptide binds to PD-L1 with a K_D of 100 mM or less.

4. The polypeptide of any one of embodiments 1-3, wherein the BC, DE, and FG loops comprise the amino acid sequences of:

[0390] (a) SEQ ID NOs: 6, 7, and 8, respectively;

[0391] (b) SEQ ID NOs: 21, 22, and 23, respectively;

[0392] (c) SEQ ID NOs: 36, 37, and 38, respectively;

[0393] (d) SEQ ID NOs: 51, 52, and 53, respectively;

[0394] (e) SEQ ID NOs: 66, 67, and 68, respectively;

[0395] (f) SEQ ID NOs: 81, 82, and 83, respectively; or

[0396] (g) SEQ ID NOs: 97, 98, and 99, respectively.

5. The polypeptide of any one of embodiments 1-4, wherein the polypeptide comprises an amino acid sequence at least 80%, 85%, 90%, 95%, 98%, 99% or 100% identical to SEQ ID NO: 5, 20, 35, 50, 65, 80, or 96.

6. The polypeptide of embodiment 5, wherein the polypeptide comprises an amino acid sequence at least 80%, 85%, 90%, 95%, 98%, 99% or 100% identical to SEQ ID NO: 80.

7. The polypeptide of embodiment 5, wherein the polypeptide comprises an amino acid sequence at least 80%, 85%, 90%, 95%, 98%, 99% or 100% identical to SEQ ID NO: 96.

8. The polypeptide of any one of embodiments 1-7, wherein the polypeptide comprises an amino acid sequence at least 80%, 85%, 90%, 95%, 98%, 99% or 100% identical to the non-BC, DE, and FG loop regions of SEQ ID NO: 5, 20, 35, 50, 65, 80, or 96.

9. The polypeptide of any one of embodiments 1-7, wherein the polypeptide comprises an amino acid sequence at least 80%, 85%, 90%, 95%, 98%, 99% or 100% identical to an amino acid sequence selected from the group consisting of: SEQ ID NOs: 9-15, 24-30, 39-45, 54-60, 69-75, 84-91, and 100-107.

10. The polypeptide of any one of embodiments 1-7 and 9, wherein the polypeptide comprises an amino acid sequence at least 80%, 85%, 90%, 95%, 98%, 99% or 100% identical to the non-BC, DE, and FG loop regions of an amino acid sequence selected from the group consisting of: SEQ ID NOs: 9-15, 24-30, 39-45, 54-60, 69-75, 84-91, and 100-107.

11. The polypeptide of any one of embodiments 1-10, wherein the polypeptide comprises an N-terminal leader selected from the group consisting of SEQ ID NOs: 112-121, and/or a C-terminal tail selected from the group consisting of SEQ ID NOs: 122-156.

12. The polypeptide of any one of embodiments 1-11, wherein the polypeptide comprises one or more pharmacokinetic (PK) moieties selected from the group consisting of polyethylene glycol, sialic acid, Fc, Fc fragment, transferrin, serum albumin, a serum albumin binding protein, and a serum immunoglobulin binding protein.

13. The polypeptide of embodiment 12, wherein the PK moiety and the polypeptide are linked via at least one disulfide bond, a peptide bond, a polypeptide, a polymeric sugar or a polyethylene glycol moiety.

14. The polypeptide of embodiment 13, wherein the PK moiety and the polypeptide are linked via a linker with an amino acid sequence selected from the group consisting of SEQ ID NOs: 167-216.

15. A nucleic acid encoding the polypeptide of any one of embodiments 1-14.

16. The nucleic acid of embodiment 15, wherein the nucleic acid comprises a nucleotide sequence selected from the

group consisting of SEQ ID NOs: 16-19, 31-34, 46-49, 61-64, 76-79, 92-95, and 108-111.

17. A vector comprising the nucleic acid of embodiment 15.

18. A cell comprising the nucleic acid of embodiment 15.

19. A composition comprising the polypeptide of any one of embodiments 1-14, and a carrier.

20. An imaging agent comprising the polypeptide of any one of embodiments 1-14, and a detectable label.

21. The imaging agent of embodiment 20, wherein the detectable label is detectable by positron emission tomography.

22. The imaging agent of embodiment 20 or 21, wherein the polypeptide is conjugated to the detectable label by an moiety selected from the group consisting of DFO, DOTA, CB-DO2A. 3p-C-DEPA. TCMC, DBCO, DIBO, BARAC, DIMAC, Oxo-DO3A, TE2A, CB-TE2A, CB-TE1A1P, CB-TE2P, MM-TE2A, DM-TE2A, diamsar, NODASA, NODAGA, NOTA, NETA, TACN-TM, DTPA, 1B4M-DTPA, CHX-A"-DTPA, TRAP, NOPO, AAZTA, DATA, H_2dedpa, H_4octapa, H_2azapa, H_5decapa, H_6phospa, HBED, SHBED, BPCA, CP256, PCTA, HEHA, PEPA, EDTA, TETA, and TRITA.

23. The imaging agent of embodiment 22, wherein the conjugating moiety is NODAGA.

24. The imaging agent of any one of embodiments 20-23, wherein the detectable label is a radionuclide.

25. The imaging agent of embodiment 24, wherein the radionuclide is selected from the group consisting of: ^{64}Cu, ^{124}I, $^{76/77}$Br, ^{86}Y, ^{89}Zr, ^{68}Ga, ^{18}F, ^{11}C, ^{125}I, ^{124}I, ^{131}I, ^{123}I, ^{131}I, ^{123}I, ^{32}Cl, ^{33}Cl, ^{34}Cl, ^{68}Ga, ^{74}Br, ^{75}Br, ^{76}Br, ^{77}Br, ^{78}Br, ^{89}Zr, ^{186}Re, ^{188}Re, ^{90}Y, ^{177}Lu, ^{99}Tc, or ^{153}Sm.

26. The imaging agent of embodiment 25, wherein the radionuclide is ^{18}F.

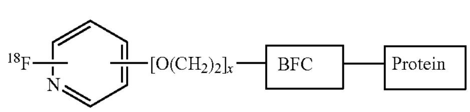
27. The imaging agent of embodiment 25, wherein the radionuclide is ^{64}Cu.

28. The imaging agent of embodiment 24, wherein the chelating agent is NODAGA and the radionuclide is ^{64}Cu.

29. The imaging agent of embodiment 24, wherein the imaging agent comprises the polypeptide of embodiment 6, the NODAGA, and the radionuclide ^{64}Cu.

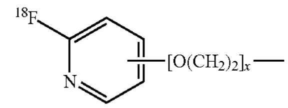
30. The imaging agent of embodiment 24, wherein the imaging agent comprises the polypeptide of embodiment 7, NODAGA, and the radionuclide ^{64}Cu.

31. An imaging agent comprising the polypeptide of any one of embodiments 1-14, a ^{18}F-radiolabeled prosthetic group and a bifunctional conjugating (BFC) moiety, wherein the imaging agent has the following structure,



wherein the ^{18}F is ortho to the N atom, x is an integer from 1 to 8, or pharmaceutically acceptable salt thereof.

32. The imaging agent of embodiment 31, wherein ^{18}F-radiolabeled prosthetic group has the following structure,

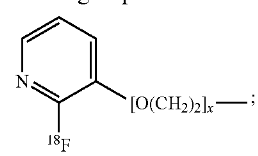


33. The imaging agent of embodiment 31 or 32, wherein the $[O(CH_2)_2]_x$ moiety is present in the 1-3 configuration relative to the nitrogen on the pyridine ring.

34. The imaging agent of embodiment 31 or 32, wherein the $[O(CH_2)_2]_x$ moiety is present in the 1-2 configuration relative to the nitrogen on the pyridine ring.

35. The imaging agent of embodiment 31 or 32, wherein the $[O(CH_2)_2]_x$ moiety is present in the 1-4 configuration relative to the nitrogen on the pyridine ring.

36. The imaging agent of embodiment 31, wherein ^{18}F-radiolabeled prosthetic group has the following structure,



37. The imaging agent of any one of the embodiments 31 to 36, wherein x is an integer from 2 to 6.

38. The imaging agent of embodiment 37, wherein x is an integer from 3 to 5.

39. The imaging agent of embodiment 37, wherein x is 4.

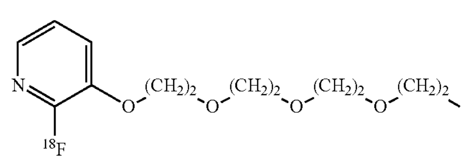
40. The imaging agent of any one of embodiments 31-39, wherein the $[O(CH_2)_2]_x$ moiety is present in the 1-3 configuration relative to the nitrogen on the pyridine ring.

41. The imaging agent of any one of the embodiments 31-40, wherein the pyridine ring comprises an additional substituent which does not interfere with the fluorination reaction.

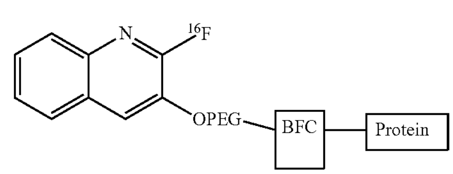
42. The imaging agent of embodiment 41, wherein the substituent on the pyridine ring is a C_{1-6} alkyl.

43. The imaging agent of embodiment 42, wherein the substituent is methyl, ethyl or propyl.

44. The imaging agent of embodiment 31, wherein the ^{18}F-radiolabeled prosthetic group has the structure



45. An imaging agent comprising the polypeptide of any one of embodiments 1-14, an ^{18}F-radiolabeled prosthetic group and a bifunctional conjugating (BFC) moiety, wherein the imaging agent has the following structure



wherein "OPEG" is $[O(CH_2)2]_x$, and x is an integer from 1 to 8, or a pharmaceutically acceptable salt thereof and wherein "Protein" is the polypeptide comprised in the imaging agent of any one of embodiments 1-14.

46. The imaging agent of embodiment 45, wherein x is an integer from 2 to 6, or a pharmaceutically acceptable salt thereof.

47. The imaging agent of embodiment 45, wherein x is an integer from 3 to 5, or a pharmaceutically acceptable salt thereof.

48. The imaging agent of embodiment 45, wherein x is 4, or a pharmaceutically acceptable salt thereof.

49. The imaging agent of any one of embodiments 31 to 48, wherein the BFC is a cyclooctyne comprising a reactive group that forms a covalent bond with an amine, carboxyl, carbonyl or thiol functional group on the protein.

50. The imaging agent of embodiment 49, wherein the cyclooctyne is selected from the group consisting of dibenzocyclooctyne (DIBO), biarylazacyclooctynone (BARAC), dimethoxyazacyclooctyne (DIMAC) and dibenzocyclooctyne (DBCO).

51. The imaging agent of embodiment 50, wherein the cyclooctyne is DBCO.

52. The imaging agent of any one of embodiments 31 to 51, wherein the BFC further comprises a polyethylene glycol $(PEG)_y$ spacer arm, wherein y is an integer from 1 to 8.

53. The imaging agent of embodiment 52, wherein y is an integer from 2 to 6.

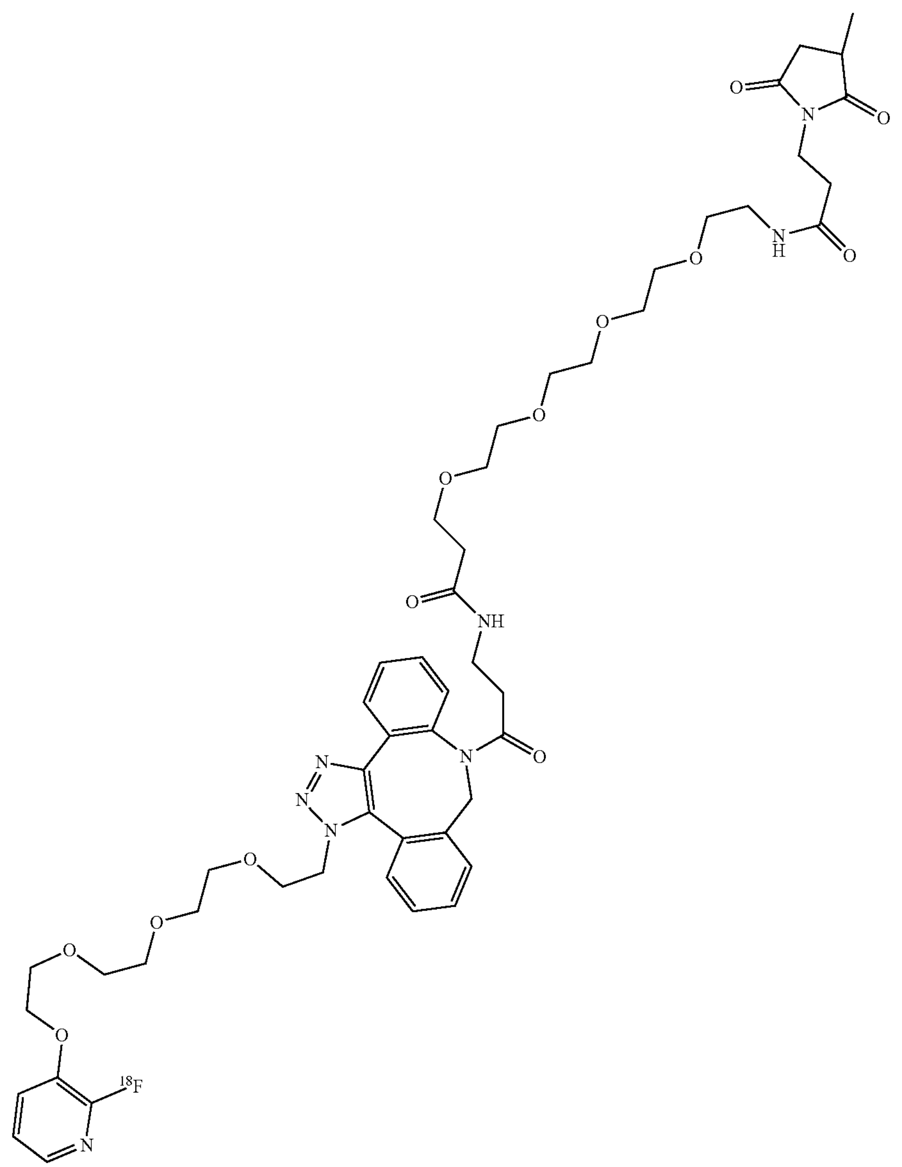
54. The imaging agent of embodiment 52, wherein y is 4 or 5.

55. The imaging agent of embodiment 52, wherein the BFC is DBCO-PEG4-NHS-Ester, DBCO-Sulfo-NHS-Ester, DBCO-PEG4-Acid, DBCO-PEG4-Amine or DBCO-PEG4-Maleimide.

56. The imaging agent of embodiment 55, wherein the BFC is DBCO-PEG4-Maleimide.

57. The imaging agent of embodiment 31, wherein the imaging agent has the structure:

X



wherein X is a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs: 13, 28, 43, 58, 73, 88, and 104.

58. The imaging agent of embodiment 57, wherein the polypeptide comprises the amino acid sequence set forth in SEQ ID NO: 88.

59. The imaging agent of embodiment 57, wherein the polypeptide comprises the amino acid sequence set forth in SEQ ID NO: 104.

60. A kit comprising the polypeptide, composition, or imaging agent of any one of embodiments 1-14 and 19-59, and instructions for use.

61. A method of detecting PD-L1 in a sample comprising contacting the sample with the polypeptide of any one of embodiments 1-14, and detecting PD-L1.

62. A method of detecting PD-L1 positive cells in a subject comprising administering to the subject an imaging agent of any one of embodiments 31-59, and detecting the imaging agent, the detected imaging agent defining the location of the PD-L1 positive cells in the subject.

63. A method of detecting PD-L1-expressing tumors in a subject comprising administering to the subject an imaging agent of any one of embodiments 31-59, and detecting the imaging agent, the detected imaging agent defining the location of the tumor in the subject.

64. The method of embodiment 62 or 63, wherein the imaging agent is detected by positron emission tomography.

65. A method of obtaining an image of the imaging agent of any one of embodiments 31-59, the method comprising,

[0397] a) administering the imaging agent to a subject; and

[0398] b) imaging in vivo the distribution of the imaging agent by positron emission tomography.

66. A method of obtaining a quantitative image of tissues or cells expressing PD-L1, the method comprising contacting the cells or tissue with the imaging agent of any one of embodiments 31-59, and detecting or quantifying the tissue expressing PD-L1 using positron emission tomography.

67. A method for detecting a PD-L1-expressing tumor comprising administering an imaging-effective amount of the imaging agent of any one of embodiments 31-59 to a subject having a PD-L1-expressing tumor, and detecting the radioactive emissions of said imaging agent in the tumor using positron emission tomography, wherein the radioactive emissions are detected in the tumor.

68. A method of diagnosing the presence of a PD-L1-expressing tumor in a subject, the method comprising

[0399] (a) administering to a subject in need thereof the imaging agent of any one of embodiments 31-59; and

[0400] (b) obtaining an radio-image of at least a portion of the subject to detect the presence or absence of the imaging agent;

[0401] wherein the presence and location of the imaging agent above background is indicative of the presence and location of the disease.

69. A method of monitoring the progress of an anti-tumor therapy against PD-L1-expressing tumors in a subject, the method comprising

[0402] (a) administering to a subject in need thereof the imaging agent of any one of embodiments 31-59 at a first time point and obtaining an image of at least a portion of the subject to determine the size of the tumor;

[0403] (b) administering an anti-tumor therapy to the subject;

[0404] (c) administering to the subject the imaging agent at one or more subsequent time points and obtaining an image of at least a portion of the subject at each time point; wherein the dimension and location of the tumor at each time point is indicative of the progress of the disease.

INCORPORATION BY REFERENCE

[0405] All documents and references, including patent documents, e.g., PCT/US15/62485 and PCT/US15/62502 and websites, described herein are individually and specifically incorporated by reference herein into this document to the same extent as if there were written in this document in full or in part.

[0406] The invention is now described by reference to the following examples, which are illustrative only, and are not intended to limit the present invention. While the invention has been described in detail and with reference to specific embodiments thereof, it will be apparent to one of skill in the art that various changes and modifications can be made thereto without departing from the spirit and scope thereof.

EXAMPLES

Example 1: Identification of PD-L1 Binding Adnectins

[0407] Anti-PD-L1 Adnectins were isolated from an Adnectin library screened with a human PD-L1 protein, or were affinity matured by PROfusion from clones identified in the library. The full length sequences, core sequences, BC, DE, and FG loop sequences of these Adnectins, as well as variants with a “PC” modified C-terminus, are presented in FIG. **1** and Table 3.

[0408] For example, the high-affinity, anti-PD-L1 Adnectin, ADX_5322_A02 (“A02”), was obtained by affinity-maturing the ATI-964 Adnectin. The gene encoding ATI-964 was re-diversified by introducing a small fraction of non-wild-type nucleotides at each nucleotide position that encoded a residue in loop BC, DE, or FG. The resulting library of Adnectin sequences related to ATI-964 was then subjected to in vitro selection by PROfusion (mRNA display) for binding to human PD-L1 under high-stringency conditions. The clones enriched after completed selection were sequenced, expressed in HTPP format, and screened for their ability to bind PD-L1 and for their fraction of monomericity. The clone with the best combination of affinity for PD-L1 and robust biophysical properties was mutated to include a C-terminal Cysteine, first with the C-terminal sequence NYRTPCH6 (the form identified as ADX_5322_A02), and later with the C-terminal sequence NYRTPC.

[0409] The same process was followed to affinity-mature ATI-967, resulting in the Adnectin ADX_5417_E01. Similarly, affinity matured ATI_1760_C02, ATI_1760_E01 ("E01") and ATI_1760_F01 were obtained by affinity maturation of ATI_1422_G05.

[0410] Additional anti-human PD-L1 adnectins were isolated. Their sequences are set forth in Table 3.

Expression and Purification of His-Tagged Anti-PD-L1 Adnectins

[0411] All DNA constructs contained an N-terminal his tag followed by a TVMV recognition sequence. The expression plasmids (pET-28 NM vector) for the anti-PD-L1 Adnectins described supra were transformed into BL21 (DE3) cells (New England Biolabs). Cells were grown in Overnight Express Autoinduction media (Novagen) in 1 L shake flasks at 37° C. for 6 hours followed by 20° C. for 16 hours at 220 RPM. Cells were harvested by centrifugation and suspended in PBS pH 7.2. Cells were lysed mechanically, then clarified by centrifugation. Soluble fractions were bound by gravity feed to Ni-NTA Agarose resin (Qiagen), washed in 20 mM Tris+10 mM Imidazole pH 8.0, followed by 20 mM Tris+40 mM Imidazole pH 8.0, and eluted with 20 mM Tris+400 mM Imidazole pH 8.0. Nickel eluates were spiked with TVMV protease at 1:23-fold molar excess of Adnectin. The TVMV-Adnectin eluate mixtures were dialyzed against 20 mM Tris pH 8.0 at 4° C. for 16 hours. To separate the TVMV protease and cleaved his tag fragments, samples were loaded onto a 10 mL HisTrap FF column (GE Healthcare) and flow through fractions were collected.

Example 2: Biophysical Assessment of PD-L1 Adnectins

[0412] The binding properties of ATI-1420D05, ATI-1420D05, AT1-1421E04 and ATI-1422G05, ATI_1760_C02, ATI_1760_E01 and ATI_1760_E01 were assessed.

TABLE 1

Binding properties of anti-PD-L1 Adnectins

Sequence Name	SEQ ID	K_D(nM)
ATI-1420B09		2.5
ATI-1420D05		9.5
AT1-1421E04		5.6

[0413] Binding properties of the purified ATI-964, ATI-967, ATI-968, ADX_5322_A02, and ADX_5417_E01 Adnectins to human or cyno PD-L1, as determined by Biacore, are shown in Table 2. Cell binding was determined by measuring binding to human PD-L1 positive cells L2987.

TABLE 2

Biophysical properties of anti-PD-Ll Adnectins

		Binding Kinetics				Melting Transition Midpoint	Cell Binding
Sequence Name	SEQ ID	k_a (1/Ms)	k_d (s)	K_D (M)	K_D (M) for cynoPD-L1	(Tm) ° C. N.D.	EC_{50} N.D.
ATI-964	30	3.6×10^5	7.7×10^{-5}	2.1×10^{-10}	1.4×10^{-10}	N.D.	4.4
ATI-965	45	4.6×10^5	3.3×10^{-4}	7.1×10^{-10}	8×10^{-10}	N.D.	4.9
ATI-966	60	2.5×10^6	6.9×10^{-5}	2.8×10^{-11}	3.8×10^{-11}	N.D.	2.3
ATI-967	75	2.1×10^6	6.7×10^{-5}	3.2×10^{-11}	6×10^{-11}	N.D.	N.D.
ATI-968	15	7.5×10^5	1.2×10^{-4}	1.6×10^{-10}	1.1×10^{-10}	60	3.4
ADX_5322_A02	91	2.5×10^6	5.7×10^{-4}	2.28×10^{-10}	N.D.	82	0.43 nM (Cys-Capped)
ADX_5417_E01	107	2.0×10^7	2.6×10^{-4}	1.3×10^{-11}	N.D.	73	N.D.

[0414] The binding data indicates that the affinity matured anti-human PD-L1 adnectins bind to human PD-L1 with affinities that are less than 1 nM or even less than 0.1 nM.

[0415] Exemplary inhibition curves are shown in FIG. **12**.

[0416] Anti-PD-L1 adnectins have the following additional characteristics:

[0417] Inhibiting the binding of human PD-1 to human PD-L1, as determined by measuring inhibition of binding of human PD-1Fc to the PD-L1 positive cells L2987 by flow cytometry, and shown, e.g., for adnectins ATI-964, ATI-965, ATI-966, ATI-967, ATI-968, A02 and E01;

[0418] Inhibiting the binding of human CD80 (B7-1) to human PD-L1, as determined by ELISA. For example, ATI-964 inhibits binding with an EC50 of 41 pM; ATI-965 inhibits binding with an EC50 of 210 pM; ATI-966 inhibits binding with an EC50 of 28 pM; and ATI-968 inhibits binding with an EC50 of 56 pM;

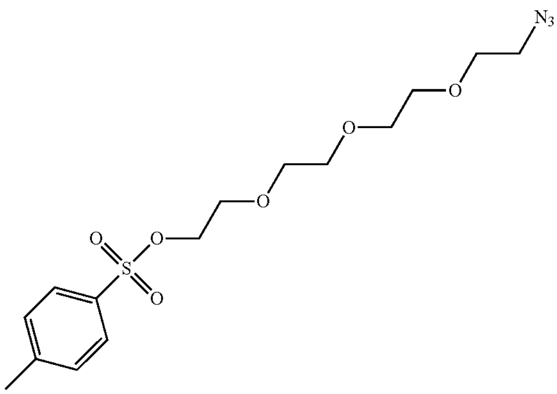
[0419] Inhibiting the binding of the anti-PD-L1 antibody 12A4 to human PD-L1, as determined by ELISA.

[0420] Anti-PD-L1 antibodies were also tested in a mixed lymphocyte reaction (MLR): ATI-964, ATI-965, and ATI-968 were active in an MLR, whereas ATI-966 and ATI-967 were not active in an MLR.

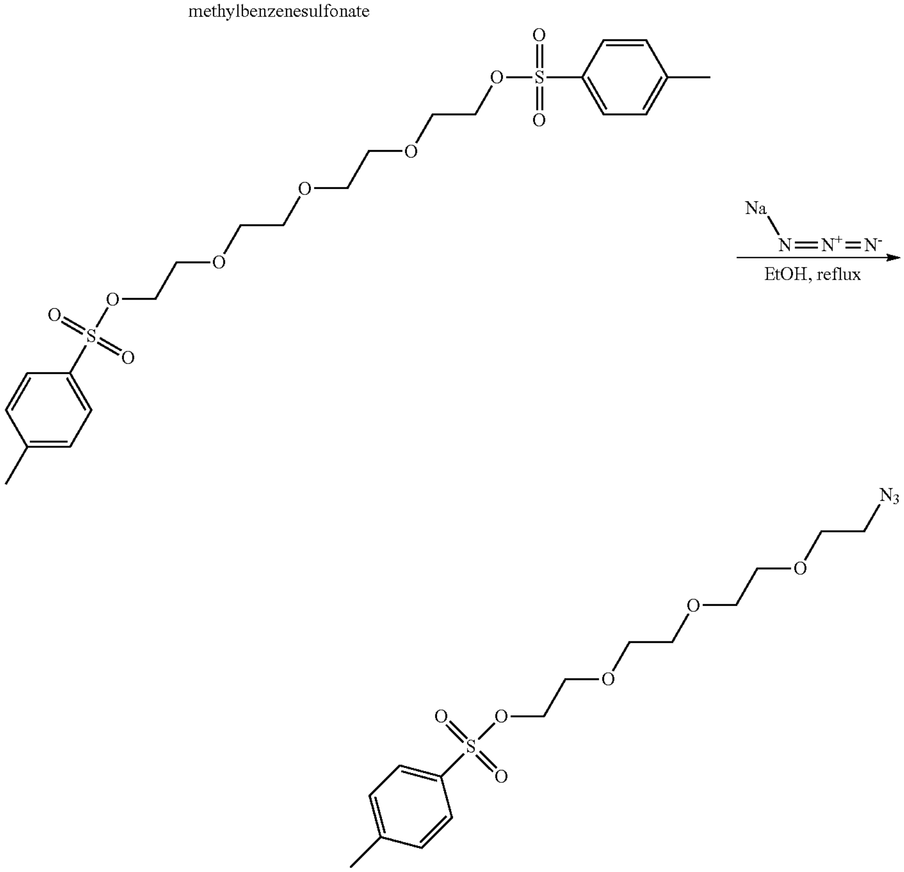
[0421] The following examples relate to the labeling of anti-PD-L1 Adnectins with ^{18}F and ^{64}Cu.

Example 3: Preparation of 2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethyl 4-methylbenzenesulfonate

[0422]



2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethyl 4-methylbenzenesulfonate

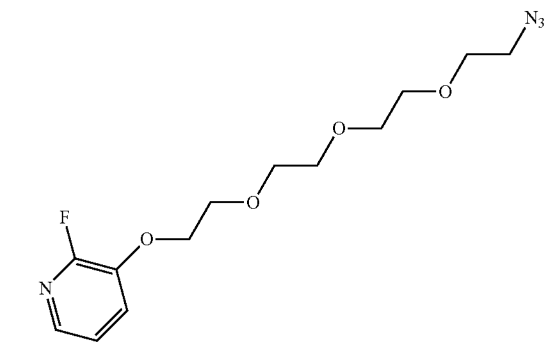


2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethyl 4-methylbenzenesulfonate

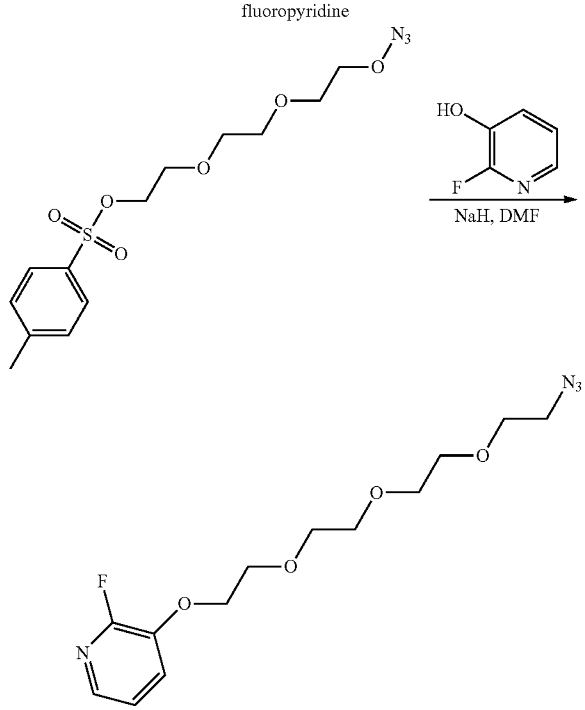
[0423] A mixture of ((oxybis(ethane-2,1-diyl))bis(oxy))bis(ethane-2,1-diyl) bis(4-methylbenzenesulfonate) (5 g, 9.95 mmol) and sodium azide (0.647 g, 9.95 mmol) were dissolved in ethanol (50 mL) and the reaction was refluxed at 90° C. over a 17 hour period. The solvent was removed using partial vacuum and then loaded onto a 40 gram silica cartridge and purified using flash chromatography (Isco-CombiFlash—eluted using a linear gradient method starting from 10% ethyl acetate in hexanes going to a 90% ethyl acetate in hexanes over a 45 minute period). The pooled fractions were checked by TLC and combined to give 2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethyl 4-methylbenzenesulfonate as a colorless oil. Due to the reactive nature of the 2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethyl 4-methylbenzenesulfonate product this material was used "as is" without any further characterizations.

Example 4: Preparation of 3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-fluoropyridine

[0424]



3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-fluoropyridine

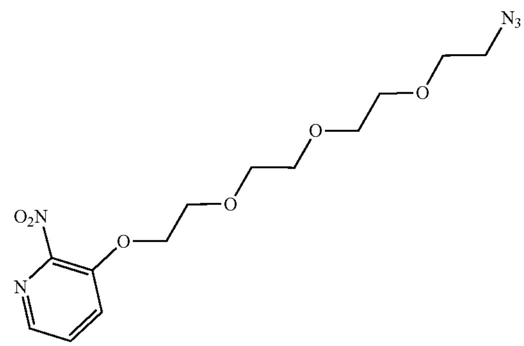


3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-fluoropyridine

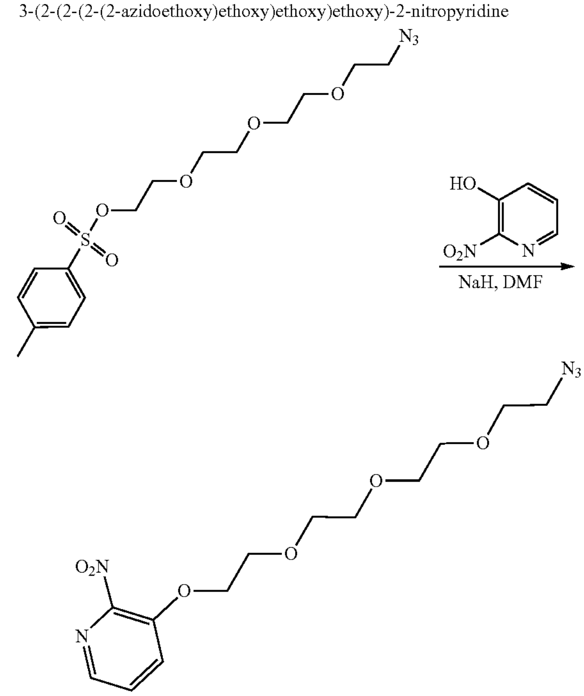
[0425] To a suspension of sodium hydride (0.129 g, 3.21 mmol) in DMF (10 mL) at 0° C. was dropwise added a stirring solution of 2-fluoropyridin-3-ol (0.363 g, 3.21 mmol) in DMF (5 mL), then followed by the dropwise addition of the solution of 2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethyl 4-methylbenzenesulfonate (1.00 g, 2.68 mmol) in DMF (5 mL). The suspension was held at 0° C. for 10 min, then brought to ambient temperature for 1 hour, followed by additional heating at 60° C. for 4 hours. The solvent was removed in vacuo. 100 ml of ethyl acetate was added followed by 3 separate wash extractions with concentrated brine solution. The organic layer was dried over sodium sulfate, filtered, and concentrated. The crude material was purified using flash chromatography (IscoCombiFlash—eluted with 10-50% EtOAc in Hex) to give a colorless oil. 3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-fluoropyridine (702 mg, 2.233 mmol, 83% yield) was isolated as a clear oil. ^{1}H NMR (400 MHz, CHLOROFORM-d) δ 7.75 (dt, J=4.9, 1.6 Hz, 1H), 7.33 (ddd, J=10.0, 8.1, 1.5 Hz, 1H), 7.10 (ddd, J=7.9, 4.9, 0.7 Hz, 1H), 4.30-4.16 (m, 2H), 3.95-3.83 (m, 2H), 3.80-3.61 (m, 10H), 3.38 (t, J=5.1 Hz, 2H) 13C NMR (101 MHz, CHLOROFORM-d) δ 142.3, 137.7, 137.5, 123.4, 123.4, 121.7, 121.6, 77.3, 76.7, 70.9, 70.7, 70.6, 70.0, 69.4, 69.0, 50.6 19F NMR (400 MHz, CHLOROFORM-d) δ−83.55. HRMS (ESI) Theory: C13H20FN4O4+m/z 315.464; found 315.1463.

Example 5: Preparation of 3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-nitropyridine

[0426]



3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-nitropyridine

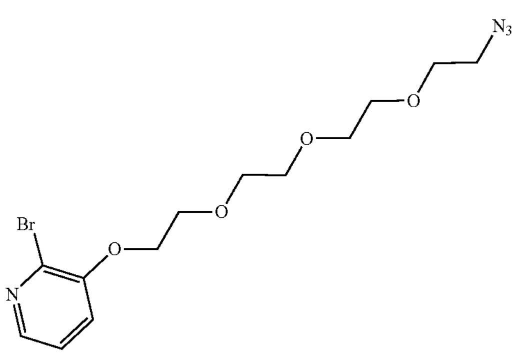


3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-nitropyridine

[0427] Sodium hydride (0.121 g, 3.01 mmol) (60% suspension in oil) was dissolved in DMF (7.0 mL) and the resulting suspension was cooled to 0° C. A solution of 2-nitropyridin-3-ol (0.384 g, 2.74 mmol) in DMF (1.5 mL) was added slowly, followed by the dropwise addition of 2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethyl 4-methylbenzenesulfonate (1.023 g, 2.74 mmol) in DMF (1.5 mL). The suspension was held at 0° C. for 10 minutes, then brought to ambient temperature for 2 hours followed by heating 60° C. for a 72 hour period. The reaction was quenched with 10 ml of DI water, followed by ethyl acetate extraction (3×10 mL). Pooled EtOAc extracts were washed with a concentrated brine solution (10 mL), dried over sodium sulfate, filtered, and evaporated under reduced pressure to give a light yellow oil. The crude was purified by flash chromatography. 24 g silica cartridge, 25 mL/min, starting from 10% ethyl acetate in hexanes, followed by a linear change to 50% ethyl acetate in hexanes over a 25 minute period. After this time, the gradient was held at this solvent composition for 10 minutes then changed to 100% ethyl acetate over a 10 minute period. 3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-nitropyridine was eluted between the 30-40 minute portion of the chromatogram and the pooled fractions were evaporated under reduced pressure, then under vacuum for 2 hours to give 3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-nitropyridine (687 mg, 1.973 mmol, 72.0% yield) as a light yellow oil. 1H NMR (400 MHz, CHLOROFORM-d) δ 8.11 (dt, J=4.9, 1.6 Hz, 1H), 7.60 (ddd, J=10.0, 8.1, 1.5 Hz, 1H), 7.52 (ddd, J=7.9, 4.9, 0.7 Hz, 1H), 4.30-4.16 (m, 2H), 3.95-3.83 (m, 2H), 3.80-3.61 (m, 10H), 3.38 (t, J=5.1 Hz, 2H) 13C NMR (101 MHz, CHLOROFORM-d) δ 147.3, 139.5, 128.4, 124.4, 71.1, 70.7, 70.6, 70.0, 69.9, 69.3, 50.7. HRMS (ESI) Theory: C13H20N5O6+m/z 342.1408; found 342.1409

Example 6: Synthesis of 3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-bromopyridine

[0428]



3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-bromopyridine

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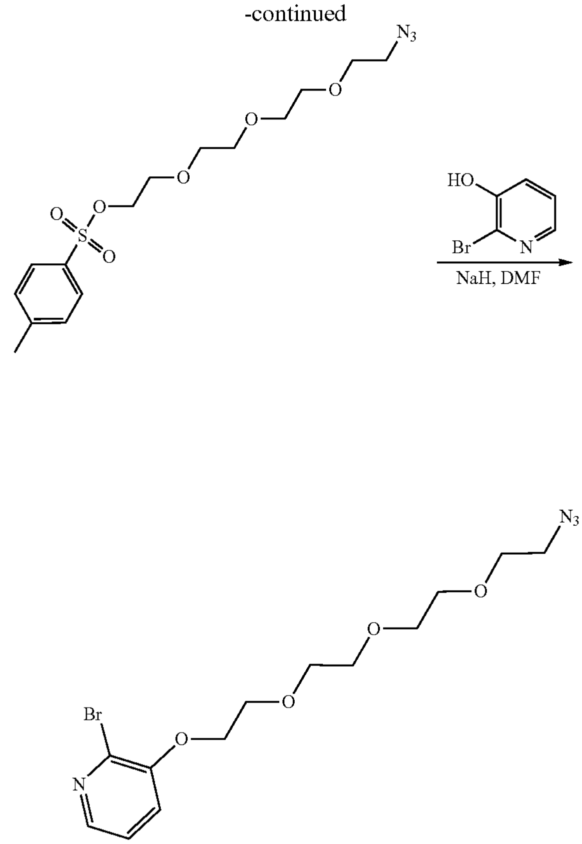
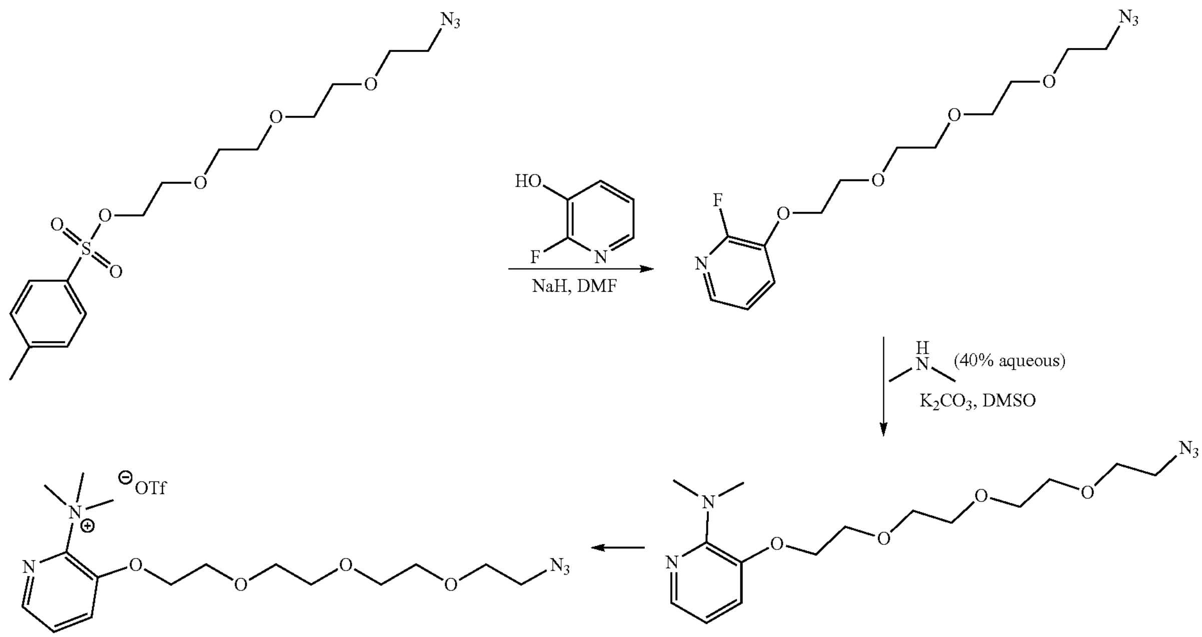


[0429] To the suspension of sodium hydride (NaH, 25.7 mg, 0.643 mmol) in dimethylformamide (DMF, 5 mL) at 0° C. was dropwise added a solution of 2-bromopyridin-3-ol (112 mg, 0.643 mmol) in DMF (1 mL), followed by the dropwise addition of the solution of 2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethyl 4-methylbenzenesulfonate (200 mg, 0.536 mmol) in DMF (1 mL). The suspension was held at 0° C. for 10 minutes, then brought to ambient temperature and held for 1 hour, followed by heating to 60° C. for 4 hours. Upon completion of heating, the solvent of the crude reaction mixture was removed in vacuo. The crude reaction was reconstituted in 50 mL of ethyl acetate, washed with 2×50 mL of a aqueous brine solution, and the organic layer was dried over magnesium sulfate, filtered, and concentrated in vacuo. The crude reaction was purified using reverse-phase HPLC to give 3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-bromopyridine, TFA (112 mg, 0.229 mmol, 42.7% yield) as a light yellow oil. HRMS ESI m/z (M+H), Theory C13H20BrN4O4 375.0664 found 375.0662; 1H NMR (400 MHz, DMSO-d_6) δ 7.97 (dd, J=4.6, 1.5 Hz, 1H), 7.54 (dd, J=8.2, 1.6 Hz, 1H), 7.40 (dd, J=8.1, 4.6 Hz, 1H), 4.24 (dd, J=5.3, 3.9 Hz, 2H), 3.85-3.78 (m, 2H), 3.68-3.62 (m, 2H), 3.62-3.52 (m, 8H), 3.42-3.34 (m, 2H).

Example 7: Scheme for Synthesis of Trimethylanilium Compound

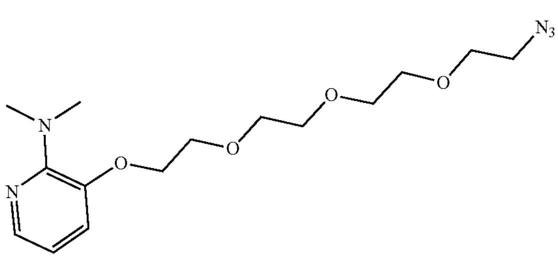
[0430]



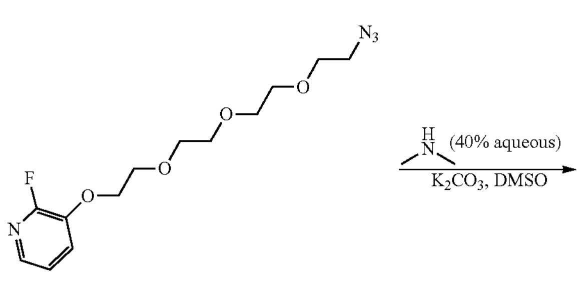
3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-N, N, N-trimethylpyridin-2-aminium

Example 8: Synthesis of 3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-N,N-dimethylpyridin-2-amine

[0431]



3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-N, N-dimethylpyridin-2-amine



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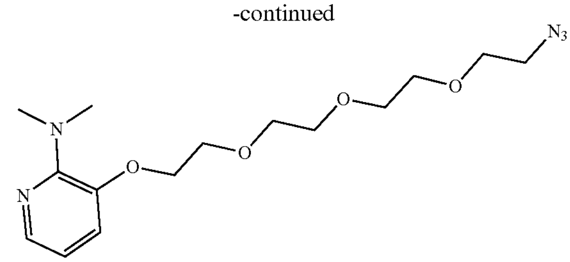


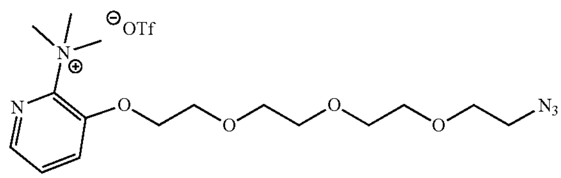
3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-N, N-dimethylpyridin-2-amine

[0432] A mixture of 3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-fluoropyridine (160 mg, 0.509 mmol), potassium carbonate (K_2CO_3, 84 mg, 0.611 mmol), and dimethylamine (40% in water, 0.097 mL, 0.764 mmol) in dimethylsulfoxide (DMSO, 2.5 mL) were heated in a sealed pressure-proof vessel at 110° C. for 14 hours. Upon completion of heating, the solvent of the crude reaction mixture was removed in vacuo. The crude reaction was reconstituted in 50 mL of ethyl acetate, washed with 2×50 mL of a aqueous brine solution, and the organic layer was dried over magnesium sulfate, filtered, and concentrated in vacuo. The crude reaction was purified using normal-phase chromatography to give 3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-N,N-dimethylpyridin-2-amine (140 mg, 0.413 mmol, 81% yield) as a colorless oil. ^{1}H NMR (400 MHz, CHLOROFORM-d) δ 7.86 (dd, J=4.9, 1.5 Hz, 1H), 7.02 (dd, J=7.8, 1.5 Hz, 1H), 6.73 (dd, J=7.8, 4.9 Hz, 1H), 4.20-4.07 (m, 2H), 3.98-3.86 (m, 2H), 3.81-3.61 (m, 9H), 3.38 (t, J=5.1

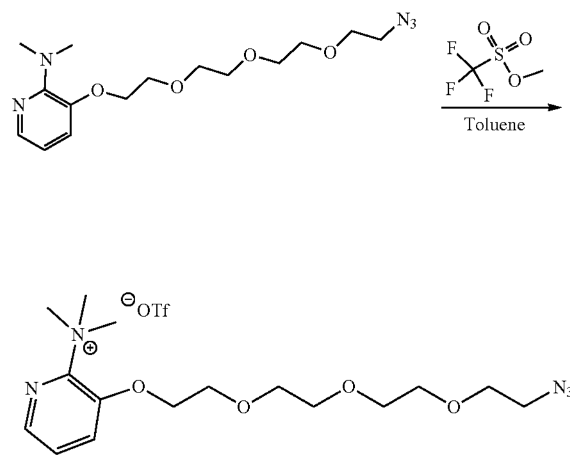
Hz, 2H), 3.13-2.94 (m, 6H), 1.69 (s, 2H). HRMS (ESI) Theory: C15H26N5O4+m/z 340.1980; found 340.1979.

Example 9: Synthesis of 3-(2-(2-(2-(2-azidoethoxy) ethoxy)ethoxy)ethoxy)-N,N,N-trimethylpyridin-2-aminium

[0433]



3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-N, N, N-trimethylpyridin-2-aminium

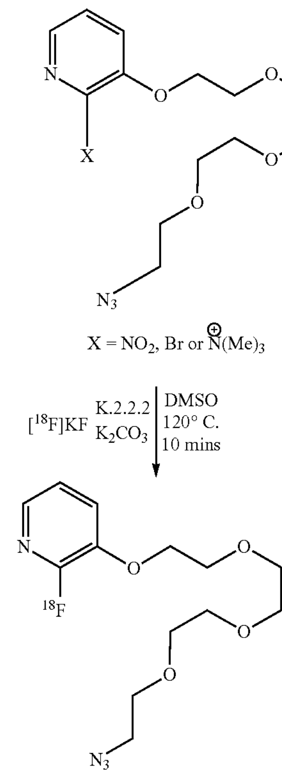


3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-N, N, N-trimethylpyridin-2-aminium

[0434] Methyl trifluoromethanesufonate (0.065 mL, 0.589 mmol) was added to the solution of 3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-N,N-dimethylpyridin-2-amine (40 mg, 0.118 mmol) in toluene (1.5 mL) in a sealed container under a steady stream of nitrogen. The reaction mixture was stirred at room temperature over a 14 hour period. The solvent was removed and the resultant residue was washed with 2×10 ml of ether, azeotropically dried with 2×1 ml of dichloromethane, and dried under high-pressure vacuum overnight to give 3-(2-(2-(2-(2-azidoethoxy) ethoxy)ethoxy)ethoxy)-N,N,N-trimethylpyridin-2-aminium, trifluoromethanesulfonate salt in quantitative yield as a thick colorless oil. LCMS m/z 354.33; ^{1}H NMR (400 MHz, DMSO-d_6) δ 8.24-8.17 (m, 1H), 7.98 (d, J=8.3 Hz, 1H), 7.75 (ddd, J=8.2, 4.6, 3.2 Hz, 1H), 4.44 (br. s., 2H), 3.88 (d, J=3.9 Hz, 2H), 3.69-3.45 (m, 21H).

Example 10: Synthesis of [^{18F}]-3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-fluoropyridine using 3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy) ethoxy)-N,N,N-trimethylpyridin-2-aminium, trifluoromethanesulfonate salt

[0435]



Synthesis of [^{18}F]-3(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-fluoropyridine

[0436] An aqueous [^{18}F]-Fluoride solution (2.0 ml, 33.3 GBq/900 mCi) was purchased from P.E.T. Net® Pharmaceuticals in West Point PA and directly transferred to a Sep-Pak light QMA [The Sep-Pak light QMA cartridge was pre-conditioned sequentially with 5 ml of 0.5 M potassium bicarbonate, 5 ml of deionized water, and 5 ml of MeCN before use.] Upon completion of this transfer, the aqueous [^{18}F] fluoride was released from the QMA Sep-Pak by the sequential addition of potassium carbonate (15 mg/ml; 0.1 ml) followed by a mixture of potassium carbonate (30 mg/ml, 0.1 ml), 4,7,13,16,21,24-hexaoxa-1,10-diazabicyclo [8.8.8]hexacosane (15 mg, 0.04 mmol) and 1.2 ml of MeCN. The solvent was evaporated under a gentle stream of nitrogen at 90° C. and vacuum. Azeotropic drying was repeated twice with 1 ml portions of acetonitrile to generate the anhydrous K.2.2.2/K[^{18}F]F complex. 3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-N,N,N-trimethylpyridin-2-aminium, trifluoromethanesulfonate salt (2 mg, 5.6 μmol) was dissolved in 500 microliters of DMSO and added to the dried cryptand. This solution was heated at 120° C. for 10 minutes. After this time, the crude reaction mixture was diluted with 3 ml of DI water. The entire contents of the crude reaction mixture was then transferred, loaded, and purified using reverse phase HPLC under the following conditions: HPLC Column: Luna C18 250×10 Solvent A: 0.1% TFA in DI water; solvent B: 0.1% TFA in acetonitrile at a flow rate of 4.6 ml/minute using isocratic method 32% B while the UV was monitored at 280 nm. [^{18}F]-3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-fluoropyridine was isolated at the 24 min mark of the chromatogram and collect over a 2 minute period. This product was collected into a 100 ml flask that contained 10 ml of DI water and the entire contents were delivered to a Sep-Pak Vac tC18 6 cc 1 g sep pack from Waters. 6.1 GBq/164 mCi of [^{18}F]-3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-fluoropyridine was isolated from this reaction. This was released from the sep-pak using 3 ml of ethanol and this solution was reduced with 98° C. heat source, a gentle stream of nitrogen, and vacuum over a 15 minute period until only a film remained in the vial. The final product was reconstituted in 100% 1×PBS buffer and was stable in this media for over 1 hour at 37° C.

[0437] The [^{18}F]-3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-fluoropyridine may be used to generate ^{18}F-labeled biologic products (e.g., ^{18}F-labeled anti-PD-L1 Adnectins, as described below) by taking advantage of "click" azide-alkyne reaction with the appropriate biologic containing an alkynes.

Example 11: Production of ^{18}F-Radiolabeled Protein Using "Click Chemistry"

A. Fluorination of the 4-PEG-tosyl-azide Precursor to Form [^{18}F]-FPPEGA

[0438] 900 mCi of ^{18}F in ^{18}O water (3 ml) activity (purchased from IBA Molecular) was transferred directly into a micro vial (no QMA) that contained 4,7,13,16,21,24-hexaoxa-1,10-diazabicyclo[8.8.8]hexacosane (2.8 mg, 7.44 μmol) and potassium carbonate (1.7 mg, 0.012 mmol). An additional 2.0 ml of acetonitrile was transferred into this crude reaction mixture and the entire mixture was azeotropically dried. This was completed by evaporating the solution using a 98° C. oil bath, and applying a gentle stream of N_2 and partial vacuum. The solution's volume was reduced to about 2 ml. An additional 2 ml of acetonitrile was added and the process was repeated 3 times over a 40 minute period. When the volume of the liquid was reduced to less than 0.3 ml, a 0.7 ml aliquot of acetonitrile was added and the solution reduced by further azeotropic distillation until the volume was ~0.1 ml. An additional 0.9 ml of acetonitrile was added and this process was completed until a white solid was formed. This process took ~55 minutes. During the final procedure, the vial was removed from the oil bath before the solution had gone to dryness and the residue in the vial was placed under full vacuum (no N_2 flow) at room temperature for 20 minutes. Total time for transfer and drying of cryptand mixture was 65 min.

[0439] To the dried cryptand mixture was added 3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-nitropyridine (2 mg, 5.86 μmol) dissolved in 500 microliters of DMSO and this mixture was heated at 120° C. for 10 minutes. After this time the crude reaction mixture was diluted with 3 ml of DI water and the entire contents were then transferred and loaded onto the following HPLC column and conditions: HPLC Column: Luna C18 250×10 mm; Solvent A: 0.1% TFA in DI water; Solvent B: 0.1% TFA in acetonitrile; flow rate 4.6 ml/min; pressure 1820 PSI; isocratic method 32% B; UV—280 nm. The [^{18}F]-3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-fluoropyridine ([^{18}F]-FPPEGA) product was isolated at the 24 minute mark of the chromatogram and was collect over a 2 minute period. This product was collected into a 100 ml flask that contained 15 ml of DI water and the entire contents were delivered to a Sep PakVac tC18 6 cc 1 g sep pack. PN WAT036795. The [^{18}F]-FPPEGA was released from the Sep Pak using 2.5 ml of ethanol and this solution was reduced with 98° C. N_2 and vacuum over a 15 minute period until dryness. This compound was dissolved in 0.1 ml 1×PBS (phosphate buffered saline). This product was analyzed using a Varian HPLC HPLC Column Luna C18 (2) 4.6×150 mm Solvent A: 0.1% TFA in DI water; Solvent B: 0.1% TFA in acetonitrile; flow rate 1.0 ml/min; gradient method 0 min 90% A 10% B; 15 mins 30% A 70% B; 17 mins 30% A 70% B; 18 mins 90% A 10% B; 20 mins 90% A 10% B; UV—280 nm. 220 mCi of [^{18}F]-FPPEGA was isolated.

B. Preparation of E01-4PEG-DBCO

[0440] This Example describes the linking of the E01 anti-PD-L1 Adnectin to PEG4-DBCO.

[0441] As maleimide chemistry is used to link the Adnectin to PEG4-DBCO, the E01 Adnectin was first modified by adding a proline followed by a cysteine at its C-terminus. The amino acid sequence of this modified E01 Adnectin is provided in SEQ ID NO: 104. The cysteine is used to link the Adnectin to PEG4-DBCO.

[0442] A 4-fold molar excess of Maleimide-PEG4-DBCO (Click Chemistry Tools) was dissolved in DMSO and added to the purified modified E01 Adnectin in the presence of 1 mM TCEP. Final DMSO concentrations did not exceed 5% in the conjugation mixtures. The conjugation mixture was left at room temperature for one hour before mass spec analysis. After MS confirmation of conjugation, the sample was purified by size-exclusion chromatography using a HiLoad 26/60 Superdex 75 column (GE Healthcare) equilibrated in PBS pH 7.2.

C. Coupling of [^{18}F]-FPPEGA to Adnectin

[0443] A schematic for synthesizing [^{18}F]-E01-4PEG-DBCO-FPPEGA is shown in FIGS. **2** and **9**.

[0444] 0.2 ml of a 5.4 mg/ml solution of the E01-4PEG-DBCO Adnectin solution (prepared as described in Section B) was incubated with 200 mCi of 0.1 ml of [^{18}F]-FPPEGA (Example 4) in 1×PBS buffer. The solution was gently mixed by pipetting the crude reaction up and down several times and was incubated together for 45 minutes at 45° C. or room temperature. The contents of this crude reaction mixture were purified using a SEC column. Superdex 200 0.5 ml/min 1×PBS buffer and the [^{18}F]-E01-4PEG-DBCO-FPPEGA product was isolated at the 37 min mark of the chromatogram over a 2 minute period.

[0445] [^{18}F]-E01-4PEG-DBCO-FPPEGA was analyzed via SEC with co-injection of non-radioactive standard, RP HPLC using a PLRPS column and gel electrophoresis.

[0446] Size Exclusion Chromatography (SEC) was performed with the following parameters:

[0447] Superdex 200 column; Solvent 100% 1×PBS buffer; 0.5 ml/min 280 UV;

[0448] Reverse phase HPLC

[0449] Column: PLRPS 8 micron 1000 A 4.6×250 mm

[0450] Solvent A: 0.1% formic acid in DI water

[0451] Solvent B: Acetonitrile

[0452] Flow rate: 1 ml/min

[0453] Pressure: 1351 PSI

[0454] Gradient:

[0455] 0 min 90% A 10% B

[0456] 30 min 45% A 55% B

[0457] 32 min 25% A 75% B

[0458] 36 min 25% A 75% B

[0459] 50 min 90% A 10% B

[0460] 15 mCi [^{18}F]-E01-4PEG-DBCO-FPPEGA was isolated with a radiochemical purity (RCP) of >99% via both SEC and RP HPLC calculations, and with a specific activity of 0.6 mCi/nmol, when the reaction was conducted at 45° C. When conducting the reaction at room temperature, 5.72 mCi was obtained. Specific activity of the [^{18}F]-FPPEGA was 0.512 mCi/nmol and RCP of 85.7% 3 hours post the end of its synthesis, when conducting the reaction at 45° C. or at room temperature, respectively. Specific activity was measured via Nanodrop (see, www.nanodrop.com). The product co-eluted with non-radioactive standard on both SEC and PLRPS. Gel electrophoresis confirmed an ^{18}F product consistent with an 11 kDa molecular weight standard.

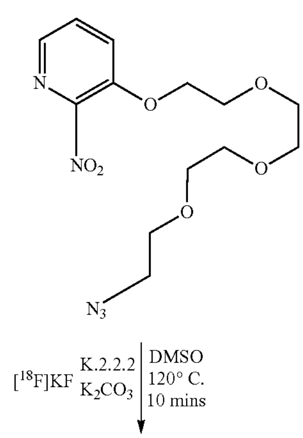
[0461] The ^{18}F-radiolabeled E01-4PEG-DBCO can be used in a variety of in vitro and/or in vivo imaging applications, including diagnostic imaging, basic research, and radiotherapeutic applications. Specific examples of possible diagnostic imaging and radiotherapeutic applications, include determining the location, the relative activity and/or quantifying of PD-L1 positive tumors, radioimmunoassay of PD-L1 positive tumors, and autoradiography to determine the distribution of PD-L1 positive tumors in a mammal or an organ or tissue sample thereof.

[0462] In particular, the ^{18}F-radiolabeled E01-4PEG-DBCO is useful for positron emission tomographic (PET) imaging of PD-L1 positive tumors in the lung, heart, kidneys, liver and skin and other organs of humans and experimental animals. PET imaging using the ^{18}F-radiolabeled E01-4PEG-DBCO can be used to obtain the following information: relationship between level of tissue occupancy by candidate PD-L1 tumor-treating medicaments and clinical efficacy in patients; dose selection for clinical trials of PD-L1 tumor-treating medicaments prior to initiation of long term clinical studies; comparative potencies of structurally novel PD-L1 tumor-treating medicaments; investigating the influence of PD-L1 tumor-treating medicaments on in vivo transporter affinity and density during the treatment of clinical targets with PD-L1 tumor-treating medicaments; changes in the density and distribution of PD-L1 positive tumors during effective and ineffective treatment.

D. Alternative Method for Preparing ^{18}F Labeled Adnectins

[0463] A slightly altered method for synthesizing [^{18}F]-3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-fluoropyridine and labelling Adnectins therewith is provided.

[0464] 900 mCi of Fluorine-18 in ^{18}O water (2 ml) activity was purchased from IBA molecular and delivered into the remote controlled synthesis unit. This sample was transferred directly into a micro vial that contained 4,7,13,16,21,24-hexaoxa-1,10-diazabicyclo[8.8.8]hexacosane (3.2 mg, 8.50 μmol) and potassium carbonate (1.4 mg, 10.13 μmol). An additional 1.5 ml of acetonitrile was transferred into this vial and the entire mixture was azeotropically dried. This solution was then evaporated by placing the vial into a 90° C. oil bath and applying a gentle stream of N_2 and partial vacuum. This was completed by first using partial vacuum for 10 minutes while heating. The total volume of the microvial was reduced to about 2 ml. An additional 2 ml of acetonitrile was added and this process was repeated 3 times over a 40 minute period. When the volume of the liquid was reduced to less than 0.3 ml, 0.7 ml aliquot of acetonitrile was added and the solution reduced by azeotropic distillation until the volume was ~0.1 ml, and additional 0.9 MeCN was added and this process was completed until a white solid was formed. During the final procedure, the vial was removed from the oil bath before the solution had gone to dryness and the residue in the vial was placed under full vacuum at room temperature for 20 minutes. 3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-nitropyridine (2 mg, 5.86 μmol) was dissolved in 500 microliters of DMSO and added to the dried cryptand. This solution was heated at 120° C. for 10 minutes. After this, the crude reaction mixture was diluted with 3 ml of DI water. The entire contents of the crude reaction mixture was then transferred, loaded and purified using reverse phase HPLC and the following conditions: HPLC Column: Luna C18 250×10 Solvent A: 0.1% TFA in DI water; solvent B: 0.1% TFA in acetonitrile at a flow rate of 4.6 ml/minute using isocratic method 32% B while the UV was monitored at 280 nm. [^{18}F]-3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-fluoropyridine was isolated at the 24 min mark of the chromatogram and was collected over a 2 minute period. This product was collected into a 100 ml flask that contained 10 ml of DI water and the entire contents were delivered to a Sep-Pak Vac tC18 6 cc 1 g sep pack from Waters. 224 mCi of [^{18}F]-3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-fluoropyridine was isolated from this reaction. This was released from the sep-pak using 3 ml of ethanol and this solution was reduced with 98° C. heat source, a gentle stream of nitrogen, and vacuum over a 15 minute period until only a film remained in this vial. The final product was reconstituted in 100% 1×PBS buffer and is stable in this media for over 1 hour at 37 C. Using [^{18}F]-3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-fluoropyridine generated several F-18 labeled biologic products by taking advantage of "click" azide-alkyne reaction with the appropriate biologic containing an alkyne.



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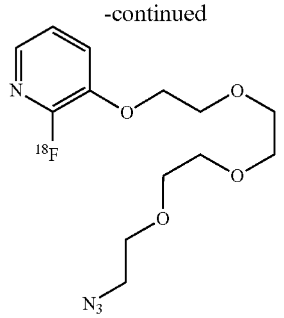


Synthesis of [^{18}F]-3(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-fluoropyridine

Example 12: Linking of PD-L1 Adnectins to NODAGA to Generate NODAGA-PD-L1 Adnectins

[0465] This Example describes the linking of the E01 and A02 anti-PD-L1 Adnectins to NODAGA. As maleimide chemistry is used to link the Adnectins to NODAGA, both Adnectins used a proline followed by a cysteine at their C-terminus (as described for E01 above). The amino acid sequences of the modified E01 and A02 Adnectins are provided in SEQ ID NOs: 104 and 88, respectively. The cysteine will be used for linking the Adnectins to NODAGA. For ^{64}Cu labeling of the Adnectins, a 50-fold molar excess of maleimide-NODAGA (CheMatech) was dissolved in PBS pH 7.4 and added to the purified Adnectins in the presence of 1 mM TCEP. Final DMSO concentrations did not exceed 5% in the conjugation mixtures. Conjugation mixtures were left at room temperature for one hour before mass spec analysis. After MS confirmation of conjugation, the samples were purified by size-exclusion chromatography using a HiLoad 26/60 Superdex 75 column (GE Healthcare) equilibrated in PBS pH 7.2.

Example 13: Synthesis of ^{64}Cu-Based Anti-PD-L1 Adnectin Probes

Synthesis of ^{64}Cu-A02-NODAGA

[0466] [^{64}Cu]-Copper chloride ($^{64}CuCl_2$) in 0.1N hydrochloric acid solution was neutralized with 0.8 mL of 0.1N sodium acetate (NaOAc) aqueous solution for 4 minutes at ambient temperature. 1 mL of the ^{64}Cu/NaOAc solution was added to A02-NODAGA (30 μL of 1.6 mg/mL) and the crude reaction was gently pipetted to allow mixing followed by resting at ambient temperature for 30 minutes. The contents of crude reaction mixture were transferred to a PD-10 desalting column that was pre-activated with 20 mL of 1×phosphate buffered saline (PBS, pH 7.4) buffer prior to loading of sample. An additional 1.5 mL of 1×PBS was added to the column, followed by an additional 0.8 ml 1×PBS solution and these fractions were discarded. [^{64}Cu]-A02-NODAGA was then collected after a 1.2 mL elution of the PD-10 column to give 10.79 mCi as the desired product. Quality control was measured using a reverse phase HPLC system using an Agilent PLRP-S HPLC column Size: 250×4.60 mm, 8 m, 280 nm and a mobile phase of 0.1% Formic Acid in distilled water and acetonitrile. A gradient method was used where the percentage of acetonitrile was increased linearly from 10% to 45% over a 30 minute time frame. [^{64}Cu]-A02-NODAGA co-eluted with reference standard at the 22 minute mark of the HPLC chromatogram. Radiochemical purity was measured to be 96% using this method. [^{64}Cu]-A02-NODAGA also co-eluted with reference material at the 20 minute mark using a size exclusion chromatography, (SEC) Column: GE Superdex 200 GL Size: 10×300 mm, 280 nm. The calculated specific activity was 956.8 mCi/mol based on Nanodrop protein concentration and isolated radioactivity of the purified sample.

Procedure for the Synthesis of ^{64}Cu-E01-NODAGA

[0467] [^{64}Cu]-Copper chloride ([^{64}Cu]$CuCl_2$) in 0.1N hydrochloric acid solution (20 mCi in 0.25 mL) was pH adjusted with 1.10 mL of 0.1N ammonium acetate buffer, then mixed and incubated with E01-NODAGA Adnectin in a 1×PBS aqueous solution (40 μL of 1.2 mg/mL, 4.62 nmol) for 30 minutes at ambient temperature. After 30 minutes of incubation, the reaction mixture (~1250 μL) was transferred to the PD-10 desalting column (GE Healthcare Life Science, Sephadex G25 Medium, 14.5×50 mm—equilibrated with 40 mL of 1×PBS), and the sample was allowed to enter the column completely by gravity and followed with 1.1 mL of 1×PBS. After the liquid completely passed through the column, the product was collected via elution in 1 mL increments with 1×PBS per sample vial. The ^{64}Cu-E01-NODAGA was isolated in the second 1 ml fraction and measured to be 9.26 mCi in 1 ml of 1×PBS. This sample was analyzed using an analytical size exclusion HPLC method using an Agilent HPLC system equipped with a UV/vis detector (X=280 nm), a posi-ram detector and Superdex 200 10/300 GL size-exclusion column (GE Healthecare Life Science, pore size 13 μm). The flow rate was 0.5 mL/min, and the aqueous mobile phase was isocratic with 1×PBS with 0.02% NaN_3 for 60 minutes. The radiochemical purity was 99% using this system, and the product co-eluted with non-radioactive reference standard. Specific activity was calculated based on the equation of the 3-points calibratio curve (y=656978x). About 100 μL of the product solution from vial 3 was injected onto the Superdex–200 size exclusion column. Product peak was collected and measured to be 0.74 mCi, UV counts of product peak was 156367 unit, and specific activity was 3.1 mCi/nmol.

Example 14: In Vitro Differentiation of PD-L1-Positive Cells from PD-L1-Negative Cells with an Anti-PD-L1 Adnectin Imaging Agent

[0468] In this experiment, the ^{64}Cu-E01 anti-PD-L1 Adnectin (NODAGA was used as a chelator) was tested for its ability to discriminate between hPD-L1-positive cells and hPD-L1-negative cells in vitro. Cell labeling was specific, as evidenced by differential association of ^{64}Cu-E01 with hPD-L1-positive L2987 cells compared to hPD-L1-negative HT-29 cells (cell associated radioactivity was 44.6× higher in hPD-L1-positive L2987 cells). Specificity was further confirmed as evidenced by a marked reduction in cell-associated ^{64}Cu-E01 when co-incubated with excess 450 nM cold (unlabeled) E01 Adnectin (99.6% reduction). Cell associated ^{18}F-E01 was minimally reduced (9.9% reduction, not significant) when cells were co-incubated with 450 nM of a cold (unlabeled) non-PD-L1 binding Adnectin (FIG. **3**).

[0469] 1×10^6 hPD-L1-positive L2987 human lung carcinoma cells or hPD-L1-negative HT-29 human colorectal adenocarcinoma cells were placed into 5 mL culture tubes (n=3 tubes per condition). ^{64}Cu-E01 Adnectin solution was prepared in PBS+0.5% BSA at a concentration of 300 nCi/200 μL. Portions of this solution were supplemented with either cold (unlabeled) E01 Adnectin or cold (unlabeled) non-PD-L1 binding Adnectin to a final concentration of 450 nM. Cell samples were centrifuged for 5 min at 200×g and then resuspended in 200 μL of the appropriate ^{64}Cu-E01 Adnectin solution and incubated on ice for 1 hour. After the incubation period, cell samples were centrifuged at 200×g and the supernatant was discarded. Cell pellets were resuspended in 1 mL PBS+0.5% BSA and the wash procedure repeated for a total of 3 washes. Following the final wash, cells were again centrifuged at 200×g and the supernatant was discarded. The radioactivity of the remaining cell pellets was then measured by gamma counter.

[0470] Taken together, these results demonstrate the ability of the 64Cu-E01 Adnectin to differentiate PD-L1(+) vs. PD-L1(−) cells in vitro. Specificity was further demonstrated by a marked reduction in cell-associated radiotracer in samples co-incubated with 450 nM unlabeled anti-PD-L1 E01 Adnectin (and only a statistically insignificant reduction when co-incubated with 450 nM of a non-PD-L1 binding Adnectin). Similar experiments using different Adnectin variants as well as ^{18}F as the radionuclide were conducted, with similar results.

Example 15: Distinguishing PD-L1-Positive Tumors from PD-L1-Negative Tumors with an Anti-PD-L1 Adnectin Imaging Agent

[0471] For PET imaging, rapid blood clearance rates provide an advantage over more slowly clearing proteins, such as antibodies, by minimizing the amount of time needed for "background" probe signals to deplete from non-relevant tissue. In the clinic, long blood half-life antibody-based-PET tracers may require several days of waiting post injection before images can be collected. Rapid clearing probes open the door to high contrast images that can be collected on the same day the probe is injected, and very importantly, they can also serve to reduce overall radiation exposure to the animals studied or patients examined.

[0472] In this experiment, the ^{64}Cu-A01 anti-PD-L1 Adnectin (NODAGA was used as the chelator), produced as described in the above Examples, was tested for its ability to discriminate between hPD-L1-positive tumors and hPD-L1-negative tumors in mice.

[0473] Mice bearing bilateral xenograft tumors were produced by introducing 1×10^6 hPD-L1(+) L2987 human lung carcinoma cells and 1.5×10^6 hPD-L1(−) HT-29 human colon carcinoma cells subcutaneously on opposite sides of the mouse. Once tumors reached approximately 300 mm^3 (approximately 2-3 weeks after cell implantation), animals were selected for imaging. For imaging, animals were placed under anesthesia with 2% isoflurane and tail vein catheters were installed. Mice were then placed into a custom animal holder with capacity for 4 animals, where they remained under anesthesia for the duration of the study. The animal holder was transferred to the microPET® F120™ scanner (Siemens Preclinical Solutions, Knoxville, Tenn.). The axial field of view of this instrument is 7.6 cm. With this limitation, animals were positioned such that the scanning region was from immediately in front of the eyes to approximately the base of the tail.

[0474] A 10-minute transmission image was first acquired using a ^{57}Co point source for the purpose of attenuation correction of the final PET images. Following the transmission scan, radiotracer solutions were administered via the previously installed tail vein catheters and a 2 hour emission image was acquired. Injected radiotracer solutions consisted of either approximately 200 μCi 64Cu-A02 (with a NODAGA chelator) or 200 μCi ^{64}Cu-A02 supplemented with 3 mg/kg final concentration of cold, unlabeled A02 Adnectin (based on individual animal weight). All injections were formulated in 200 μL saline prior to injection. Exact injected doses were calculated by taking direct measurements of the formulated dose and subtracting the radioactivity remaining in the syringe and the tail vein catheter.

[0475] Images were reconstructed using a maximum a posteriori (MAP) algorithm with attenuation correction using the collected transmission images and corrected for radioisotope decay. In the final images, regions of interest (ROIs) were drawn around the tumor boundary using ASIPro software (Siemens Preclinical Solutions). Time-activity curves were calculated for each ROI to yield a quantitative view of radiotracer within the tumor volume over the course of the 2 hour emission image. For final comparison, individual time-activity curves were normalized based on the injected radiotracer dose for each specific animal. Radiotracer uptake was compared across tumors using the final 10 minutes of each time-activity curve (1 hour 50 minutes-2h post-radiotracer injection). Using this methodology, radiotracer uptake in hPD-L1(+) L2987 xenografts was 3.05× that seen hPD-L1(−) HT-29 xenografts in animals receiving only the ^{64}Cu-A02 radiotracer. In animals co-injected with the ^{64}Cu-A02 radiotracer and 3 mg/kg unlabeled A02 Adnectin uptake in the hPD-L1(+) L2987 xenografts was only 1.04× that seen in hPD-L1(−) HT-29 xenografts (FIGS. **4**A and **4**B).

[0476] Similar experiments using ^{18}F as the radionuclide were conducted in mice, and similar results were obtained, reaching a maximum radiotracer uptake ratio of 3.53:1 in hPD-L1(+) L2987 xenografts vs. hPD-L1(−) HT-29 xenografts using the ^{18}F-A02 Adnectin radiotracer. Briefly, nude mice were subcutaneously implanted bilaterally with HT-29 and L2987 cells. Once tumors reached approximately 200-300 mm^3, animals were selected for imaging. Mice were anesthetized with 2% isoflurane in oxygen and placed onto the imaging bed of a Focus 120 PET imaging system (Siemens Preclinical Solutions). Approximately 150 μCi ^{18}F-A02 was then injected via a tail vein and animals were imaged continuously for 120 minutes. A 10-minute transmission image was then collected using a ^{57}Co point source for use as attenuation correction. Images were reconstructed using a 3D maximum a posteriori algorithm with attenuation correction using AsiPro software (Siemens Preclinical Solutions). The results demonstrated clear differential uptake in hPD-L1 (=) L2987 xenografts compared to hPD-L1 (−) HT29 xenografts in mice reciving only the radiotracer.

[0477] For some studies, animals were sacrificed via cervical dislocation immediately following imaging. Necropsy was then performed on the animals, and individual tissues were collected (blood, heart, lung, liver, spleen, kidney, muscle, stomach, bone, L2987 tumor, and HT-29 tumor) into pre-weighed tubes. All tissues were then weighed again to determine the weight of each tissue. The radioactivity in each tissue was then directly measured ex vivo using a Perkin-Elmer Wizard3 gamma counter. For all tissues, measured values in counts per minute (CPM) were normalized to the injected radioactive dose for the individual animals and corrected for radioactive decay. These results were then plotted to show the biodistribution of the radiotracer. An example of this analysis for the ^{18}F-A02 Adnectin radiotracer is shown in FIG. **5**. These results demonstrate clear differential uptake of the radiotracer in hPD-L1(+) L2987 xenografts compared to hPD-L1(−) HT-29 xenografts. Furthermore, the only tissue with higher PD-L1 uptake was the kidney, which is expected as clearance of the ^{18}F-A02 Adnectin is expected to be via kidney filtration based on the molecular weight of the molecule.

[0478] Taken together, these results provide direct visualization of differentiation of hPD-L1(+) versus hPD-L1(−) xenograft tumors in vivo. Specificity was further demonstrated by co-injection of 3 mg/kg unlabeled anti-PD-L1 A02 Adnectin, resulting in a reduction of radiotracer uptake in hPD-L1(+) tumors to the level of hPD-L1(−) xenografts. This further validates the use of anti-PD-L1 Adnectins for visualization of PD-L1 tissue expression using PET imaging.

[0479] The anti-PD-L1 Adnecin-based imaging agents also showed similar results when performed in cynomolgus monkeys. In these studies, the ^{18}F-E01 anti-PD-L1 Adnectin, produced as described in the above Examples, was tested for its ability to produce high-contrast images in cynomolgus monkeys. The anti-PD-L1 Adnectins described here maintain high affinity for cynomolgus PD-L1 (but have low affinity for rodent PD-L1). Furthermore, as cynomolgus monkeys do not contain PD-L1(+) tumors as in mouse models, imaging performance was assessed primarily on the background levels measured in the images in the context of endogenous PD-L1 expression (with low background enabling the potential for high-sensitivity detection of PD-L1(+) tissues). In these studies, background levels in the resulting PET images were very low, with notable radiotracer accumulation noted mainly in the kidneys, spleen, and bladder.

[0480] Cynomolgus male monkeys with a previously installed vascular access port (VAP) were anesthetized with 0.02 mg/kg atropine, 5 mg/kg Telazol and 0.01 mg/kg buprenorphine I.M. (all drawn into a single syringe). An i.v. catheter is then placed in the cephalic vessel for fluid administration during the imaging procedure to maintain hydration. Animals were intubated with an endotracheal tube—usually 3.0 mm and transferred to the imaging bed of a microPET® F220™ PET instrument (Siemens Preclinical Solutions, Knoxville, Tenn.). Anesthesia was maintained with isoflurane and oxygen and I.V. fluids (LRS) were administered at a rate of 6 ml/kg/hr during the imaging procedure. As the axial field of view of the microPET® F220™ instrument is only 7.6 cm, images over 5 distinct bed positions were acquired to create a composite image of the animals from just above the heart through approximately the pelvis.

[0481] For each field of view, a 10 minute transmission image was first acquired using a ^{57}Co point source for the purpose of attenuation correction of the final PET images. Once transmission images were acquired for all bed positions, approximately 1.5 mCi (approximately 0.015 mg/kg) of the ^{18}F-E01 Adnectin radiotracer was administered via the installed VAP. 5 minute duration emission scans were then sequentially acquired for each bed position, beginning at position 1 centered aproximately at the heart and moving toward the pelvis of the animal. Once images were acquired at each position (1 through 5), the imaging bed was moved back to bed position 1 and the process was repeated. Using this procedure, a total of 5 distinct images were acquired for each bed position over the duration of the imaging study.

[0482] Individual images were reconstructed using a filtered back projection (FBP) algorithm with attenuation correction using the collected transmission images and corrected for radioisotope decay. Final composite images were then produced by aligning images from all 5 bed positions obtained from a single pass (i.e. a single composite image was produced from each set of sequential images from bed positions 1 through 5) covering the duration of the imaging study. Final images were visually inspected to note areas of visible radiotracer uptake (i.e. spleen, kidney, bladder) and background tissue (muscle) (FIG. **6**). Background accumulation of ^{18}F-E01 Adnectin was very low, with little signal visible in background tissues such as muscle. Additionally, uptake was verified in the spleen, which is believed to be PD-L1(+) based on mRNA expression. Thus, studies in cynomolgus monkeys demonstrate the potential for high-sensitivity PD-L1 imaging in the context of endogenous PD-L1.

[0483] In aggregate, PET studies in rodent and cynomolgus monkey show that ^{64}Cu and ^{18}F labeled anti-human PD-L1 Adnectins provide strong and specific probes for in vivo labeling of PD-L1 positive tissues with the potential for high-sensitivity detection of tissues with low level PD-L1 expression.

[0484] In vivo imaging experiments were also conducted with an anti-PD-L1 antibody, and the areas that this imaging agent detected were the same areas that were detected with the PD-L1 imaging agent, therefore confirming that anti-PD-L1 Adnectin imaging agents successfully detect PD-L1 positive cells in vivo.

Example 16: In Vitro Autoradiography of Human and Xenograft Tissue with [^{18}F]-E01 Anti-PD-L1 Adnectin

[0485] Human lung tumor tissues were embedded in OCT and chilled in 2-methylbutane for 2-5 minutes until frozen. Samples were stored in −80° C. degree freezer until use. Human xenograft tissues were also included in the assay. Mice bearing bilateral xenografts were produced by introducing 4×10^6 hPD-L1(+) L2987 cells and 1.5×10^6 hPD-L1 (−) HT-29 t cells subcutaneously into opposite flanks of nu/nu mice. Once resulting xenograft tumors reached appropriate size (approx. 200-300 mm^3), mice were anesthetized with 2% isoflurane and sacrificed via cervical dislocation. Fresh tumor tissues were excised, immersed into OCT and chilled in 2-methylbutane for 2-5 minutes until frozen. The tissues were then wrapped in foil/ZIPLOC® bag and stored at −80° C. until use. For all tissues (human lung tumor and xenografts) sections of 5 μm thickness (collected as 2 sections/slide) were cut using a cryostat, thaw-mounted on glass microscope slides, and allowed to air dry for approximately 30 minutes.

[0486] Blocking studies with cold (unlabeled) A02 Adnectin at 0.025 nM, 0.25 nM, 2.5 nM and 25 nM respectively and 25 nM non-PD-L1 binding Adnectin were conducted using the following conditions. The individual slides, 1 slide per concentration, were placed in plastic slide cassettes and pre-incubated in Dako serum-free protein block solution for 30 minutes. Slides were then transferred to glass slide incubation chambers for further incubation. Separately, a stock solution of 0.25 nM ^{18}F-A02 Adnectin was produced by diluting 10.6 μl of the original stock radioligand solution (7064 nM at the time of experiment) with 300 ml of PBS+0.5% BSA. From this stock solution, 40 ml was added to each incubation chamber. One of these chambers contained only the radioligand buffer solution, which is referred to as the total binding section. Other incubation chambers received 40 ml of this stock solution along with the relevant concentration of blocking compound (unlabeled A02 Adnectin at 0.025 nM, 0.25 nM, 2.5 nM, or 25 nM or unlabeled non-PD-L1 binding Adnectin at 25 nM). Slides were incubated in the individual buffer solutions for 1 hour at room temperature to reach maximum binding. After incubation, slides from each treatment group were removed from the incubation solutions and placed in an ice-cold wash buffer (PBS+0.5% BSA) for 3 minutes and rinsed 4 separate times. Slides were then dried under a stream of cold air for approximately 30 minutes. The air-dried slides were exposed by placing the slides onto an imaging plate (BAS-SR 3545S) overnight at room temperature. The imaging plate was scanned using the bioimaging analyzer (Fujifilm Fluorescent Image Analyzer, FLA-9000). The pixel size of the autoradiogram images was 100 μm. Image analysis was performed using the Multi-Gauge software. The regions of interest (ROIs) were drawn to surround the entire tumor tissue in all study groups. Autogradiography signal from tissue-associated radioactivity was quantified from these ROIs.

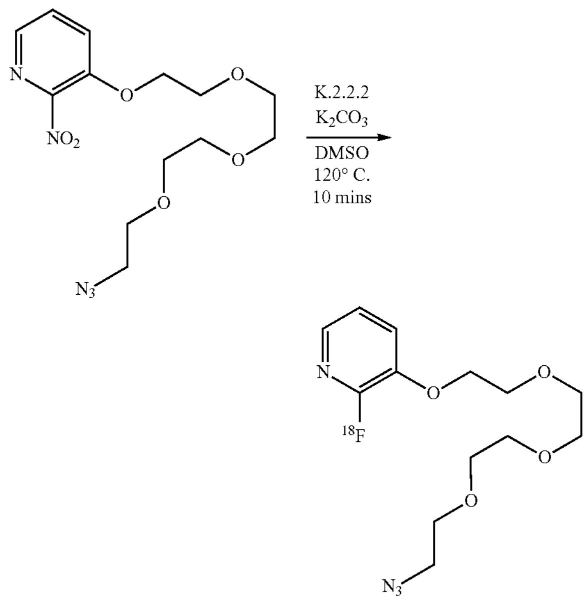
[0487] The apparent displacement of the ^{18}F-A02 Adnectin radioligand when compared to the total binding sections was determined for 4 different concentrations (0.025 nM, 0.25 nM, 2.5 nM and 25 nM) of unlabeled A02 Adnectin in both human lung tumor sections as well as human xenograft sections. A dose dependent displacement of ^{18}F-A02 was seen in all tissue sections with the addition of unlabeled A02 Adnectin, while 25 nM non-PD-L1 binding Adnectin showed minimal blockade in all tissues compared to total binding (FIG. **7**).

[0488] Serial 5 μm tissue sections from each tissue were subjected to an anti-human-PD-L1 immunohistochemical procedure to verify the level of PD-L1 antigen expression in the samples (FIG. **8**).

[0489] Taken together, these results provide direct visualization of PD-L1 in both human lung tumor samples as well as human xenograft tissues. The level of radioligand binding in the individual tissues corresponds with the intensity of PD-L1 staining of frozen sections by IHC. In addition, the dose dependent blockade of the receptor with unlabeled anti-PD-L1 A02 Adnectin (and lack of blockade with unlabeled non-PD-L1 binding Adnectin), further validates the use of ^{18}F-A02 for visualization of PD-L1 tissue expression using PET imaging.

Example 17: Automated preparation of [^{18}F]-3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-fluoropyridine according to the general procedure for radiosynthesis using commercial GE TRACERlab FX2 N synthesis unit

[0490]



Procedure:

[0491] The automated synthesis of [^{18}F]-3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-fluoropyridine was carried out using a non-cassette type GE TRACERlab FX2 N Synthesis module. The setup of the synthesis unit is summarized in Table 4. The aqueous [^{18}F]-Fluoride solution (2.0 ml, 29.6 GBq/800 mCi) was delivered to a Sep-Pak light QMA [The Sep-Pak light QMA cartridge was preconditioned sequentially with 5 ml of 0.5 M potassium bicarbonate, 5 ml of deionized water, and 5 ml of acetonitrile before use.] Upon completion of this transfer, the aqueous [^{18}F] fluoride was released from the QMA Sep-Pak by the addition of the elution mixture (from "V1") into the reactor. The solvent was evaporated under a gentle stream of nitrogen and vacuum. The solution of precursor (from "V3") was added to the dried cryptand residue and this reaction mixture was heated 120° C. for 10 minutes. Then 4 ml of distilled water (from "V4") was added to the crude reaction mixture in the reactor and the mixture was transferred to the 5 ml sample injection loop of the semi-preparative HPLC via a liquid sensor which controls the end of the loading. The mixture was loaded onto the semi-preparative HPLC column (Luna C18(2). 250×10 mm, Phenomenex). A mixture of 35% acetonitrile in an aqueous 0.1% trifluoroacetic acid solution was flushed through the column at a rate of 4.6 ml per minute. The product was collected from this HPLC column into the dilution flask which contained 15 ml distilled water and its entire contents were transferred to a tC18 1 gram, solid phase extraction cartridge. 352 mCi (13 GBq) of [^{18}F]-3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-

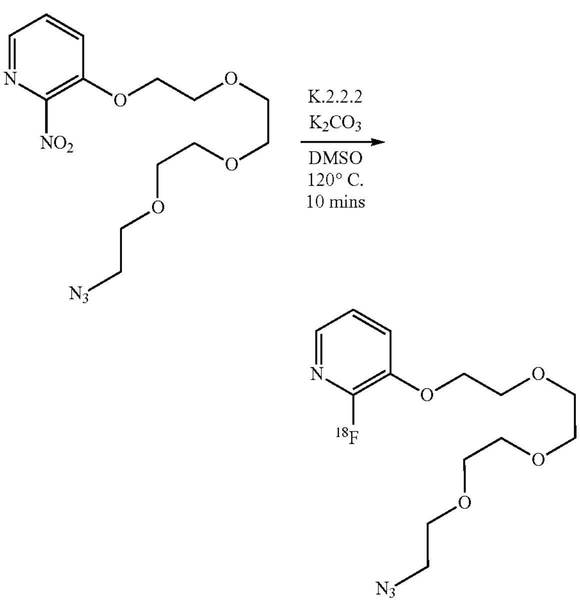
2-fluoropyridine was released from this cartridge (from "V14") with 3 ml of ethanol and may be used to generate ^{18}F labeled biologic products by taking advantage of "click" azide-alkyne reaction with the appropriate biologic containing an alkynes.

TABLE 4

Vial 1 (V1)	16 mg K.2.2.2, 3 mg Potassium carbonate, dissolved in 0.1 ml of distilled water and 1.4 ml of acetonitrile
Vial 3 (V3)	2 mg 3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-nitropyridine in 0.5 ml DMSO
Vial 4 (V4)	4 ml of distilled water
Vial 14 (V14)	3 ml of 100% ethanol
Dilution Flask	15 ml of distilled water
Cartridge 1 (C1)	tC18 6 cc 1 g sep pack
HPLC Column	Luna C18(2), 250 × 10 mm, 5 μm, Phenomenex
HPLC Solvent	35% acetonitrile in an aqueous 0.1% trifluoroacetitic acid solution
HPLC flow	4.6 ml/min

Example 18 Automated preparation of [^{18}F]-3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-fluoropyridine according to the general procedure for radiosynthesis on IBA Synthera synthesis unit

[0492]



Procedure:

[0493] The automated synthesis of [^{18}F]-3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-fluoropyridine was carried out using a cassette type IBA Synthera Synthesis module and an appropriately assembled integrator fluidic processor kit. The integrator fluidic processor (IFP) kit was loaded with appropriate precursors for this synthesis and is summarized in Table 5. The purification was performed on an Varian HPLC unit. The filling of the injection loop of the HPLC was controlled by a steady stream of nitrogen on the HPLC unit. The setup of both automates are summarized in Table 5. The aqueous [^{18}F]-Fluoride solution (2.0 ml, 29.6 GBq/800 mCi) was delivered to a Sep-Pak light QMA [The Sep-Pak light QMA cartridge was pre-conditioned sequentially with 5 ml of 0.5 M potassium bicarbonate, 5 ml of deionized water, and 5 ml of acetonitrile before use.] Upon completion of this transfer, the aqueous [^{18}F] fluoride was released from the QMA Sep-Pak by the addition of the elution mixture (from "V1") into the reactor. The solvent was evaporated under a gentle stream of nitrogen and vacuum. The solution of precursor (from "V2") was added to the dried cryptand residue and this reaction mixture was heated 120° C. for 10 minutes. Then 3 ml of distilled water (from "V4") was added to the crude reaction mixture in the reactor and the mixture is transferred to the 5 ml sample injection loop of the semi-preparative HPLC via a liquid sensor which controls the end of the loading. The mixture was loaded onto the semi-preparative HPLC column (Luna C18(2). 250×10 mm, Phenomenex). A mixture of 35% acetonitrile in an aqueous 0.1% trifluoroacetic acid solution was flushed through the column at a rate of 4.6 ml per minute. The product was collected from this HPLC column into the dilution flask which contained 15 ml distilled water and its entire contents were transferred to a tC18 1 gram, solid phase extraction cartridge. 325 mCi (12 GBq) of [^{18}F]-3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-fluoropyridine was released from this cartridge with 3 ml of ethanol and may be used to generate ^{18}F labeled biologic products by taking advantage of "click" azide-alkyne reaction with the appropriate biologic containing an alkynes.

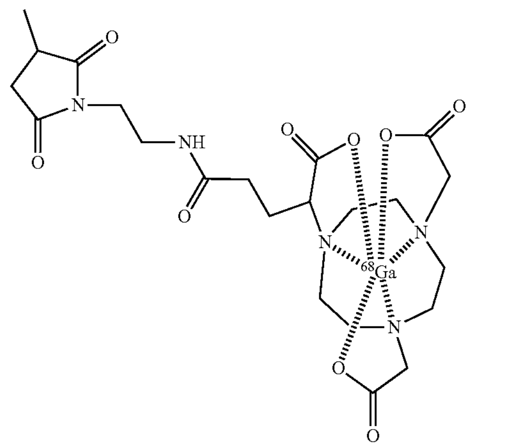
TABLE 5

Vial 1 (V1)	22 mg K.2.2.2, 4 mg Potassium carbonate, dissolved in 0.3 ml of distilled water and 0.3 ml of acetonitrile
Vial 2 (V2)	2 mg 3-(2-(2-(2-(2-azidoethoxy)ethoxy)ethoxy)ethoxy)-2-nitropyridine in 0.5 ml DMSO
Vial 4 (V4)	3 ml of distilled water
Dilution Flask	15 ml of distilled water
Cartridge 1 (C1)	tC18 6 cc 1 g sep pack
HPLC Column	Luna C18(2), 250 × 10 mm, 5 μm, Phenomenex
HPLC Solvent	35% acetonitrile in an aqueous 0.1% trifluoroacetitic acid solution
HPLC flow	4.6 ml/min

Example 19: Synthesis of ^{68}Ga-Based Anti-PD-L1 Adnectin Probes

Synthesis of ^{68}Ga-E01-NODAGA

[0494] [^{68}Ga]-Gallium chloride in 0.1N hydrochloric acid solution was neutralized with 32 mg of sodium acetate (NaOAc) for 4 minutes at ambient temperature, the resultant solution was stirred to ensure the entire volume was properly mixed. This solution was then added to E01-NODAGA (15 μL of 1.3 mg/mL) solution and the crude reaction was gently pipetted to allow mixing followed by resting at ambient temperature for 15 minutes. The contents of crude reaction mixture were transferred to a PD-10 desalting column that was pre-activated with 20 mL of 1× phosphate buffered saline (PBS, pH 7.4) buffer prior to loading of sample. An additional 1.5 mL of 1×PBS was added to the column, followed by an additional 0.8 ml 1×PBS solution and these fractions were discarded. [6^{8}Ga]-E01-NODAGA was then collected after a 1.4 mL elution of the PD-10 column to give 5.78 mCi (214 MBq) as the desired product. Quality control was measured using a reverse phase HPLC system using an Agilent PLRP-S HPLC column Size: 250×4.60 mm, 8 m, 280 nm and a mobile phase of 0.1% Formic Acid in distilled water and acetonitrile. A gradient method was used where the percentage of acetonitrile was increased linearly from 10% to 45% over a 30 minute time frame. [^{68}Ga]-E01-NODAGA co-eluted with reference standard at the 22 minute mark of the HPLC chromatogram. Radiochemical purity was measured to be 98% using this method. [^{68}Ga]-E01-NODAGA also co-eluted with reference material at the 20 minute mark using a size exclusion chromatography, (SEC) Column: GE Superdex 200 GL Size: 10×300 mm, 280 nm.



1 MGVSD VPRDL EVVAA TPTSL LISWR AQLSP SFYYR ITYGE
41 TGGNS PVQEF TVPND VMTAT ISGLK PGVDY TITVY AVTTH
81 GVYFY SPISI NYRTP CHHHH HH

Example 20: Pharmacokinetics of [^{19}F]-E01 Anti-PD-L1 Adnectin

[0495] The following experiment was conducted to compare the pharmacokinetics of ^{19}F labelled-E01 anti-PD-L1 adnectin and E01-4PEG-DBCO (unlabeled anti-PD-L1-adnectin-DBCO precursor) in cynomolgus monkeys (n=3). This was a cross-over design study with a 2-week washout between doses. Serum samples were collected and analyzed by either a LBA using specific adnectin-binding reagents that do not differentiate E01-4PEG-DBCO from [^{19}F]-E01, or LC/MS assays that differentiate between E01-4PEG-DBCO and [^{19}F]-E01.

[0496] A summary of the PK parameters is shown in Table 6.

TABLE 6

	[^{19}F]-E01	E01-4PEG-DBCO
AUC(INF) (μg*h/mL)	4.72 ± 0.79	2.92 ± 0.40
CLTs (mL/min/kg)	4.54 ± 0.81	5.78 ± 0.76
Vss (L/kg)	0.29 ± 0.05	0.40 ± 0.04
T-HALF (h)	1.69 ± 0.13	1.65 ± 0.13
MRT (h)	1.05 ± 0.06	1.14 ± 0.05

[0497] Following an i.v. dose to cynomolgus monkeys, the CLTs of [^{19}F]-E01 was low in both studies. The T-HALF was also short, at about 1.7 hours. The PK of E01-4PEG-DBCO was similar to that of [^{19}F]-E01. The PK parameters were also similar by LC/MS.

TABLE 3

SEQUENCE LISTING

SEQ ID	DESCRIPTION	SEQUENCE
1	Full length wild-type human ^{10}Fn3 domain	VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNS PVQEFTVPGSKSTATISGLKPGVDYTITVYAVTGRGDSPASSK PISINYRT
2	Core wild-type human ^{10}Fn3 domain	EVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVP GSKSTATISGLKPGVDYTITVYAVTGRGDSPASSKPISINYRT
3	Core ^{10}Fn3-based scaffold with variable AB, BC, CD, DE, EF, and FG loops	EVVAA(Z)$_a$LLISW(Z)$_x$YRITY(Z)$_b$FTV(Z)yATISGL(Z)$_c$Y TITVYA(Z)$_z$ISINYRT
4	Core ^{10}Fn3-based scaffold with variable BC, DE, and FG loops	EVVAATPTSLLISW(Z)$_x$YRITYGETGGNSPVQEFTV(Z)$_y$ATISG LKPGVDYTITVYA(Z)$_z$ISINYRT
5	ATI-968 core (aka ADX_1760_C01)	EVVAATPTSLLISWIAPFYNVIYYRITYGETGGNSPVQEFTVPGTG YTATISGLKPGVDYTITVYAVTDGASIASYAFPISINYRT
6	ATI-968 BC loop	IAPFYNVIY
7	ATI-968 DE loop	PGTGYT
8	ATI-968 FG loop	VTDGASIASYAFP
9	ATI-968 w/ N leader	GVSDVPRDLEVVAATPTSLLISWIAPFYNVIYYRITYGETGGNSPV QEFTVPGTGYTATISGLKPGVDYTITVYAVTDGASIASYAFPISIN YRT

TABLE 3-continued

SEQUENCE LISTING

SEQ ID	DESCRIPTION	SEQUENCE
10	ATI-968 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWIAPFYNVIYYRITYGETGGNSPVQEFTVPGTGYTATISGLKPGVDYTITVYAVTDGASIASYAFPISINYRTHHHHHH
11	ATI-968 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWIAPFYNVIYYRITYGETGGNSPVQEFTVPGTGYTATISGLKPGVDYTITVYAVTDGASIASYAFPISINYRTEIDKPSQ
12	ATI-968 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWIAPFYNVIYYRITYGETGGNSPVQEFTVPGTGYTATISGLKPGVDYTITVYAVTDGASIASYAFPISINYRTEIDKPSQHHHHHH
13	ATI-968 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWIAPFYNVIYYRITYGETGGNSPVQEFTVPGTGYTATISGLKPGVDYTITVYAVTDGASIASYAFPISINYRTPC
14	ATI-968 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWIAPFYNVIYYRITYGETGGNSPVQEFTVPGTGYTATISGLKPGVDYTITVYAVTDGASIASYAFPISINYRTPCHHHHHH
15	ATI-968-full length	MGVSDVPRDLEVVAATPTSLLISWIAPFYNVIYYRITYGETGGNSPVQEFTVPGTGYTATISGLKPGVDYTITVYAVTDGASIASYAFPISINYRTEIDKPSQHHHHHH
16	ATI-968-core (nucleotide sequence)	GAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGATCGCTCCGTTCTACAATGTCATCTATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTACTGGTTATACAGCTACAATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGATGGAGCATCCATTGCTTCATACGCGTTTCCAATTTCCATTAATTACCGCACA
17	ATI-968 w/ N leader (nucleotide sequence with N-terminal methionine)	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGATCGCTCCGTTCTACAATGTCATCTATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTACTGGTTATACAGCTACAATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGATGGAGCATCCATTGCTTCATACGCGTTTCCAATTTCCATTAATTACCGCACA
18	ATI-968 w/ N leader and modified C-terminus including PC (nucleotide sequence with N-terminal methionine)	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGATCGCTCCGTTCTACAATGTCATCTATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTACTGGTTATACAGCTACAATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGATGGAGCATCCATTGCTTCATACGCGTTTCCAATTTCCATTAATTACCGCACACCGTGC
19	ATI-968 w/ N leader and C tail + his tag (nucleotide sequence with N-terminal methionine)	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGATCGCTCCGTTCTACAATGTCATCTATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTACTGGTTATACAGCTACAATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGATGGAGCATCCATTGCTTCATACGCGTTTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA
20	ATI-964 core (parent of ADX_5322_A02)	EVVAATPTSLLISWSYDGSIERYYRITYGETGGNSPVQEFTVPPDQKTATISGLKPGVDYTITVYAVRLEEAHYYRESPISINYRT
21	ATI-964 BC loop	SYDGSIERY
22	ATI-964 DE loop	PPDQKT
23	ATI-964 FG loop	VRLEEAHYYRESP
24	ATI-964 w/ N leader	GVSDVPRDLEVVAATPTSLLISWSYDGSIERYYRITYGETGGNSPVQEFTVPPDQKTATISGLKPGVDYTITVYAVRLEEAHYYRESPISINYRT
25	ATI-964 w/ N leader +his tag	GVSDVPRDLEVVAATPTSLLISWSYDGSIERYYRITYGETGGNSPVQEFTVPPDQKTATISGLKPGVDYTITVYAVRLEEAHYYRESPISINYRTHHHHHH

TABLE 3-continued

SEQUENCE LISTING		
SEQ ID	DESCRIPTION	SEQUENCE
26	ATI-964 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWSYDGSIERYYRITYGETGGNSPVQEFTVPPDQKTATISGLKPGVDYTITVYAVRLEEAHYYRESPISINYRTEIDKPSQ
27	ATI-964 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWSYDGSIERYYRITYGETGGNSPVQEFTVPPDQKTATISGLKPGVDYTITVYAVRLEEAHYYRESPISINYRTEIDKPSQHHHHHH
28	ATI-964 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWSYDGSIERYYRITYGETGGNSPVQEFTVPPDQKTATISGLKPGVDYTITVYAVRLEEAHYYRESPISINYRTPC
29	ATI-964 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWSYDGSIERYYRITYGETGGNSPVQEFTVPPDQKTATISGLKPGVDYTITVYAVRLEEAHYYRESPISINYRTPCHHHHHH
30	ATI-964-full length	MGVSDVPRDLEVVAATPTSLLISWSYDGSIERYYRITYGETGGNSPVQEFTVPPDQKTATISGLKPGVDYTITVYAVRLEEAHYYRESPISINYRTEIDKPSQHHHHHH
31	ATI-964-core (nucleotide sequence)	GAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTCTTACGACGGTTCGATTGAACGTTATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTCCGGATCAGAAGACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCAGGCTGGAAGAAGCTCATTACTATCGAGAGTCTCCAATTTCCATTAATTACCGCACA
32	ATI-964 w/ N leader (nucleotide sequence with N-terminal methionine)	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTCTTACGACGGTTCGATTGAACGTTATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTCCGGATCAGAAGACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCAGGCTGGAAGAAGCTCATTACTATCGAGAGTCTCCAATTTCCATTAATTACCGCACA
33	ATI-964 w/ N leader and modified C-terminus including PC (nucleotide sequence with N-terminal methionine)	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTCTTACGACGGTTCGATTGAACGTTATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTCCGGATCAGAAGACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCAGGCTGGAAGAAGCTCATTACTATCGAGAGTCTCCAATTTCCATTAATTACCGCACACCGTGC
34	ATI-964 w/ N leader and C tail + his tag (nucleotide sequence with N-terminal methionine)	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTCTTACGACGGTTCGATTGAACGTTATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTCCGGATCAGAAGACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCAGGCTGGAAGAAGCTCATTACTATCGAGAGTCTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA
35	ATI-965 core	EVVAATPTSLLISWTAYDSVDKYYRITYGETGGNSPVQEFTVGPRHHTATISGLKPGVDYTITVYAVYHTEPGYHAHMPISINYRT
36	ATI-965 BC loop	TAYDSVDKY
37	ATI-965 DE loop	GPRHHT
38	ATI-965 FG loop	VYHTEPGYHAHMP
39	ATI-965 w/ N leader	GVSDVPRDLEVVAATPTSLLISWTAYDSVDKYYRITYGETGGNSPVQEFTVGPRHHTATISGLKPGVDYTITVYAVYHTEPGYHAHMPISINYRT
40	ATI-965 w/ N leader +his tag	GVSDVPRDLEVVAATPTSLLISWTAYDSVDKYYRITYGETGGNSPVQEFTVGPRHHTATISGLKPGVDYTITVYAVYHTEPGYHAHMPISINYRTHHHHHH

TABLE 3-continued

SEQUENCE LISTING

SEQ ID	DESCRIPTION	SEQUENCE
41	ATI-965 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWTAYDSVDKYYRITYGETGGNSPV QEFTVGPRHHTATISGLKPGVDYTITVYAVYHTEPGYHAHMPISIN YRTEIDKPSQ
42	ATI-965 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWTAYDSVDKYYRITYGETGGNSPV QEFTVGPRHHTATISGLKPGVDYTITVYAVYHTEPGYHAHMPISIN YRTEIDKPSQHHHHHH
43	ATI-965 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWTAYDSVDKYYRITYGETGGNSPV QEFTVGPRHHTATISGLKPGVDYTITVYAVYHTEPGYHAHMPISIN YRTPC
44	ATI-965 w/ N leader and modified C-terminus including PC +his tag	GVSDVPRDLEVVAATPTSLLISWTAYDSVDKYYRITYGETGGNSPV QEFTVGPRHHTATISGLKPGVDYTITVYAVYHTEPGYHAHMPISIN YRTPCHHHHHH
45	ATI-965-full length	MGVSDVPRDLEVVAATPTSLLISWTAYDSVDKYYRITYGE TGGNSPVQEFTVGPRHHTATISGLKPGVDYTITVYAVYHTEPGYHA HMPISINYRTEIDKPSQHHHHHH
46	ATI-965-core (nucleotide sequence)	GAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGACTG CATACGACTCTGTTGACAAATATTACCGCATCACTTACGGCGAAAC AGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGGGCCCTAGACAT CACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCA TCACTGTGTATGCTGTCTATCACACTGAACCGGGCTATCATGCTCA TATGCCAATTTCCATTAATTACCGCACA
47	ATI-965 w/ N leader (nucleotide sequence with N-terminal methionine)	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCA CCCCCACCAGCCTGCTGATCAGCTGGACTGCATACGACTCTGTTGA CAAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCT GTCCAGGAGTTCACTGTGGGCCCTAGACATCACACAGCTACCATCA GCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGT CTATCACACTGAACCGGGCTATCATGCTCATATGCCAATTTCCATT AATTACCGCACA
48	ATI-965 w/ N leader and modified C-terminus including PC (nucleotide sequence with N-terminal methionine)	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCA CCCCCACCAGCCTGCTGATCAGCTGGACTGCATACGACTCTGTTGA CAAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCT GTCCAGGAGTTCACTGTGGGCCCTAGACATCACACAGCTACCATCA GCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGT CTATCACACTGAACCGGGCTATCATGCTCATATGCCAATTTCCATT AATTACCGCACACCGTGC
49	ATI-965 w/ N leader and C tail +his tag (nucleotide sequence with N-terminal methionine)	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCA CCCCCACCAGCCTGCTGATCAGCTGGACTGCATACGACTCTGTTGA CAAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCT GTCCAGGAGTTCACTGTGGGCCCTAGACATCACACAGCTACCATCA GCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGT CTATCACACTGAACCGGGCTATCATGCTCATATGCCAATTTCCATT AATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACC ACCACTGA
50	ATI-966 core	EVVAATPTSLLISWHRFSSIMAYYRITYGETGGNSPVQEFTVAGSV NTATISGLKPGVDYTITVYAVTIHNVSFPISINYRT
51	ATI-966 BC loop	HRFSSIMAY
52	ATI-966 DE loop	AGSVNT
53	ATI-966 FG loop	VTIHNVSFP
54	ATI-966 w/ N leader	GVSDVPRDLEVVAATPTSLLISWHRFSSIMAYYRITYGETGGNSPV QEFTVAGSVNTATISGLKPGVDYTITVYAVTIHNVSFPISINYRT
55	ATI-966 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWHRFSSIMAYYRITYGETGGNSPV QEFTVAGSVNTATISGLKPGVDYTITVYAVTIHNVSFPISINYRTH HHHHH
56	ATI-966 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWHRFSSIMAYYRITYGETGGNSPV QEFTVAGSVNTATISGLKPGVDYTITVYAVTIHNVSFPISINYRTE IDKPSQ

TABLE 3-continued

SEQUENCE LISTING

SEQ ID	DESCRIPTION	SEQUENCE
57	ATI-966 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWHRFSSIMAYYRITYGETGGNSPV QEFTVAGSVNTATISGLKPGVDYTITVYAVTIHNVSFPISINYRTE IDKPSQHHHHHH
58	ATI-966 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWHRFSSIMAYYRITYGETGGNSPV QEFTVAGSVNTATISGLKPGVDYTITVYAVTIHNVSFPISINYRTP C
59	ATI-966 w/ N leader and modified C-terminus including PC +his tag	GVSDVPRDLEVVAATPTSLLISWHRFSSIMAYYRITYGETGGNSPV QEFTVAGSVNTATISGLKPGVDYTITVYAVTIHNVSFPISINYRTP CHHHHHH
60	ATI-966-full length	MGVSDVPRDLEVVAATPTSLLISWHRFSSIMAYYRITYGETGGNSP VQEFTVAGSVNTATISGLKPGVDYTITVYAVTIHNVSFPISINYRT EIDKPSQHHHHHH
61	ATI-966-core (nucleotide sequence)	GAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGCATA GGTTCTCTTCTATCATGGCGTATTACCGCATCACTTACGGCGAAAC AGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGGCTGGCTCTGTT AACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCA TCACTGTGTATGCTGTCACGATCCATAACGTTTCTTTCCCAATTTC CATTAATTACCGCACA
62	ATI-966w/ N leader (nucleotide sequence with N-terminal methionine)	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCA CCCCCACCAGCCTGCTGATCAGCTGGCATAGGTTCTCTTCTATCAT GGCGTATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCT GTCCAGGAGTTCACTGTGGCTGGCTCTGTTAACACAGCTACCATCA GCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGT CACGATCCATAACGTTTCTTTCCCAATTTCCATTAATTACCGCACA
63	ATI-966 w/ N leader and modified C-terminus including PC (nucleotide sequence with N-terminal methionine)	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCA CCCCCACCAGCCTGCTGATCAGCTGGCATAGGTTCTCTTCTATCAT GGCGTATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCT GTCCAGGAGTTCACTGTGGCTGGCTCTGTTAACACAGCTACCATCA GCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGT CACGATCCATAACGTTTCTTTCCCAATTTCCATTAATTACCGCACA CCGTGC
64	ATI-966 w/ N leader and C tail + his tag (nucleotide sequence with N-terminal methionine)	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCA CCCCCACCAGCCTGCTGATCAGCTGGCATAGGTTCTCTTCTATCAT GGCGTATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCT GTCCAGGAGTTCACTGTGGCTGGCTCTGTTAACACAGCTACCATCA GCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGT CACGATCCATAACGTTTCTTTCCCAATTTCCATTAATTACCGCACA GAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGA
65	ATI-967 core (parent of ADX_5417_E01)	EVVAATPTSLLISWQGQLSPSFYYRITYGETGGNSPVQEFTVPVAS GTATISGLKPGVDYTITVYAVTSHGIYFYAPISINYRT
66	ATI-967 BC loop	QGQLSPSFY
67	ATI-967 DE loop	PVASGT
68	ATI-967 FG loop	VTSHGIYFYAP
69	ATI-967 w/ N leader	GVSDVPRDLEVVAATPTSLLISWQGQLSPSFYYRITYGETGGNSPV QEFTVPVASGTATISGLKPGVDYTITVYAVTSHGIYFYAPISINYR T
70	ATI-967 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWQGQLSPSFYYRITYGETGGNSPV QEFTVPVASGTATISGLKPGVDYTITVYAVTSHGIYFYAPISINYR THHHHHH
71	ATI-967 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWQGQLSPSFYYRITYGETGGNSPV QEFTVPVASGTATISGLKPGVDYTITVYAVTSHGIYFYAPISINYR TEIDKPSQ
72	ATI-967 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWQGQLSPSFYYRITYGETGGNSPV QEFTVPVASGTATISGLKPGVDYTITVYAVTSHGIYFYAPISINYR TEIDKPSQHHHHHH

TABLE 3-continued

SEQUENCE LISTING		
SEQ ID	DESCRIPTION	SEQUENCE
73	ATI-967 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWQGQLSPSFYYRITYGETGGNSPVQEFTVPVASGTATISGLKPGVDYTITVYAVTSHGIYFYAPISINYRTPC
74	ATI-967 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWQGQLSPSFYYRITYGETGGNSPVQEFTVPVASGTATISGLKPGVDYTITVYAVTSHGIYFYAPISINYRTPCHHHHHH
75	ATI-967-full length	MGVSDVPRDLEVVAATPTSLLISWQGQLSPSFYYRITYGETGGNSPVQEFTVPVASGTATISGLKPGVDYTITVYAVTSHGIYFYAPISINYRTEIDKPSQHHHHHH
76	ATI-967-core (nucleotide sequence)	GAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGCAGGGACAGCTGTCTCCGTCTTTCTATTACCGAATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGTTGCTAGTGGGACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTTCTCATGGCATATACTTCTACGCTCCAATTTCCATTAATTACCGCACA
77	ATI-967 w/ N leader (nucleotide sequence with N-terminal methionine)	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGCAGGGACAGCTGTCTCCGTCTTTCTATTACCGAATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGTTGCTAGTGGGACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTTCTCATGGCATATACTTCTACGCTCCAATTTCCATTAATTACCGCACA
78	ATI-967 w/ N leader and modified C-terminus including PC (nucleotide sequencewithN-terminal methionine)	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGCAGGGACAGCTGTCTCCGTCTTTCTATTACCGAATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGTTGCTAGTGGGACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTTCTCATGGCATATACTTCTACGCTCCAATTTCCATTAATTACCGCACACCGTGC
79	ATI-967 w/ N leader and C tail + his tag (nucleotide sequence with N-terminal methionine)	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGCAGGGACAGCTGTCTCCGTCTTTCTATTACCGAATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGTTGCTAGTGGGACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTTCTCATGGCATATACTTCTACGCTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCACTGAT
80	ADX_5322_A02 core	EVVAATPTSLLISWSYDGPIDRYYRITYGETGGNSPVQEFTVPPDQKTATISGLKPGVDYTITVYAVRLEEAHYNREFPISINYRT
81	ADX_5322_A02 BC loop	SYDGPIDRY
82	ADX_5322_A02 DE loop	PPDQKT
83	ADX_5322_A02 FG loop	VRLEEAHYNREFP
84	ADX_5322_A02 w/ N leader	GVSDVPRDLEVVAATPTSLLISWSYDGPIDRYYRITYGETGGNSPVQEFTVPPDQKTATISGLKPGVDYTITVYAVRLEEAHYNREFPISINYRT
85	ADX_5322_A02 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWSYDGPIDRYYRITYGETGGNSPVQEFTVPPDQKTATISGLKPGVDYTITVYAVRLEEAHYNREFPISINYRTHHHHHH
86	ADX_5322_A02 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWSYDGPIDRYYRITYGETGGNSPVQEFTVPPDQKTATISGLKPGVDYTITVYAVRLEEAHYNREFPISINYRTEIDKPSQ
87	ADX_5322_A02 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWSYDGPIDRYYRITYGETGGNSPVQEFTVPPDQKTATISGLKPGVDYTITVYAVRLEEAHYNREFPISINYRTEIDKPSQHHHHHH
88	ADX_5322_A02 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWSYDGPIDRYYRITYGETGGNSPVQEFTVPPDQKTATISGLKPGVDYTITVYAVRLEEAHYNREFPISINYRTPC

TABLE 3-continued

SEQ ID	DESCRIPTION	SEQUENCE
	SEQUENCE LISTING	
89	ADX_5322_A02 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWSYDGPIDRYYRITYGETGGNSPV QEFTVPPDQKTATISGLKPGVDYTITVYAVRLEEAHYNREFPISIN YRTPCHHHHHH
90	ADX_5322_A02-Mal-DBCO-FFPF18	GVSDVPRDLEVVAATPTSLLISWSYDGPIDRYYRITYGETGGNSPV QEFTVPPDQKTATISGLKPGVDYTITVYAVRLEEAHYNREFPISIN YRTPC-[Maleamide-DBCO-FFP(18F)]
91	ADX_5322_A02 full length	MGVSDVPRDLEVVAATPTSLLISWSYDGPIDRYYRITYGETGGNSP VQEFTVPPDQKTATISGLKPGVDYTITVYAVRLEEAHYNREFPISI NYRTPCHHHHHH
92	ADX_5322_A02-core (nucleotide sequence)	GAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTCTT ACGATGGCCCAATTGACCGGTATTACCGCATCACTTACGGCGAAAC AGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTCCGGATCAG AAGACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCA TCACTGTGTATGCTGTCCGGCTGGAAGAAGCTCATTACAATCGAGA GTTTCCAATTTCCATTAATTACCGCACA
93	ADX_5322_A02 w/ N leader (nucleotide sequence with N-terminal methionine)	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCA CCCCCACCAGCCTGCTGATCAGCTGGTCTTACGATGGCCCAATTGA CCGGTATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCT GTCCAGGAGTTCACTGTGCCTCCGGATCAGAAGACAGCTACCATCA GCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGT CCGGCTGGAAGAAGCTCATTACAATCGAGAGTTTCCAATTTCCATT AATTACCGCACA
94	ADX_5322_A02 w/ N leader and modified C-terminus including PC (nucleotide sequence with N-terminal methionine)	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCA CCCCCACCAGCCTGCTGATCAGCTGGTCTTACGATGGCCCAATTGA CGGTATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCT GTCCAGGAGTTCACTGTGCCTCCGGATCAGAAGACAGCTACCATCA GCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGT CCGGCTGGAAGAAGCTCATTACAATCGAGAGTTTCCAATTTCCATT AATTACCGCACACCGTGC
95	ADX_5322_A02 w/ N leader and C tail + his tag (nucleotide sequence with N-terminal methionine)	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCA CCCCCACCAGCCTGCTGATCAGCTGGTCTTACGATGGCCCAATTGA CCGGTATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCT GTCCAGGAGTTCACTGTGCCTCCGGATCAGAAGACAGCTACCATCA GCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGT CCGGCTGGAAGAAGCTCATTACAATCGAGAGTTTCCAATTTCCATT AATTACCGCACACCGTGCCACCATCACCACCACCACTGA
96	ADX_5417_E01 core	EVVAATPTSLLISWRAQLSPSFYYRITYGETGGNSPVQEFTVPNDV MTATISGLKPGVDYTITVYAVTTHGVYFYSPISINYRT
97	ADX_5417_E01 BC loop	RAQLSPSFY
98	ADX_5417_E01 DE loop	PNDVMT
99	ADX_5417_E01 FG loop	VTTHGVYFYSP
100	ADX_5417_E01 w/ N leader	GVSDVPRDLEVVAATPTSLLISWRAQLSPSFYYRITYGETGGNSPV QEFTVPNDVMTATISGLKPGVDYTITVYAVTTHGVYFYSPISINYR T
101	ADX_5417_E01 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWRAQLSPSFYYRITYGETGGNSPV QEFTVPNDVMTATISGLKPGVDYTITVYAVTTHGVYFYSPISINYR THHHHHH
102	ADX_5417_E01 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWRAQLSPSFYYRITYGETGGNSPV QEFTVPNDVMTATISGLKPGVDYTITVYAVTTHGVYFYSPISINYR TEIDKPSQ
103	ADX_5417_E01 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWRAQLSPSFYYRITYGETGGNSPV QEFTVPNDVMTATISGLKPGVDYTITVYAVTTHGVYFYSPISINYR TEIDKPSQHHHHHH

TABLE 3-continued

SEQ ID	DESCRIPTION	SEQUENCE
104	ADX_5417_E01 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWRAQLSPSFYYRITYGETGGNSPVQEFTVPNDVMTATISGLKPGVDYTITVYAVTTHGVYFYSPISINYRTPC
105	ADX_5417_E01 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWRAQLSPSFYYRITYGETGGNSPVQEFTVPNDVMTATISGLKPGVDYTITVYAVTTHGVYFYSPISINYRTPCHHHHHH
106	ADX-5417_E01-Mal-DBCO-FFPF18	GVSDVPRDLEVVAATPTSLLISWSYDGPIDRYYRITYGETGGNSPVQEFTVPPDQKTATISGLKPGVDYTITVYAVRLEEAHYNREFPISINYRTPC-[Maleamide-DBCO-FFP(18F)]
107	ADX-5417_E01 full length	MGVSDVPRDLEVVAATPTSLLISWRAQLSPSFYYRITYGETGGNSPVQEFTVPNDVMTATISGLKPGVDYTITVYAVTTHGVYFYSPISINYRTPCHHHHHH
108	ADX-5417_E01-core (nucleotide sequence)	GAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGAGGGCTCAGCTGTCTCCGTCTTTCTATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTAATGATGTAATGACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTACTCATGGTGTTTATTTCTACTCACCAATTTCCATTAATTACCGCACA
109	ADX_5417_E01 w/ N leader (nucleotide sequence with N-terminal methionine)	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGAGGGCTCAGCTGTCTCCGTCTTTCTATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTAATGATGTAATGACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTACTCATGGTGTTTATTTCTACTCACCAATTTCCATTAATTACCGCACA
110	ADX_5417_E01 w/ N leader and modified C-terminus including PC (nucleotide sequence with N-terminal methionine)	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGAGGGCTCAGCTGTCTCCGTCTTTCTATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTAATGATGTAATGACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTACTCATGGTGTTTATTTCTACTCACCAATTTCCATTAATTACCGCACACCGTGC
111	ADX_5417_E01 w/ N leader and C tail +his tag (nucleotide sequence with N-terminal methionine)	ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGAGGGCTCAGCTGTCTCCGTCTTTCTATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTAATGATGTAATGACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTACTCATGGTGTTTATTTCTACTCACCAATTTCCATTAATTACCGCACACCGTGCCACCATCACCACCACCACTGA
112	ATI_1420_A10 core	EVVAATPTSLLISWPYPSYYIEYRITYGETGGNSPVQEFTVQSMKATISGLKPGVDYTITVYAIRHPGMLEFGISINYRT
113	ATI_1420_A10 BC loop	PYPSYYIE
114	ATI_1420_A10 DE loop	IRHPGMLEFG
115	ATI_1420_A10 FG loop	VTDGASIASYAFP
116	ATI_1420_A10 w/ N leader	GVSDVPRDLEVVAATPTSLLISWPYPSYYIEYRITYGETGGNSPVQEFTVQSMKATISGLKPGVDYTITVYAIRHPGMLEFGISINYRT
117	ATI_1420_A10 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWPYPSYYIEYRITYGETGGNSPVQEFTVQSMKATISGLKPGVDYTITVYAIRHPGMLEFGISINYRTHHHHHH
118	ATI_1420_A10 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWPYPSYYIEYRITYGETGGNSPVQEFTVQSMKATISGLKPGVDYTITVYAIRHPGMLEFGISINYRTEIDKPSQ
119	ATI_1420_A10 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWPYPSYYIEYRITYGETGGNSPVQEFTVQSMKATISGLKPGVDYTITVYAIRHPGMLEFGISINYRTEIDKPSQHHHHHH

TABLE 3-continued

SEQUENCE LISTING

SEQ ID	DESCRIPTION	SEQUENCE
120	ATI_1420_A10 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWPYPSYYIEYRITYGETGGNSPVQEFTVQSMKATISGLKPGVDYTITVYAIRHPGMLEFGISINYRTPC
121	ATI_1420_A10 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWPYPSYYIEYRITYGETGGNSPVQEFTVQSMKATISGLKPGVDYTITVYAIRHPGMLEFGISINYRTPCHHHHHH
122	ATI_1420 A10-full length	MGVSDVPRDLEVVAATPTSLLISWPYPSYYIEYRITYGETGGNSPVQEFTVQSMKATISGLKPGVDYTITVYAIRHPGMLEFGISINYRTEIDKPSQHHHHHH
123	ATI_1420_B09 core	EVVAATPTSLLISWHKFSSLMSYRITYGETGGNSPVQEFTVGSVNATISGLKPGVDYTITVYAIHNVGFISINYRT
124	ATI_1420_B09 BC loop	HKFSSLMS
125	ATI_1420_B09 DE loop	GSVN
126	ATI_1420_B09 FG loop	IHNVGF
127	ATI_1420_B09 w/ N leader	GVSDVPRDLEVVAATPTSLLISWHKFSSLMSYRITYGETGGNSPVQEFTVGSVNATISGLKPGVDYTITVYAIHNVGFISINYRT
128	ATI_1420_B09 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWHKFSSLMSYRITYGETGGNSPVQEFTVGSVNATISGLKPGVDYTITVYAIHNVGFISINYRTHHHHHH
129	AATI_1420_B09 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWHKFSSLMSYRITYGETGGNSPVQEFTVGSVNATISGLKPGVDYTITVYAIHNVGFISINYRTEIDKPSQ
130	ATI_1420_B09 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWHKFSSLMSYRITYGETGGNSPVQEFTVGSVNATISGLKPGVDYTITVYAIHNVGFISINYRTEIDKPSQHHHHHH
131	ATI_1420_B09 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWHKFSSLMSYRITYGETGGNSPVQEFTVGSVNATISGLKPGVDYTITVYAIHNVGFISINYRTPC
132	ATI_1420_B09 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWHKFSSLMSYRITYGETGGNSPVQEFTVGSVNATISGLKPGVDYTITVYAIHNVGFISINYRTPCHHHHHH
133	ATI_1420_B09-full length	MGVSDVPRDLEVVAATPTSLLISWHKFSSLMSYRITYGETGGNSPVQEFTVGSVNATISGLKPGVDYTITVYAIHNVGFISINYRTEIDKPSQHHHHHH
134	ATI_1420_C02 core	EVVAATPTSLLISWRIKSYYAYRITYGETGGNSPVQEFTVRQHVATISGLKPGVDYTITVYARLGDVELVYEISINYRT
135	ATI_1420_C02 BC loop	RIKSYYA
136	ATI_1420_C02 DE loop	RQHV
137	ATI_1420_C02 FG loop	RLGDVELVYE
138	ATI_1420_C02 w/ N leader	GVSDVPRDLEVVAATPTSLLISWRIKSYYAYRITYGETGGNSPVQEFTVRQHVATISGLKPGVDYTITVYARLGDVELVYEISINYRT
139	ATI_1420_C02 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWHKFSSLMSYRITYGETGGNSPVQEFTVGSVNATISGLKPGVDYTITVYAIHNVGFISINYRTHHHHHH
140	ATI_1420_C02 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWRIKSYYAYRITYGETGGNSPVQEFTVRQHVATISGLKPGVDYTITVYARLGDVELVYEISINYRTEIDKPSQ

TABLE 3-continued

SEQ ID	DESCRIPTION	SEQUENCE
	SEQUENCE LISTING	
141	ATI_1420_C02 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWRIKSYYAYRITYGETGGNSPVQEFTVRQHVATISGLKPGVDYTITVYARLGDVELVYEISINYRTEIDKPSQHHHHHH
142	ATI_1420_C02 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWRIKSYYAYRITYGETGGNSPVQEFTVRQHVATISGLKPGVDYTITVYARLGDVELVYEISINYRTPC
143	ATI_1420_C02 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWHKFSSLMSYRITYGETGGNSPVQEFTVGSVNATISGLKPGVDYTITVYAIHNVGFISINYRTPCHHHHHH
144	ATI_1420_C02-full length	MGVSDVPRDLEVVAATPTSLLISWRIKSYYAYRITYGETGGNSPVQEFTVRQHVATISGLKPGVDYTITVYARLGDVELVYEISINYRTEIDKPSQHHHHHH
145	ATI_1420_C11 core	EVVAATPTSLLISWMYPLKSVPYRITYGETGGNSPVQEFTVYSSGATISGLKPGVDYTITVYAMSYSTYHAFMISINYRT
146	ATI_1420_C11 BC loop	MYPLKSVP
147	ATI_1420_C11 DE loop	YSSG
148	ATI_1420_C11 FG loop	MSYSTYHAFM
149	ATI_1420_C11 w/ N leader	GVSDVPRDLEVVAATPTSLLISWMYPLKSVPYRITYGETGGNSPVQEFTVYSSGATISGLKPGVDYTITVYAMSYSTYHAFMISINYRT
150	ATI_420_C11 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWMYPLKSVPYRITYGETGGNSPVQEFTVYSSGATISGLKPGVDYTITVYAMSYSTYHAFMISINYRTHHHHHH
151	ATI_1420_C11 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWMYPLKSVPYRITYGETGGNSPVQEFTVYSSGATISGLKPGVDYTITVYAMSYSTYHAFMISINYRTEIDKPSQ
152	ATI_1420_C11 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWMYPLKSVPYRITYGETGGNSPVQEFTVYSSGATISGLKPGVDYTITVYAMSYSTYHAFMISINYRTEIDKPSQHHHHHH
153	ATI_1420_C11 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWMYPLKSVPYRITYGETGGNSPVQEFTVYSSGATISGLKPGVDYTITVYAMSYSTYHAFMISINYRTPC
154	ATI_1420_C11 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWMYPLKSVPYRITYGETGGNSPVQEFTVYSSGATISGLKPGVDYTITVYAMSYSTYHAFMISINYRTPCHHHHHH
155	AATI_1420_C11-full length	MGVSDVPRDLEVVAATPTSLLISWMYPLKSVPYRITYGETGGNSPVQEFTVYSSGATISGLKPGVDYTITVYAMSYSTYHAFMISINYRTEIDKPSQHHHHHH
156	ATI_1420_D01 core	EVVAATPTSLLISWRTVPETDYRITYGETGGNSPVQEFTVPDNTATISGLKPGVDYTITVYALETAHYNRDYISINYRT
157	ATI_1420_D01 BC loop	RTVPETD
158	ATI_1420_D01 DE loop	PDNT
159	ATI_1420_D01 FG loop	LETAHYNRDY
160	ATI_1420_D01 w/ N leader	GVSDVPRDLEVVAATPTSLLISWRTVPETDYRITYGETGGNSPVQEFTVPDNTATISGLKPGVDYTITVYALETAHYNRDYISINYRT
161	ATI_1420_D01 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWRTVPETDYRITYGETGGNSPVQEFTVPDNTATISGLKPGVDYTITVYALETAHYNRDYISINYRTHHHHHH

TABLE 3-continued

SEQUENCE LISTING		
SEQ ID	DESCRIPTION	SEQUENCE
162	ATI_1420_D01 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWRTVPETDYRITYGETGGNSPVQEFTVPDNTATISGLKPGVDYTITVYALETAHYNRDYISINYRTEIDKPSQ
163	ATI_1420_D01 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWRTVPETDYRITYGETGGNSPVQEFTVPDNTATISGLKPGVDYTITVYALETAHYNRDYISINYRTEIDKPSQHHHHHH
164	ATI_1420_D01 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWRTVPETDYRITYGETGGNSPVQEFTVPDNTATISGLKPGVDYTITVYALETAHYNRDYISINYRTPC
165	ATI_1420_D01 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWRTVPETDYRITYGETGGNSPVQEFTVPDNTATISGLKPGVDYTITVYALETAHYNRDYISINYRTPCHHHHHH
166	ATI_1420_D01-full length	MGVSDVPRDLEVVAATPTSLLISWRTVPETDYRITYGETGGNSPVQEFTVPDNTATISGLKPGVDYTITVYALETAHYNRDYISINYRTEIDKPSQHHHHHH
167	ATI_1420_D05 core	EVVAATPTSLLISWTAYYSTIKYRITYGETGGNSPVQEFTVGPKHHATISGLKPGVDYTITVYAYNTKPGYHAHQISINYRT
168	ATI_1420_D05 BC loop	TAYYSTIK
169	ATI_1420_D05 DE loop	GPKHH
170	ATI_1420_D05 FG loop	YNTKPGYHAHQ
171	ATI_1420_D05 w/ N leader	GVSDVPRDLEVVAATPTSLLISWTAYYSTIKYRITYGETGGNSPVQEFTVGPKHHATISGLKPGVDYTITVYAYNTKPGYHAHQISINYRT
172	ATI_1420_D05 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWTAYYSTIKYRITYGETGGNSPVQEFTVGPKHHATISGLKPGVDYTITVYAYNTKPGYHAHQISINYRTHHHHHH
173	ATI_1420_D05 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWTAYYSTIKYRITYGETGGNSPVQEFTVGPKHHATISGLKPGVDYTITVYAYNTKPGYHAHQISINYRTEIDKPSQ
174	ATI_1420_D05 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWTAYYSTIKYRITYGETGGNSPVQEFTVGPKHHATISGLKPGVDYTITVYAYNTKPGYHAHQISINYRTEIDKPSQHHHHHH
175	ATI_1420_D05 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWTAYYSTIKYRITYGETGGNSPVQEFTVGPKHHATISGLKPGVDYTITVYAYNTKPGYHAHQISINYRTPC
176	ATI_1420_D05 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWTAYYSTIKYRITYGETGGNSPVQEFTVGPKHHATISGLKPGVDYTITVYAYNTKPGYHAHQISINYRTPCHHHHHH
177	ATI_1420_D05-full length	MGVSDVPRDLEVVAATPTSLLISWTAYYSTIKYRITYGETGGNSPVQEFTVGPKHHATISGLKPGVDYTITVYAYNTKPGYHAHQISINYRTEIDKPSQHHHHHH
178	ATI_1420_D10 core	EVVAATPTSLLISWRIPSYHIQYRITYGETGGNSPVQEFTVYQKYATISGLKPGVDYTITVYAVSPPKQLRFGISINYRT
179	ATI_1420_D10 BC loop	RIPSYHIQ
180	ATI_1420_D10 DE loop	YQKY
181	ATI_1420_D10 FG loop	VSPPKQLRFG
182	ATI_1420_D10 w/ N leader	GVSDVPRDLEVVAATPTSLLISWRIPSYHIQYRITYGETGGNSPVQEFTVYQKYATISGLKPGVDYTITVYAVSPPKQLRFGISINYRT

TABLE 3-continued

SEQUENCE LISTING

SEQ ID	DESCRIPTION	SEQUENCE
183	ATI_1420_D10 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWRIPSYHIQYRITYGETGGNSPVQEFTVYQKYATISGLKPGVDYTITVYAVSPPKQLRFGISINYRTHHHHHH
184	ATI_1420_D10 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWRIPSYHIQYRITYGETGGNSPVQEFTVYQKYATISGLKPGVDYTITVYAVSPPKQLRFGISINYRTEIDKPSQ
185	ATI_1420_D10 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWRIPSYHIQYRITYGETGGNSPVQEFTVYQKYATISGLKPGVDYTITVYAVSPPKQLRFGISINYRTEIDKPSQHHHHHH
186	ATI_1420_D10 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWRIPSYHIQYRITYGETGGNSPVQEFTVYQKYATISGLKPGVDYTITVYAVSPPKQLRFGISINYRTPC
187	ATI_1420_D10 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWRIPSYHIQYRITYGETGGNSPVQEFTVYQKYATISGLKPGVDYTITVYAVSPPKQLRFGISINYRTPCHHHHHH
188	ATI_1420_D010-full length	MGVSDVPRDLEVVAATPTSLLISWRIPSYHIQYRITYGETGGNSPVQEFTVYQKYATISGLKPGVDYTITVYAVSPPKQLRFGISINYRTEIDKPSQHHHHHH
189	ATI_1420_F10 core	EVVAATPTSLLISWPAPPSYVFYRITYGETGGNSPVQEFTVYPYMATISGLKPGVDYTITVYAYTSGFSISINYRT
190	ATI_1420_F10 BC loop	PAPPSYVF
191	ATI_1420_F10 DE loop	YPYM
192	ATI_1420_F10 FG loop	YTSGFS
193	ATI_1420_F10 w/ N leader	GVSDVPRDLEVVAATPTSLLISWPAPPSYVFYRITYGETGGNSPVQEFTVYPYMATISGLKPGVDYTITVYAYTSGFSISINYRT
194	ATI_1420_F10 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWPAPPSYVFYRITYGETGGNSPVQEFTVYPYMATISGLKPGVDYTITVYAYTSGFSISINYRTHHHHHH
195	ATI_1420_F10 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWPAPPSYVFYRITYGETGGNSPVQEFTVYPYMATISGLKPGVDYTITVYAYTSGFSISINYRTEIDKPSQ
196	ATI_1420_F10 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWPAPPSYVFYRITYGETGGNSPVQEFTVYPYMATISGLKPGVDYTITVYAYTSGFSISINYRTEIDKPSQHHHHHH
197	ATI_1420_F10 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWPAPPSYVFYRITYGETGGNSPVQEFTVYPYMATISGLKPGVDYTITVYAYTSGFSISINYRTPC
198	ATI_1420_F10 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWPAPPSYVFYRITYGETGGNSPVQEFTVYPYMATISGLKPGVDYTITVYAYTSGFSISINYRTPCHHHHHH
199	ATI_1420_F10-full length	MGVSDVPRDLEVVAATPTSLLISWPAPPSYVFYRITYGETGGNSPVQEFTVYPYMATISGLKPGVDYTITVYAYTSGFSISINYRTEIDKPSQHHHHHH
200	ATI_1421_C05 core	EVVAATPTSLLISWYMDHKSKYRITYGETGGNSPVQEFTVPDQRATISGLKPGVDYTITVYALSEAHYLRDKISINYRT
201	ATI_1421_C05 BC loop	YMDHKSK
202	ATI_1421_C05 DE loop	PDQR
203	ATI_1421_C05 FG loop	LSEAHYLRDK

TABLE 3-continued

SEQUENCE LISTING

SEQ ID	DESCRIPTION	SEQUENCE
204	ATI_1421_C05 w/ N leader	GVSDVPRDLEVVAATPTSLLISWYMDHKSKYRITYGETGGNSPV QEFTVPDQRATISGLKPGVDYTITVYALSEAHYLRDKISINYRT
205	ATI_1421_C05 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWYMDHKSKYRITYGETGGNSPV QEFTVPDQRATISGLKPGVDYTITVYALSEAHYLRDKISINYRT HHHHHH
206	ATI_1421_C05 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWYMDHKSKYRITYGETGGNSPV QEFTVPDQRATISGLKPGVDYTITVYALSEAHYLRDKISINYRT EIDKPSQ
207	ATI_1421_C05 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWYMDHKSKYRITYGETGGNSPV QEFTVPDQRATISGLKPGVDYTITVYALSEAHYLRDKISINYRT EIDKPSQHHHHHH
208	ATI_1421_C05 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWYMDHKSKYRITYGETGGNSPV QEFTVPDQRATISGLKPGVDYTITVYALSEAHYLRDKISINYRT PC
209	ATI_1421_C05 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWYMDHKSKYRITYGETGGNSPV QEFTVPDQRATISGLKPGVDYTITVYALSEAHYLRDKISINYRT PCHHHHHH
210	ATI_1421_C05-full length	MGVSDVPRDLEVVAATPTSLLISWYMDHKSKYRITYGETGGNSP VQEFTVPDQRATISGLKPGVDYTITVYALSEAHYLRDKISINYR TEIDKPSQHHHHHH
211	ATI_1421_C06 core	EVVAATPTSLLISWENLASYQYRITYGETGGNSPVQEFTVPDQA ATISGLKPGVDYTITVYALQTAHYYRQHISINYRT
212	ATI_1421_C06 BC loop	ENLASYQ
213	ATI_1421_C06 DE loop	PDQA
214	ATI_1421_C06 FG loop	LQTAHYYRQH
215	ATI_1421_C06 w/ N leader	GVSDVPRDLEVVAATPTSLLISWENLASYQYRITYGETGGNSPV QEFTVPDQAATISGLKPGVDYTITVYALQTAHYYRQHISINYRT
216	ATI_1421_C06 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWENLASYQYRITYGETGGNSPV QEFTVPDQAATISGLKPGVDYTITVYALQTAHYYRQHISINYRT HHHHHH
217	ATI_1421_C06 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWENLASYQYRITYGETGGNSPV QEFTVPDQAATISGLKPGVDYTITVYALQTAHYYRQHISINYRT EIDKPSQ
218	ATI_1421_C06 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWENLASYQYRITYGETGGNSPV QEFTVPDQAATISGLKPGVDYTITVYALQTAHYYRQHISINYRT EIDKPSQHHHHHH
219	ATI_1421_C06 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWENLASYQYRITYGETGGNSPV QEFTVPDQAATISGLKPGVDYTITVYALQTAHYYRQHISINYRT PC
220	ATI_1421_C06 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWENLASYQYRITYGETGGNSPV QEFTVPDQAATISGLKPGVDYTITVYALQTAHYYRQHISINYRT PCHHHHHH
221	ATI_1421_C06-full length	MGVSDVPRDLEVVAATPTSLLISWENLASYQYRITYGETGGNSP VQEFTVPDQAATISGLKPGVDYTITVYALQTAHYYRQHISINYR TEIDKPSQHHHHHH
222	ATI_1421_D05 core	EVVAATPTSLLISWYYVQYNDYRITYGETGGNSPVQEFTVPDQS ATISGLKPGVDYTITVYALEKAHYYRQNISINYRT
223	ATI_1421_D05 BC loop	YYVQYND
224	ATI_1421_D05 DE loop	PDQS

TABLE 3-continued

SEQUENCE LISTING		
SEQ ID	DESCRIPTION	SEQUENCE
225	ATI_1421_D05 FG loop	LEKAHYYRQN
226	ATI_1421_D05 w/ N leader	GVSDVPRDLEVVAATPTSLLISWYYVQYNDYRITYGETGGNSPVQEFTVPDQSATISGLKPGVDYTITVYALEKAHYYRQNISINYRT
227	ATI_1421_D05 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWYYVQYNDYRITYGETGGNSPVQEFTVPDQSATISGLKPGVDYTITVYALEKAHYYRQNISINYRTHHHHHH
228	ATI_1421_D05 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWYYVQYNDYRITYGETGGNSPVQEFTVPDQSATISGLKPGVDYTITVYALEKAHYYRQNISINYRTEIDKPSQ
229	ATI_1421_D05 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWYYVQYNDYRITYGETGGNSPVQEFTVPDQSATISGLKPGVDYTITVYALEKAHYYRQNISINYRTEIDKPSQHHHHHH
230	ATI_1421_D05 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWYYVQYNDYRITYGETGGNSPVQEFTVPDQSATISGLKPGVDYTITVYALEKAHYYRQNISINYRTPC
231	ATI_1421_D05 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWYYVQYNDYRITYGETGGNSPVQEFTVPDQSATISGLKPGVDYTITVYALEKAHYYRQNISINYRTPCHHHHHH
232	ATI_1421_D05-full length	MGVSDVPRDLEVVAATPTSLLISWYYVQYNDYRITYGETGGNSPVQEFTVPDQSATISGLKPGVDYTITVYALEKAHYYRQNISINYRTEIDKPSQHHHHHH
233	ATI_1421_D06 core	EVVAATPTSLLISWGHNYDDEYRITYGETGGNSPVQEFTVPDQYATISGLKPGVDYTITVYALAEAHVRKNHISINYRT
234	ATI_1421_D06 BC loop	GHNYDDE
235	ATI_1421_D06 DE loop	PDQY
236	ATI_1421_D06 FG loop	LAEAHVRKNH
237	ATI_1421_D06 w/ N leader	GVSDVPRDLEVVAATPTSLLISWGHNYDDEYRITYGETGGNSPVQEFTVPDQYATISGLKPGVDYTITVYALAEAHVRKNHISINYRT
238	ATI_1421_D06 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWGHNYDDEYRITYGETGGNSPVQEFTVPDQYATISGLKPGVDYTITVYALAEAHVRKNHISINYRTHHHHHH
239	ATI_1421_D06 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWGHNYDDEYRITYGETGGNSPVQEFTVPDQYATISGLKPGVDYTITVYALAEAHVRKNHISINYRTEIDKPSQ
240	ATI_1421_D06 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWGHNYDDEYRITYGETGGNSPVQEFTVPDQYATISGLKPGVDYTITVYALAEAHVRKNHISINYRTEIDKPSQHHHHHH
241	ATI_1421_D06 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWGHNYDDEYRITYGETGGNSPVQEFTVPDQYATISGLKPGVDYTITVYALAEAHVRKNHISINYRTPC
242	ATI_1421_D06 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWGHNYDDEYRITYGETGGNSPVQEFTVPDQYATISGLKPGVDYTITVYALAEAHVRKNHISINYRTPCHHHHHH
243	ATI_1421_D06-full length	MGVSDVPRDLEVVAATPTSLLISWGHNYDDEYRITYGETGGNSPVQEFTVPDQYATISGLKPGVDYTITVYALAEAHVRKNHISINYRTEIDKPSQHHHHHH
244	ATI_1421_E03 core	EVVAATPTSLLISWVYHYDAQYRITYGETGGNSPVQEFTVPDQKATISGLKPGVDYTITVYALSEAHHKRDSISINYRT
245	ATI_1421_E03 BC loop	VYHYDAQ

TABLE 3-continued

SEQ ID	DESCRIPTION	SEQUENCE
	SEQUENCE LISTING	
246	ATI_1421_E03 DE loop	PDQK
247	ATI_1421_E03 FG loop	LSEAHHKRDS
248	ATI_1421_E03 w/ N leader	GVSDVPRDLEVVAATPTSLLISWVYHYDAQYRITYGETGGNSPV QEFTVPDQKATISGLKPGVDYTITVYALSEAHHKRDSISINYRT HHHHHH
249	ATI_1421_E03 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWVYHYDAQYRITYGETGGNSPV QEFTVPDQKATISGLKPGVDYTITVYALSEAHHKRDSISINYRT EIDKPSQ
250	ATI_1421_E03 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWVYHYDAQYRITYGETGGNSPV QEFTVPDQKATISGLKPGVDYTITVYALSEAHHKRDSISINYRT EIDKPSQHHHHHH
251	ATI_1421_E03 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWVYHYDAQYRITYGETGGNSPV QEFTVPDQKATISGLKPGVDYTITVYALSEAHHKRDSISINYRT PC
252	ATI_1421_E03 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWVYHYDAQYRITYGETGGNSPV QEFTVPDQKATISGLKPGVDYTITVYALSEAHHKRDSISINYRT PCHHHHHH
253	ATI_1421_E03 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWVYHYDAQYRITYGETGGNSPV QEFTVPDQKATISGLKPGVDYTITVYALSEAHHKRDSISINYRT
254	ATI_1421_E03-full length	MGVSDVPRDLEVVAATPTSLLISWVYHYDAQYRITYGETGGNSP VQEFTVPDQKATISGLKPGVDYTITVYALSEAHHKRDSISINYR TEIDKPSQHHHHHH
255	ATI_1421_E04 core	EVVAATPTSLLISWSYNGPIEYRITYGETGGNSPVQEFTVPDQQ ATISGLKPGVDYTITVYALEEAHYSRQSISINYRT
256	ATI_1421_E04 BC loop	SYNGPIE
257	ATI_1421_E04 DE loop	PDQQ
258	ATI_1421_E04 FG loop	LEEAHYSRQS
259	ATI_1421_E04 w/ N leader	GVSDVPRDLEVVAATPTSLLISWSYNGPIEYRITYGETGGNSPV QEFTVPDQQATISGLKPGVDYTITVYALEEAHYSRQSISINYRT
260	ATI_1421_E04 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWSYNGPIEYRITYGETGGNSPV QEFTVPDQQATISGLKPGVDYTITVYALEEAHYSRQSISINYRT HHHHHH
261	ATI_1421_E04 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWSYNGPIEYRITYGETGGNSPV QEFTVPDQQATISGLKPGVDYTITVYALEEAHYSRQSISINYRT EIDKPSQ
262	ATI_1421_E04 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWSYNGPIEYRITYGETGGNSPV QEFTVPDQQATISGLKPGVDYTITVYALEEAHYSRQSISINYRT EIDKPSQHHHHHH
263	ATI_1421_E04 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWSYNGPIEYRITYGETGGNSPV QEFTVPDQQATISGLKPGVDYTITVYALEEAHYSRQSISINYRT PC
264	ATI_1421_E04 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWSYNGPIEYRITYGETGGNSPV QEFTVPDQQATISGLKPGVDYTITVYALEEAHYSRQSISINYRT PCHHHHHH
265	ATI_1421_E04-full length	MGVSDVPRDLEVVAATPTSLLISWSYNGPIEYRITYGETGGNSP VQEFTVPDQQATISGLKPGVDYTITVYALEEAHYSRQSISINYR TEIDKPSQHHHHHH
266	ATI_1421_F03 core	EVVAATPTSLLISWISVQTYDYRITYGETGGNSPVQEFTVPDQS ATISGLKPGVDYTITVYALEKAHYYRQNISINYRT
267	ATI_1421_F03 BC loop	ISVQTYD

TABLE 3-continued

SEQUENCE LISTING		
SEQ ID	DESCRIPTION	SEQUENCE
268	ATI_1421_F03 DE loop	PDQS
269	ATI_1421_F03 FG loop	LEKAHYYRQN
270	ATI_1421_F03 w/ N leader	GVSDVPRDLEVVAATPTSLLISWISVQTYDYRITYGETGGNSPV QEFTVPDQSATISGLKPGVDYTITVYALEKAHYYRQNISINYRT
271	ATI_1421_F03 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWISVQTYDYRITYGETGGNSPV QEFTVPDQSATISGLKPGVDYTITVYALEKAHYYRQNISINYRT HHHHHH
272	ATI_1421_F03 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWISVQTYDYRITYGETGGNSPV QEFTVPDQSATISGLKPGVDYTITVYALEKAHYYRQNISINYRT EIDKPSQ
273	ATI_1421_F03 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWISVQTYDYRITYGETGGNSPV QEFTVPDQSATISGLKPGVDYTITVYALEKAHYYRQNISINYRT EIDKPSQHHHHHH
274	ATI_1421_F03 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWISVQTYDYRITYGETGGNSPV QEFTVPDQSATISGLKPGVDYTITVYALEKAHYYRQNISINYRT PC
275	ATI_1421_F03 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWISVQTYDYRITYGETGGNSPV QEFTVPDQSATISGLKPGVDYTITVYALEKAHYYRQNISINYRT PCHHHHHH
276	ATI_1421_F03-full length	MGVSDVPRDLEVVAATPTSLLISWISVQTYDYRITYGETGGNSP VQEFTVPDQSATISGLKPGVDYTITVYALEKAHYYRQNISINYR TEIDKPSQHHHHHH
277	ATI_1421_F05 core	EVVAATPTSLLISWLARHDARYRITYGETGGNSPVQEFTVPDRM ATISGLKPGVDYTITVYALEQAHYYRLYISINYRT
278	ATI_1421_F05 BC loop	LARHDAR
279	ATI_1421_F05 DE loop	PDRM
280	ATI_1421_F05 FG loop	LEQAHYYRLY
281	ATI_1421_F05 w/ N leader	GVSDVPRDLEVVAATPTSLLISWLARHDARYRITYGETGGNSPV QEFTVPDRMATISGLKPGVDYTITVYALEQAHYYRLYISINYRT
282	ATI_1421_F05 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWLARHDARYRITYGETGGNSPV QEFTVPDRMATISGLKPGVDYTITVYALEQAHYYRLYISINYRT HHHHHH
283	ATI_1421_F05 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWLARHDARYRITYGETGGNSPV QEFTVPDRMATISGLKPGVDYTITVYALEQAHYYRLYISINYRT EIDKPSQ
284	ATI_1421_F05 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWLARHDARYRITYGETGGNSPV QEFTVPDRMATISGLKPGVDYTITVYALEQAHYYRLYISINYRT EIDKPSQHHHHHH
285	ATI_1421_F05 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWLARHDARYRITYGETGGNSPV QEFTVPDRMATISGLKPGVDYTITVYALEQAHYYRLYISINYRT PC
286	ATI_1421_F05 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWLARHDARYRITYGETGGNSPV QEFTVPDRMATISGLKPGVDYTITVYALEQAHYYRLYISINYRT PCHHHHHH
287	ATI_1421_F05-full length	MGVSDVPRDLEVVAATPTSLLISWLARHDARYRITYGETGGNSP VQEFTVPDRMATISGLKPGVDYTITVYALEQAHYYRLYISINYR TEIDKPSQHHHHHH
288	ATI_1421_G07 core	EVVAATPTSLLISWHSPTSGITYRITYGETGGNSPVQEFTVPYD PSATISGLKPGVDYTITVYAPYGSQYYPGYHISINYRT
289	ATI_1421_G07 BC loop	HSPTSGIT

TABLE 3-continued

SEQUENCE LISTING

SEQ ID	DESCRIPTION	SEQUENCE
290	ATI_1421_G07 DE loop	PYDPS
291	ATI_1421_G07 FG loop	PYGSQYYPGYH
292	ATI_1421_G07 w/ N leader	GVSDVPRDLEVVAATPTSLLISWHSPTSGITYRITYGETGGNSP VQEFTVPYDPSATISGLKPGVDYTITVYAPYGSQYYPGYHISIN YRT
293	ATI_1421_G07 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWHSPTSGITYRITYGETGGNSP VQEFTVPYDPSATISGLKPGVDYTITVYAPYGSQYYPGYHISIN YRTHHHHHH
294	ATI_1421_G07 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWHSPTSGITYRITYGETGGNSP VQEFTVPYDPSATISGLKPGVDYTITVYAPYGSQYYPGYHISIN YRTEIDKPSQ
295	ATI_1421_G07 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWHSPTSGITYRITYGETGGNSP VQEFTVPYDPSATISGLKPGVDYTITVYAPYGSQYYPGYHISIN YRTEIDKPSQHHHHHH
296	ATI_1421_G07 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWHSPTSGITYRITYGETGGNSP VQEFTVPYDPSATISGLKPGVDYTITVYAPYGSQYYPGYHISIN YRTPC
297	ATI_1421_G07 w/ N leader and modified C-terminus including PC +30 his tag	GVSDVPRDLEVVAATPTSLLISWHSPTSGITYRITYGETGGNSP VQEFTVPYDPSATISGLKPGVDYTITVYAPYGSQYYPGYHISIN YRTPCHHHHHH
298	ATI_1421_G07-full length	MGVSDVPRDLEVVAATPTSLLISWHSPTSGITYRITYGETGGNS PVQEFTVPYDPSATISGLKPGVDYTITVYAPYGSQYYPGYHISI NYRTEIDKPSQHHHHHH
299	ATI_1421_H03 core	EVVAATPTSLLISWVYHYDAQYRITYGETGGNSPVQEFTVPDSS ATISGLKPGVDYTITVYALEQAHIDRTTISINYRT
300	ATI_1421_H03 BC loop	VYHYDAQ
301	ATI_1421_H03 DE loop	PDSS
302	ATI_1421_H03 FG loop	LEQAHIDRTT
303	ATI_1421_H03 w/ N leader	GVSDVPRDLEVVAATPTSLLISWVYHYDAQYRITYGETGGNSPV QEFTVPDSSATISGLKPGVDYTITVYALEQAHIDRTTISINYRT
304	ATI_1421_H03 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWVYHYDAQYRITYGETGGNSPV QEFTVPDSSATISGLKPGVDYTITVYALEQAHIDRTTISINYRT HHHHHH
305	ATI_1421_H03 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWVYHYDAQYRITYGETGGNSPV QEFTVPDSSATISGLKPGVDYTITVYALEQAHIDRTTISINYRT EIDKPSQ
306	ATI_1421_H03 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWVYHYDAQYRITYGETGGNSPV QEFTVPDSSATISGLKPGVDYTITVYALEQAHIDRTTISINYRT EIDKPSQHHHHHH
307	ATI_1421_H03 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWVYHYDAQYRITYGETGGNSPV QEFTVPDSSATISGLKPGVDYTITVYALEQAHIDRTTISINYRT PC
308	ATI_1421_H03 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWVYHYDAQYRITYGETGGNSPV QEFTVPDSSATISGLKPGVDYTITVYALEQAHIDRTTISINYRT PCHHHHHH
309	ATI_1421_H03-full length	MGVSDVPRDLEVVAATPTSLLISWVYHYDAQYRITYGETGGNSP VQEFTVPDSSATISGLKPGVDYTITVYALEQAHIDRTTISINYR TEIDKPSQHHHHHH

TABLE 3-continued

SEQUENCE LISTING

SEQ ID	DESCRIPTION	SEQUENCE
310	ATI_1421_H05 core	EVVAATPTSLLISWTSVLLKDYRITYGETGGNSPVQEFTVPDQH ATISGLKPGVDYTITVYALQNAHHERLYISINYRT
311	ATI_1421_H05 BC loop	TSVLLKD
312	ATI_1421_H05 DE loop	PDQH
313	ATI_1421_H05 FG loop	LQNAHHERLY
314	ATI_1421_H05 w/ N leader	GVSDVPRDLEVVAATPTSLLISWTSVLLKDYRITYGETGGNSPV QEFTVPDQHATISGLKPGVDYTITVYALQNAHHERLYISINYRT
315	ATI_1421_H05 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWTSVLLKDYRITYGETGGNSPV QEFTVPDQHATISGLKPGVDYTITVYALQNAHHERLYISINYRT HHHHHH
316	ATI_1421_H05 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWTSVLLKDYRITYGETGGNSPV QEFTVPDQHATISGLKPGVDYTITVYALQNAHHERLYISINYRT EIDKPSQ
317	ATI_1421_H05 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWTSVLLKDYRITYGETGGNSPV QEFTVPDQHATISGLKPGVDYTITVYALQNAHHERLYISINYRT EIDKPSQHHHHHH
318	ATI_1421_H05 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWTSVLLKDYRITYGETGGNSPV QEFTVPDQHATISGLKPGVDYTITVYALQNAHHERLYISINYRT PC
319	ATI_1421_H05 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWTSVLLKDYRITYGETGGNSPV QEFTVPDQHATISGLKPGVDYTITVYALQNAHHERLYISINYRT PCHHHHHH
320	ATI_1421_H05-full length	MGVSDVPRDLEVVAATPTSLLISWTSVLLKDYRITYGETGGNSP VQEFTVPDQHATISGLKPGVDYTITVYALQNAHHERLYISINYR TEIDKPSQHHHHHH
321	ATI_1422_E06 core	EVVAATPTSLLISWLPSYYITYRITYGETGGNSPVQEFTVSKDL ATISGLKPGVDYTITVYAFNGSSYYTFGISINYRT
322	ATI_1422_E06 BC loop	LPSYYIT
323	ATI_1422_E06 DE loop	SKDL
324	ATI_1422_E06 FG loop	ENGSSYYTFG
325	ATI_1422_E06 w/ N leader	GVSDVPRDLEVVAATPTSLLISWLPSYYITYRITYGETGGNSPV QEFTVSKDLATISGLKPGVDYTITVYAFNGSSYYTFGISINYRT
326	ATI_1422_E06 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWLPSYYITYRITYGETGGNSPV QEFTVSKDLATISGLKPGVDYTITVYAFNGSSYYTFGISINYRT EIDKPSQHHHHHH
327	ATI_1422_E06 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWLPSYYITYRITYGETGGNSPV QEFTVSKDLATISGLKPGVDYTITVYAFNGSSYYTFGISINYRT EIDKPSQHHHHHH
328	ATI_1422_E06 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWLPSYYITYRITYGETGGNSPV QEFTVSKDLATISGLKPGVDYTITVYAFNGSSYYTFGISINYRT PC
329	ATI_1422_E06 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWLPSYYITYRITYGETGGNSPV QEFTVSKDLATISGLKPGVDYTITVYAFNGSSYYTFGISINYRT PCHHHHHH
330	ATI_1422_E06 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWLPSYYITYRITYGETGGNSPV QEFTVSKDLATISGLKPGVDYTITVYAFNGSSYYTFGISINYRT EIDKPSQHHHHHH

TABLE 3-continued

SEQ ID	DESCRIPTION	SEQUENCE
331	ATI_1422_E06-full length	MGVSDVPRDLEVVAATPTSLLISWLPSYYITYRITYGETGGNSP VQEFTVSKDLATISGLKPGVDYTITVYAFNGSSYYTFGISINYR T
332	ATI_1422_F04 core	EVVAATPTSLLISWSIPSYFISYRITYGETGGNSPVQEFTVYKN YATISGLKPGVDYTITVYASEGIMFYNISINYRT
333	ATI_1422_F04 BC loop	SIPSYFIS
334	ATI_1422_F04 DE loop	YKNY
335	ATI_1422_F04 FG loop	SEGIMFYN
336	ATI_1422_F04 w/ N leader	GVSDVPRDLEVVAATPTSLLISWSIPSYFISYRITYGETGGNSP VQEFTVYKNYATISGLKPGVDYTITVYASEGIMFYNISINYRT
337	ATI_1422_F04 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWSIPSYFISYRITYGETGGNSP VQEFTVYKNYATISGLKPGVDYTITVYASEGIMFYNISINYRTH HHHHH
338	ATI_1422_F04 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWSIPSYFISYRITYGETGGNSP VQEFTVYKNYATISGLKPGVDYTITVYASEGIMFYNISINYRTE IDKPSQ
339	ATI_1422_F04 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWSIPSYFISYRITYGETGGNSP VQEFTVYKNYATISGLKPGVDYTITVYASEGIMFYNISINYRTE IDKPSQHHHHHH
340	ATI_1422_F04 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWSIPSYFISYRITYGETGGNSP VQEFTVYKNYATISGLKPGVDYTITVYASEGIMFYNISINYRTP C
341	ATI_1422_F04 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWSIPSYFISYRITYGETGGNSP VQEFTVYKNYATISGLKPGVDYTITVYASEGIMFYNISINYRTP CHHHHHH
342	ATI_1422_F04-full length	MGVSDVPRDLEVVAATPTSLLISWSIPSYFISYRITYGETGGNS PVQEFTVYKNYATISGLKPGVDYTITVYASEGIMFYNISINYRT EIDKPSQHHHHHH
343	ATI_1422_F05 core	EVVAATPTSLLISWPYPRGPYVEYRITYGETGGNSPVQEFTVYP GQATISGLKPGVDYTITVYAYTSGYVISINYRT
344	ATI_1422_F05 BC loop	PYPRGPYVF
345	ATI_1422_F05 DE loop	YPGQ
346	ATI_1422_F05 FG loop	YTSGYV
347	ATI_1422_F05 w/ N leader	GVSDVPRDLEVVAATPTSLLISWPYPRGPYVEYRITYGETGGNS PVQEFTVYPGQATISGLKPGVDYTITVYAYTSGYVISINYRT
348	ATI_1422_F05 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWPYPRGPYVEYRITYGETGGNS PVQEFTVYPGQATISGLKPGVDYTITVYAYTSGYVISINYRTEI DKPSQHHHHHH
349	ATI_1422_F05 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWPYPRGPYVEYRITYGETGGNS PVQEFTVYPGQATISGLKPGVDYTITVYAYTSGYVISINYRTEI DKPSQ
350	ATI_1422_F05 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWPYPRGPYVEYRITYGETGGNS PVQEFTVYPGQATISGLKPGVDYTITVYAYTSGYVISINYRTEI DKPSQHHHHHH
351	ATI_1422_F05 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWPYPRGPYVEYRITYGETGGNS PVQEFTVYPGQATISGLKPGVDYTITVYAYTSGYVISINYRTPC
352	ATI_1422_F05 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWPYPRGPYVEYRITYGETGGNS PVQEFTVYPGQATISGLKPGVDYTITVYAYTSGYVISINYRTPC HHHHHH

TABLE 3-continued

SEQUENCE LISTING

SEQ ID	DESCRIPTION	SEQUENCE
353	ATI_1422_F05-full length	MGVSDVPRDLEVVAATPTSLLISWPYPRGPYVEYRITYGETGGN SPVQEFTVYPGQATISGLKPGVDYTITVYAYTSGYVISINYRTE IDKPSQHHHHHH
354	ATI_1422_H04 core	EVVAATPTSLLISWYLPSYYVQYRITYGETGGNSPVQEFTVKSY NATISGLKPGVDYTITVYARMGVYYLSYSISINYRT
355	ATI_1422_H04 BC loop	YLPSYYVQ
356	ATI_1422_H04 DE loop	KSYN
357	ATI_1422_H04 FG loop	RMGVYYLSYS
358	ATI_1422_H04 w/ N leader	GVSDVPRDLEVVAATPTSLLISWYLPSYYVQYRITYGETGGNSP VQEFTVKSYNATISGLKPGVDYTITVYARMGVYYLSYSISINYR T
359	ATI_1422_H04 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWYLPSYYVQYRITYGETGGNSP VQEFTVKSYNATISGLKPGVDYTITVYARMGVYYLSYSISINYR THHHHHH
360	ATI_1422_H04 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWYLPSYYVQYRITYGETGGNSP VQEFTVKSYNATISGLKPGVDYTITVYARMGVYYLSYSISINYR TEIDKPSQ
361	ATI_1422_H04 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWYLPSYYVQYRITYGETGGNSP VQEFTVKSYNATISGLKPGVDYTITVYARMGVYYLSYSISINYR TEIDKPSQHHHHHH
362	ATI_1422_H04 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWYLPSYYVQYRITYGETGGNSP VQEFTVKSYNATISGLKPGVDYTITVYARMGVYYLSYSISINYR TPC
363	ATI_1422_H04 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWYLPSYYVQYRITYGETGGNSP VQEFTVKSYNATISGLKPGVDYTITVYARMGVYYLSYSISINYR TPCHHHHHH
364	ATI_1422_H04-full length	MGVSDVPRDLEVVAATPTSLLISWYLPSYYVQYRITYGETGGNS PVQEFTVKSYNATISGLKPGVDYTITVYARMGVYYLSYSISINY RTEIDKPSQHHHHHH
365	ATI_1422_H05 core	EVVAATPTSLLISWQGQLSPSFYRITYGETGGNSPVQEFTVVAG MATISGLKPGVDYTITVYATSDVYFYSISINYRT
366	ATI_1422_H05 BC loop	QGQLSPSF
367	ATI_1422_H05 DE loop	VAGM
368	ATI_1422_H05 FG loop	TSDVYFYS
369	ATI_1422_H05 w/ N leader	GVSDVPRDLEVVAATPTSLLISWQGQLSPSFYRITYGETGGNSP VQEFTVVAGMATISGLKPGVDYTITVYATSDVYFYSISINYRT
370	ATI_1422_H05 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWQGQLSPSFYRITYGETGGNSP VQEFTVVAGMATISGLKPGVDYTITVYATSDVYFYSISINYRTH HHHHH
371	ATI_1422_H05 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWQGQLSPSFYRITYGETGGNSP VQEFTVVAGMATISGLKPGVDYTITVYATSDVYFYSISINYRTE IDKPSQ
372	ATI_1422_H05 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWQGQLSPSFYRITYGETGGNSP VQEFTVVAGMATISGLKPGVDYTITVYATSDVYFYSISINYRTE IDKPSQHHHHHH
373	ATI_1422_H05 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWQGQLSPSFYRITYGETGGNSP VQEFTVVAGMATISGLKPGVDYTITVYATSDVYFYSISINYRTP C

TABLE 3-continued

SEQUENCE LISTING		
SEQ ID	DESCRIPTION	SEQUENCE
374	ATI_1422_H05 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWQGQLSPSFYRITYGETGGNSPVQEFTVVAGMATISGLKPGVDYTITVYATSDVYFYSISINYRTPCHHHHHH
375	-full length	MGVSDVPRDLEVVAATPTSLLISWQGQLSPSFYRITYGETGGNSPVQEFTVVAGMATISGLKPGVDYTITVYATSDVYFYSISINYRTEIDKPSQHHHHHH
376	ATI_1422_G05 core	EVVAATPTSLLISWIAPYYSVIYRITYGETGGNSPVQEFTVTGSGYATISGLKPGVDYTITVYATYCASVASYAFISINYRT
377	ATI_1422_G05 BC loop	IAPYYSVI
378	ATI_1422_G05 DE loop	TGSGY
379	ATI_1422_G05 FG loop	TYCASVASYAF
380	ATI_1422_G05 w/ N leader	GVSDVPRDLEVVAATPTSLLISWIAPYYSVIYRITYGETGGNSPVQEFTVTGSGYATISGLKPGVDYTITVYATYCASVASYAFISINYRT
381	ATI_1422_G05 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWIAPYYSVIYRITYGETGGNSPVQEFTVTGSGYATISGLKPGVDYTITVYATYCASVASYAFISINYRTHHHHHH
382	ATI_1422_G05 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWIAPYYSVIYRITYGETGGNSPVQEFTVTGSGYATISGLKPGVDYTITVYATYCASVASYAFISINYRTEIDKPSQ
383	ATI_1422_G05 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWIAPYYSVIYRITYGETGGNSPVQEFTVTGSGYATISGLKPGVDYTITVYATYCASVASYAFISINYRTEIDKPSQHHHHHH
384	ATI_1422_G05 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWIAPYYSVIYRITYGETGGNSPVQEFTVTGSGYATISGLKPGVDYTITVYATYCASVASYAFISINYRTPC
385	ATI_1422_G05 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWIAPYYSVIYRITYGETGGNSPVQEFTVTGSGYATISGLKPGVDYTITVYATYCASVASYAFISINYRTPCHHHHHH
386	ATI_1422_G05-full length	MGVSDVPRDLEVVAATPTSLLISWIAPYYSVIYRITYGETGGNSPVQEFTVTGSGYATISGLKPGVDYTITVYATYCASVASYAFISINYRTEIDKPSQHHHHHH
387	ATI_1760_C02 core	EVVAATPTSLLISWIAPYYSVIYRITYGETGGNSPVQEFTVPGSAYATISGLKPGVDYTITVYASSGASIAAYAFISINYRT
388	ATI_1760_C02 BC loop	IAPYYSVI
389	ATI_1760_C02 DE loop	PGSAY
390	ATI_1760_C02 FG loop	sSGASIAAYAF
391	ATI_1760_C02 w/ N leader	GVSDVPRDLEVVAATPTSLLISWIAPYYSVIYRITYGETGGNSPVQEFTVPGSAYATISGLKPGVDYTITVYASSGASIAAYAFISINYRT
392	ATI_1760_C02 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWIAPYYSVIYRITYGETGGNSPVQEFTVPGSAYATISGLKPGVDYTITVYASSGASIAAYAFISINYRTHHHHHH
393	ATI_1760_C02 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWIAPYYSVIYRITYGETGGNSPVQEFTVPGSAYATISGLKPGVDYTITVYASSGASIAAYAFISINYRTEIDKPSQ
394	ATI_1760_C02 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWIAPYYSVIYRITYGETGGNSPVQEFTVPGSAYATISGLKPGVDYTITVYASSGASIAAYAFISINYRTEIDKPSQHHHHHH

TABLE 3-continued

SEQ ID	DESCRIPTION	SEQUENCE
395	ATI_1760_C02 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWIAPYYSVIYRITYGETGGNSPVQEFTVPGSAYATISGLKPGVDYTITVYASSGASIAAYAFISINYRTPC
396	ATI_1760_C02 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWIAPYYSVIYRITYGETGGNSPVQEFTVPGSAYATISGLKPGVDYTITVYASSGASIAAYAFISINYRTPCHHHHHH
397	ATI_1760_C02-full length	MGVSDVPRDLEVVAATPTSLLISWIAPYYSVIYRITYGETGGNSPVQEFTVPGSAYATISGLKPGVDYTITVYASSGASIAAYAFISINYRTEIDKPSQHHHHHH
398	ATI_1760_E01 core	EVVAATPTSLLISWIAPYYSVKYRITYGETGGNSPVQEFTVAGADYATISGLKPGVDYTITVYATYGASIASYAFISINYRT
399	ATI_1760_E01 BC loop	IAPYYSVK
400	ATI_1760_E01 DE loop	AGADY
401	ATI_1760_E01 FG loop	TYGASIASYAF
402	ATI_1760_E01 w/ N leader	GVSDVPRDLEVVAATPTSLLISWIAPYYSVKYRITYGETGGNSPVQEFTVAGADYATISGLKPGVDYTITVYATYGASIASYAFISINYRT
403	ATI_1760_E01 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWIAPYYSVKYRITYGETGGNSPVQEFTVAGADYATISGLKPGVDYTITVYATYGASIASYAFISINYRTHHHHHH
404	ATI_1760_E01 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWIAPYYSVKYRITYGETGGNSPVQEFTVAGADYATISGLKPGVDYTITVYATYGASIASYAFISINYRTEIDKPSQ
405	ATI_1760_E01 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWIAPYYSVKYRITYGETGGNSPVQEFTVAGADYATISGLKPGVDYTITVYATYGASIASYAFISINYRTEIDKPSQHHHHHH
406	ATI_1760_E01 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWIAPYYSVKYRITYGETGGNSPVQEFTVAGADYATISGLKPGVDYTITVYATYGASIASYAFISINYRTPC
407	ATI_1760_E01 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWIAPYYSVKYRITYGETGGNSPVQEFTVAGADYATISGLKPGVDYTITVYATYGASIASYAFISINYRTPCHHHHHH
408	ATI_1760 E01-full length	MGVSDVPRDLEVVAATPTSLLISWIAPYYSVKYRITYGETGGNSPVQEFTVAGADYATISGLKPGVDYTITVYATYGASIASYAFISINYRTEIDKPSQHHHHHH
409	ATI_1760_F01 core	EVVAATPTSLLISWIAPYYAVMYRITYGETGGNSPVQEFTVPGGGYATISGLKPGVDYTITVYATGGASIAAYAFISINYRT
410	ATI_1760_F01 BC loop	IAPYYAVM
411	ATI_1760_F01 DE loop	PGGGY
412	ATI_1760_F01 FG loop	TGGASIAAYAF
413	ATI_1760_F01 w/ N leader	GVSDVPRDLEVVAATPTSLLISWIAPYYAVMYRITYGETGGNSPVQEFTVPGGGYATISGLKPGVDYTITVYATGGASIAAYAFISINYRT
414	ATI_1760_F01 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWIAPYYAVMYRITYGETGGNSPVQEFTVPGGGYATISGLKPGVDYTITVYATGGASIAAYAFISINYRTHHHHHH
415	ATI_1760_F01 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWIAPYYAVMYRITYGETGGNSPVQEFTVPGGGYATISGLKPGVDYTITVYATGGASIAAYAFISINYRTEIDKPSQ

TABLE 3-continued

SEQUENCE LISTING

SEQ ID	DESCRIPTION	SEQUENCE
416	ATI_1760_F01 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWIAPYYAVMYRITYGETGGNSPVQEFTVPGGGYATISGLKPGVDYTITVYATGGASIAAYAFISINYRTEIDKPSQHHHHHH
417	ATI_1760_F01 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWIAPYYAVMYRITYGETGGNSPVQEFTVPGGGYATISGLKPGVDYTITVYATGGASIAAYAFISINYRTPC
418	ATI_1760_F01 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWIAPYYAVMYRITYGETGGNSPVQEFTVPGGGYATISGLKPGVDYTITVYATGGASIAAYAFISINYRTPCHHHHHH
419	ATI_1760_F01-full length	MGVSDVPRDLEVVAATPTSLLISWIAPYYAVMYRITYGETGGNSPVQEFTVPGGGYATISGLKPGVDYTITVYATGGASIAAYAFISINYRTEIDKPSQHHHHHH
420	ATI_1494_D03 core	EVVAATPTSLLISWSYPSYHLYRITYGETGGNSPVQEFTVHIDYATISGLKPGVDYTITVYAQSPPYDIYYEISINYRT
421	ATI_1494_D03 BC loop	SYPSYHL
422	ATI_1494_D03 DE loop	HIDY
423	ATI_1494_D03 FG loop	QSPPYDIYYE
424	ATI_1494_D03 w/ N leader	GVSDVPRDLEVVAATPTSLLISWSYPSYHLYRITYGETGGNSPVQEFTVHIDYATISGLKPGVDYTITVYAQSPPYDIYYEISINYRT
425	ATI_1494_D03 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWSYPSYHLYRITYGETGGNSPVQEFTVHIDYATISGLKPGVDYTITVYAQSPPYDIYYEISINYRTHHHHHH
426	ATI_1494_D03 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWSYPSYHLYRITYGETGGNSPVQEFTVHIDYATISGLKPGVDYTITVYAQSPPYDIYYEISINYRTEIDKPSQ
427	ATI_1494_D03 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWSYPSYHLYRITYGETGGNSPVQEFTVHIDYATISGLKPGVDYTITVYAQSPPYDIYYEISINYRTEIDKPSQHHHHHH
428	ATI_1494_D03 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWSYPSYHLYRITYGETGGNSPVQEFTVHIDYATISGLKPGVDYTITVYAQSPPYDIYYEISINYRTPC
429	ATI_1494_D03 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWSYPSYHLYRITYGETGGNSPVQEFTVHIDYATISGLKPGVDYTITVYAQSPPYDIYYEISINYRTPCHHHHHH
430	ATI_1494_D03-full length	MGVSDVPRDLEVVAATPTSLLISWSYPSYHLYRITYGETGGNSPVQEFTVHIDYATISGLKPGVDYTITVYAQSPPYDIYYEISINYRTEIDKPSQHHHHHH
431	ATI_1494_D04 core	EVVAATPTSLLISWMESSSNSYRITYGETGGNSPVQEFTVPDQLATISGLKPGVDYTITVYALANAHYMRVGISINYRT
432	ATI_1494_D04 BC loop	MESSSNS
433	ATI_1494_D04 DE loop	PDQL
434	ATI_1494_D04 FG loop	LANAHYMRVG
435	ATI_1494_D04 w/ N leader	GVSDVPRDLEVVAATPTSLLISWMESSSNSYRITYGETGGNSPVQEFTVPDQLATISGLKPGVDYTITVYALANAHYMRVGISINYRT
436	ATI_1494_D04 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWMESSSNSYRITYGETGGNSPVQEFTVPDQLATISGLKPGVDYTITVYALANAHYMRVGISINYRTHHHHHH
437	ATI_1494_D04 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWMESSSNSYRITYGETGGNSPVQEFTVPDQLATISGLKPGVDYTITVYALANAHYMRVGISINYRTEIDKPSQ

TABLE 3-continued

SEQ ID	DESCRIPTION	SEQUENCE
438	ATI_1494_D04 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWMESSSNSYRITYGETGGNSPV QEFTVPDQLATISGLKPGVDYTITVYALANAHYMRVGISINYRT EIDKPSQHHHHHH
439	ATI_1494_D04 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWMESSSNSYRITYGETGGNSPV QEFTVPDQLATISGLKPGVDYTITVYALANAHYMRVGISINYRT PC
440	ATI_1494_D04 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWMESSSNSYRITYGETGGNSPV QEFTVPDQLATISGLKPGVDYTITVYALANAHYMRVGISINYRT PCHHHHHH
441	ATI_1494_D04-full length	MGVSDVPRDLEVVAATPTSLLISWMESSSNSYRITYGETGGNSP VQEFTVPDQLATISGLKPGVDYTITVYALANAHYMRVGISINYR TEIDKPSQHHHHHH
442	ATI_1523_A08 core	EVVAATPTSLLISWISVQTYXYRITYGETGGNSPVQEFTVPDQS ATISGLKPGVDYTITVYALEKAHYYRQNISINYRT
443	ATI_1523_A08 BC loop	ISVQTYX
444	ATI_1523_A08 DE loop	PDQS
445	ATI_1523_A08 FG loop	LEKAHYYRQN
446	ATI_1523_A08 w/ N leader	GVSDVPRDLEVVAATPTSLLISWISVQTYXYRITYGETGGNSPV QEFTVPDQSATISGLKPGVDYTITVYALEKAHYYRQNISINYRT
447	ATI_1523_A08 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWISVQTYXYRITYGETGGNSPV QEFTVPDQSATISGLKPGVDYTITVYALEKAHYYRQNISINYRT HHHHHH
448	ATI_1523_A08 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWISVQTYXYRITYGETGGNSPV QEFTVPDQSATISGLKPGVDYTITVYALEKAHYYRQNISINYRT EIDKPSQ
449	ATI_1523_A08 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWISVQTYXYRITYGETGGNSPV QEFTVPDQSATISGLKPGVDYTITVYALEKAHYYRQNISINYRT EIDKPSQHHHHHH
450	ATI_1523_A08 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWISVQTYXYRITYGETGGNSPV QEFTVPDQSATISGLKPGVDYTITVYALEKAHYYRQNISINYRT PC
451	ATI_1523_A08 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWISVQTYXYRITYGETGGNSPV QEFTVPDQSATISGLKPGVDYTITVYALEKAHYYRQNISINYRT PCHHHHHH
452	ATI_1523 A08-full length	MGVSDVPRDLEVVAATPTSLLISWISVQTYXYRITYGETGGNSP VQEFTVPDQSATISGLKPGVDYTITVYALEKAHYYRQNISINYR TEIDKPSQHHHHHH
453	ATI_1523_B10 core	EVVAATPTSLLISWVYHYDXQYRITYGETGGNSPVQEFTVPDQK ATISGLKPGVDYTITVYALSEAHHKRDSISINYRT
454	ATI_1523_B10 BC loop	VYHYDXQ
455	ATI_1523_B10 DE loop	PDQK
456	ATI_1523_B10 FG loop	LSEAHHKRDS
457	ATI_1523_B10 w/ N leader	GVSDVPRDLEVVAATPTSLLISWVYHYDXQYRITYGETGGNSPV QEFTVPDQKATISGLKPGVDYTITVYALSEAHHKRDSISINYRT
458	ATI_1523_B10 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWVYHYDXQYRITYGETGGNSPV QEFTVPDQKATISGLKPGVDYTITVYALSEAHHKRDSISINYRT HHHHHH

TABLE 3-continued

SEQ ID	DESCRIPTION	SEQUENCE
459	ATI_1523_B10 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWVYHYDXQYRITYGETGGNSPVQEFTVPDQKATISGLKPGVDYTITVYALSEAHHKRDSISINYRTEIDKPSQ
460	ATI_1523_B10 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWVYHYDXQYRITYGETGGNSPVQEFTVPDQKATISGLKPGVDYTITVYALSEAHHKRDSISINYRTEIDKPSQHHHHHH
461	ATI_1523_B10 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWVYHYDXQYRITYGETGGNSPVQEFTVPDQKATISGLKPGVDYTITVYALSEAHHKRDSISINYRTPC
462	ATI_1523_B10 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWVYHYDXQYRITYGETGGNSPVQEFTVPDQKATISGLKPGVDYTITVYALSEAHHKRDSISINYRTPCHHHHHH
463	ATI_1523_B10-full length	MGVSDVPRDLEVVAATPTSLLISWVYHYDXQYRITYGETGGNSPVQEFTVPDQKATISGLKPGVDYTITVYALSEAHHKRDSISINYRTEIDKPSQHHHHHH
464	ATI_1523_C07 core	EVVAATPTSLLISWRMHTDPDYRITYGETGGNSPVQEFTVPDQEATISGLKPGVDYTITVYAIQTAHYYRINISINYRT
465	ATI_1523_C07 BC loop	RMHTDPD
466	ATI_1523_C07 DE loop	PDQE
467	ATI_1523_C07 FG loop	IQTAHYYRIN
468	ATI_1523_C07 w/ N leader	GVSDVPRDLEVVAATPTSLLISWRMHTDPDYRITYGETGGNSPVQEFTVPDQEATISGLKPGVDYTITVYAIQTAHYYRINISINYRT
469	ATI_1523_C07 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWRMHTDPDYRITYGETGGNSPVQEFTVPDQEATISGLKPGVDYTITVYAIQTAHYYRINISINYRTHHHHHH
470	ATI_1523_C07 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWRMHTDPDYRITYGETGGNSPVQEFTVPDQEATISGLKPGVDYTITVYAIQTAHYYRINISINYRTEIDKPSQ
471	ATI_1523_C07 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWRMHTDPDYRITYGETGGNSPVQEFTVPDQEATISGLKPGVDYTITVYAIQTAHYYRINISINYRTEIDKPSQHHHHHH
472	ATI_1523_C07 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWRMHTDPDYRITYGETGGNSPVQEFTVPDQEATISGLKPGVDYTITVYAIQTAHYYRINISINYRTPC
473	ATI_1523_C07 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWRMHTDPDYRITYGETGGNSPVQEFTVPDQEATISGLKPGVDYTITVYAIQTAHYYRINISINYRTPCHHHHHH
474	ATI_1523_C07-full length	MGVSDVPRDLEVVAATPTSLLISWRMHTDPDYRITYGETGGNSPVQEFTVPDQEATISGLKPGVDYTITVYAIQTAHYYRINISINYRTEIDKPSQHHHHHH
475	ATI_1523_D07 core	EVVAATPTSLLISWENLASYQYRITYGETGGNSPVQEFTVPDVQATISGLKPGVDYTITVYALPYIHMKQRVISINYRT
476	ATI_1523_D07 BC loop	ENLASYQ
477	ATI_1523_D07 DE loop	PDVQ
478	ATI_1523_D07 FG loop	LPYIHMKQRV
479	ATI_1523_D07 w/ N leader	GVSDVPRDLEVVAATPTSLLISWENLASYQYRITYGETGGNSPVQEFTVPDVQATISGLKPGVDYTITVYALPYIHMKQRVISINYRT

TABLE 3-continued

SEQ ID	DESCRIPTION	SEQUENCE
480	ATI_1523_D07 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWENLASYQYRITYGETGGNSPV QEFTVPDVQATISGLKPGVDYTITVYALPYIHMKQRVISINYRT HHHHHH
481	ATI_1523_D07 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWENLASYQYRITYGETGGNSPV QEFTVPDVQATISGLKPGVDYTITVYALPYIHMKQRVISINYRT EIDKPSQ
482	ATI_1523_D07 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWENLASYQYRITYGETGGNSPV QEFTVPDVQATISGLKPGVDYTITVYALPYIHMKQRVISINYRT EIDKPSQHHHHHH
483	ATI_1523_D07 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWENLASYQYRITYGETGGNSPV QEFTVPDVQATISGLKPGVDYTITVYALPYIHMKQRVISINYRT PC
484	ATI_1523_D07 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWENLASYQYRITYGETGGNSPV QEFTVPDVQATISGLKPGVDYTITVYALPYIHMKQRVISINYRT PCHHHHHH
485	ATI_1523_D07-full length	MGVSDVPRDLEVVAATPTSLLISWENLASYQYRITYGETGGNSP VQEFTVPDVQATISGLKPGVDYTITVYALPYIHMKQRVISINYR TEIDKPSQHHHHHH
486	ATI_1523_D08 core	EVVAATPTSLLISWMRYYDAYYRITYGETGGNSPVQEFTVPDQS ATISGLKPGVDYTITVYALEKAHYYRQNISINYRT
487	ATI_1523_D08 BC loop	MRYYDAY
488	ATI_1523_D08 DE loop	PDQS
489	ATI_1523_D08 FG loop	LEKAHYYRQN
490	ATI_1523_D08 w/ N leader	GVSDVPRDLEVVAATPTSLLISWMRYYDAYYRITYGETGGNSPV QEFTVPDQSATISGLKPGVDYTITVYALEKAHYYRQNISINYRT
491	ATI_1523_D08 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWMRYYDAYYRITYGETGGNSPV QEFTVPDQSATISGLKPGVDYTITVYALEKAHYYRQNISINYRT HHHHHH
492	ATI_1523_D08 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWMRYYDAYYRITYGETGGNSPV QEFTVPDQSATISGLKPGVDYTITVYALEKAHYYRQNISINYRT EIDKPSQ
493	ATI_1523_D08 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWMRYYDAYYRITYGETGGNSPV QEFTVPDQSATISGLKPGVDYTITVYALEKAHYYRQNISINYRT EIDKPSQHHHHHH
494	ATI_1523_D08 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWMRYYDAYYRITYGETGGNSPV QEFTVPDQSATISGLKPGVDYTITVYALEKAHYYRQNISINYRT PC
495	ATI_1523_D08 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWMRYYDAYYRITYGETGGNSPV QEFTVPDQSATISGLKPGVDYTITVYALEKAHYYRQNISINYRT PCHHHHHH
496	ATI_1523_D08-full length	MGVSDVPRDLEVVAATPTSLLISWMRYYDAYYRITYGETGGNSP VQEFTVPDQSATISGLKPGVDYTITVYALEKAHYYRQNISINYR TEIDKPSQHHHHHH
497	ATI_1523_E08 core	EVVAATPTSLLISWHHYQHYEYRITYGETGGNSPVQEFTVPDMG ATISGLKPGVDYTITVYALEEAHSDRSSISINYRT
498	ATI_1523_E08 BC loop	HHYQHYE
499	ATI_1523_E08 DE loop	PDMG
500	ATI_1523_E08 FG loop	LEEAHSDRSS

TABLE 3-continued

SEQUENCE LISTING

SEQ ID	DESCRIPTION	SEQUENCE
501	ATI_1523_E08 w/ N leader	GVSDVPRDLEVVAATPTSLLISWHHYQHYEYRITYGETGGNSPV QEFTVPDMGATISGLKPGVDYTITVYALEEAHSDRSSISINYRT
502	ATI_1523_E08 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWHHYQHYEYRITYGETGGNSPV QEFTVPDMGATISGLKPGVDYTITVYALEEAHSDRSSISINYRT HHHHHH
503	ATI_1523_E08 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWHHYQHYEYRITYGETGGNSPV QEFTVPDMGATISGLKPGVDYTITVYALEEAHSDRSSISINYRT EIDKPSQ
504	ATI_1523_E08 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWHHYQHYEYRITYGETGGNSPV QEFTVPDMGATISGLKPGVDYTITVYALEEAHSDRSSISINYRT EIDKPSQHHHHHH
505	ATI_1523_E08 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWHHYQHYEYRITYGETGGNSPV QEFTVPDMGATISGLKPGVDYTITVYALEEAHSDRSSISINYRT PC
506	ATI_1523_E08 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWHHYQHYEYRITYGETGGNSPV QEFTVPDMGATISGLKPGVDYTITVYALEEAHSDRSSISINYRT PCHHHHHH
507	ATI_1523_E08-full length	MGVSDVPRDLEVVAATPTSLLISWHHYQHYEYRITYGETGGNSP VQEFTVPDMGATISGLKPGVDYTITVYALEEAHSDRSSISINYR TEIDKPSQHHHHHH
508	ATI_1523_F01 core	EVVAATPTSLLISWYKPSTIVTYRITYGETGGNSPVQEFTVYGY NATISGLKPGVDYTITVYAVHGVRFISINYRT
509	ATI_1523_F01 BC loop	YKPSTIVT
510	ATI_1523_F01 DE loop	YGYN
511	ATI_1523_F01 FG loop	VHGVRF
512	ATI_1523_F01 w/ N leader	GVSDVPRDLEVVAATPTSLLISWYKPSTIVTYRITYGETGGNSP VQEFTVYGYNATISGLKPGVDYTITVYAVHGVRFISINYRT
513	ATI_1523_F01 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWYKPSTIVTYRITYGETGGNSP VQEFTVYGYNATISGLKPGVDYTITVYAVHGVRFISINYRTHHH HHH
514	ATI_1523_F01 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWYKPSTIVTYRITYGETGGNSP VQEFTVYGYNATISGLKPGVDYTITVYAVHGVRFISINYRTEID KPSQ
515	ATI_1523_F01 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWYKPSTIVTYRITYGETGGNSP VQEFTVYGYNATISGLKPGVDYTITVYAVHGVRFISINYRTEID KPSQHHHHHH
516	ATI_1523_F01 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWYKPSTIVTYRITYGETGGNSP VQEFTVYGYNATISGLKPGVDYTITVYAVHGVRFISINYRTPC
517	ATI_1523_F01 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWYKPSTIVTYRITYGETGGNSP VQEFTVYGYNATISGLKPGVDYTITVYAVHGVRFISINYRTPCH HHHHH
518	ATI_1523_F01-full length	MGVSDVPRDLEVVAATPTSLLISWYKPSTIVTYRITYGETGGNS PVQEFTVYGYNATISGLKPGVDYTITVYAVHGVRFISINYRTEI DKPSQHHHHHH
519	ATI_1523_F04 core	EVVAATPTSLLISWGGSLSPTFYRITYGETGGNSPVQEFTVTYQ GATISGLKPGVDYTITVYATEGIVYYQISINYRT
520	ATI_1523_F04 BC loop	GGSLSPTF
521	ATI_1523_F04 DE loop	TYQG
522	ATI_1523_F04 FG loop	TEGIVYYQ

TABLE 3-continued

SEQUENCE LISTING

SEQ ID	DESCRIPTION	SEQUENCE
523	ATI_1523_F04 w/ N leader	GVSDVPRDLEVVAATPTSLLISWGGSLSPTFYRITYGETGGNSP VQEFTVTYQGATISGLKPGVDYTITVYATEGIVYYQISINYRT
524	ATI_1523_F04 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWGGSLSPTFYRITYGETGGNSP VQEFTVTYQGATISGLKPGVDYTITVYATEGIVYYQISINYRTH HHHHH
525	ATI_1523_F04 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWGGSLSPTFYRITYGETGGNSP VQEFTVTYQGATISGLKPGVDYTITVYATEGIVYYQISINYRTE IDKPSQ
526	ATI_1523_F04 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWGGSLSPTFYRITYGETGGNSP VQEFTVTYQGATISGLKPGVDYTITVYATEGIVYYQISINYRTE IDKPSQHHHHHH
527	ATI_1523_F04 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWGGSLSPTFYRITYGETGGNSP VQEFTVTYQGATISGLKPGVDYTITVYATEGIVYYQISINYRTP C
528	ATI_1523_F04 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWGGSLSPTFYRITYGETGGNSP VQEFTVTYQGATISGLKPGVDYTITVYATEGIVYYQISINYRTP CHHHHHH
529	ATI_1523_F04-full length	MGVSDVPRDLEVVAATPTSLLISWGGSLSPTFYRITYGETGGNS PVQEFTVTYQGATISGLKPGVDYTITVYATEGIVYYQISINYRT EIDKPSQHHHHHH
530	ATI_1523_F08 core	EVVAATPTSLLISWVYHYDAQYRITYGETGGNSPVQEFTVPDQK ATISGLKPGVDYTITVYALPRAHMDRSHISINYRT
531	ATI_1523_F08 BC loop	VYHYDAQ
532	ATI_1523_F08 DE loop	PDQK
533	ATI_1523_F08 FG loop	LPRAHMDRSH
534	ATI_1523_F08 w/ N leader	GVSDVPRDLEVVAATPTSLLISWVYHYDAQYRITYGETGGNSPV QEFTVPDQKATISGLKPGVDYTITVYALPRAHMDRSHISINYRT
535	ATI_1523_F08 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWVYHYDAQYRITYGETGGNSPV QEFTVPDQKATISGLKPGVDYTITVYALPRAHMDRSHISINYRT HHHHHH
536	ATI_1523_F08 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWVYHYDAQYRITYGETGGNSPV QEFTVPDQKATISGLKPGVDYTITVYALPRAHMDRSHISINYRT EIDKPSQ
537	ATI_1523_F08 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWVYHYDAQYRITYGETGGNSPV QEFTVPDQKATISGLKPGVDYTITVYALPRAHMDRSHISINYRT EIDKPSQHHHHHH
538	ATI_1523_F08 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWVYHYDAQYRITYGETGGNSPV QEFTVPDQKATISGLKPGVDYTITVYALPRAHMDRSHISINYRT PC
539	ATI_1523_F08 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWVYHYDAQYRITYGETGGNSPV QEFTVPDQKATISGLKPGVDYTITVYALPRAHMDRSHISINYRT PCHHHHHH
540	ATI_1523_F08-full length	MGVSDVPRDLEVVAATPTSLLISWVYHYDAQYRITYGETGGNSP VQEFTVPDQKATISGLKPGVDYTITVYALPRAHMDRSHISINYR TEIDKPSQHHHHHH
541	ATI_1523_G06 core	EVVAATPTSLLISWRIKSYHKYRITYGETGGNSPVQEFTVRSYA ATISGLKPGVDYTITVYAIMEETHLAYAISINYRT
542	ATI_1523_G06 BC loop	RIKSYHK
543	ATI_1523_G06 DE loop	RSYA
544	ATI_1523_G06 FG loop	IMEETHLAYA

TABLE 3-continued

SEQUENCE LISTING

SEQ ID	DESCRIPTION	SEQUENCE
545	ATI_1523_G06 w/ N leader	GVSDVPRDLEVVAATPTSLLISWRIKSYHKYRITYGETGGNSPVQEFTVRSYAATISGLKPGVDYTITVYAIMEETHLAYAISINYRT
546	ATI_1523_G06 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWRIKSYHKYRITYGETGGNSPVQEFTVRSYAATISGLKPGVDYTITVYAIMEETHLAYAISINYRTHHHHHH
547	ATI_1523_G06 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWRIKSYHKYRITYGETGGNSPVQEFTVRSYAATISGLKPGVDYTITVYAIMEETHLAYAISINYRTEIDKPSQ
548	ATI_1523_G06 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWRIKSYHKYRITYGETGGNSPVQEFTVRSYAATISGLKPGVDYTITVYAIMEETHLAYAISINYRTEIDKPSQHHHHHH
549	ATI_1523_G06 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWRIKSYHKYRITYGETGGNSPVQEFTVRSYAATISGLKPGVDYTITVYAIMEETHLAYAISINYRTPC
550	ATI_1523_G06 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWRIKSYHKYRITYGETGGNSPVQEFTVRSYAATISGLKPGVDYTITVYAIMEETHLAYAISINYRTPCHHHHHH
551	ATI_1523_G06-full length	MGVSDVPRDLEVVAATPTSLLISWRIKSYHKYRITYGETGGNSPVQEFTVRSYAATISGLKPGVDYTITVYAIMEETHLAYAISINYRTEIDKPSQHHHHHH
552	ATI_1523_G07 core	EVVAATPTSLLISWVYPQADDYRITYGETGGNSPVQEFTVPDQNATISGLKPGVDYTITVYALAEAHLVRIYISINYRT
553	ATI_1523_G07 BC loop	VYPQADD
554	ATI_1523_G07 DE loop	PDQN
555	ATI_1523_G07 FG loop	LAEAHLVRIY
556	ATI_1523_G07 w/ N leader	GVSDVPRDLEVVAATPTSLLISWVYPQADDYRITYGETGGNSPVQEFTVPDQNATISGLKPGVDYTITVYALAEAHLVRIYISINYRT
557	ATI_1523_G07 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWVYPQADDYRITYGETGGNSPVQEFTVPDQNATISGLKPGVDYTITVYALAEAHLVRIYISINYRTHHHHHH
558	ATI_1523_G07 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWVYPQADDYRITYGETGGNSPVQEFTVPDQNATISGLKPGVDYTITVYALAEAHLVRIYISINYRTEIDKPSQ
559	ATI_1523_G07 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWVYPQADDYRITYGETGGNSPVQEFTVPDQNATISGLKPGVDYTITVYALAEAHLVRIYISINYRTEIDKPSQHHHHHH
560	ATI_1523_G07 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWVYPQADDYRITYGETGGNSPVQEFTVPDQNATISGLKPGVDYTITVYALAEAHLVRIYISINYRTPC
561	ATI_1523_G07 w/ N leader and modified C-terminus including PC +3 his tag	GVSDVPRDLEVVAATPTSLLISWVYPQADDYRITYGETGGNSPVQEFTVPDQNATISGLKPGVDYTITVYALAEAHLVRIYISINYRTPCHHHHHH
562	ATI_1523_G07-full length	MGVSDVPRDLEVVAATPTSLLISWVYPQADDYRITYGETGGNSPVQEFTVPDQNATISGLKPGVDYTITVYALAEAHLVRIYISINYRTEIDKPSQHHHHHH
563	ATI_1523_H07 core	EVVAATPTSLLISWVYHYDAXYRITYGETGGNSPVQEFTVPDQKATISGLKPGVDYTITVYALSEAHHKRDSISINYRT
564	ATI_1523_H07 BC loop	VYHYDAX
565	ATI_1523_H07 DE loop	PDQK

TABLE 3-continued

SEQUENCE LISTING		
SEQ ID	DESCRIPTION	SEQUENCE
566	ATI_1523_H07 FG loop	LSEAHHKRDS
567	ATI_1523_H07 w/ N leader	GVSDVPRDLEVVAATPTSLLISWVYHYDAXYRITYGETGGNSPV QEFTVPDQKATISGLKPGVDYTITVYALSEAHHKRDSISINYRT
568	ATI_1523_H07 w/ N leader + his tag	GVSDVPRDLEVVAATPTSLLISWVYHYDAXYRITYGETGGNSPV QEFTVPDQKATISGLKPGVDYTITVYALSEAHHKRDSISINYRT HHHHHH
569	ATI_1523_H07 w/ N leader and C tail	GVSDVPRDLEVVAATPTSLLISWVYHYDAXYRITYGETGGNSPV QEFTVPDQKATISGLKPGVDYTITVYALSEAHHKRDSISINYRT EIDKPSQ
570	ATI_1523_H07 w/ N leader and C tail + his tag	GVSDVPRDLEVVAATPTSLLISWVYHYDAXYRITYGETGGNSPV QEFTVPDQKATISGLKPGVDYTITVYALSEAHHKRDSISINYRT EIDKPSQHHHHHH
571	ATI_1523_H07 w/ N leader and modified C-terminus including PC	GVSDVPRDLEVVAATPTSLLISWVYHYDAXYRITYGETGGNSPV QEFTVPDQKATISGLKPGVDYTITVYALSEAHHKRDSISINYRT PC
572	ATI_1523_H07 w/ N leader and modified C-terminus including PC + his tag	GVSDVPRDLEVVAATPTSLLISWVYHYDAXYRITYGETGGNSPV QEFTVPDQKATISGLKPGVDYTITVYALSEAHHKRDSISINYRT PCHHHHHH
573	ATI_1523_H07-full length	GVSDVPRDLEVVAATPTSLLISWVYHYDAXYRITYGETGGNSPV QEFTVPDQKATISGLKPGVDYTITVYALSEAHHKRDSISINYRT EIDKPSQHHHHHH
574	N-terminal leader	MGVSDVPRDL
575	N-terminal leader	GVSDVPRDL
576	N-terminal leader	X_nEDVPRDL
577	N-terminal leader	X_nDVPRDL
578	N-terminal leader	X_nVPRDL
579	N-terminal leader	X_nPRDL
580	N-terminal leader	X_nRDL
581	N-terminal leader	X_nDL
582	N-terminal leader	MASTSG
583	N-terminal leader	METDTLLLWVLLLWVPGSTG
584	C-terminal tail	EIEK
585	C-terminal tail	EGSGC
586	C-terminal tail	EIEKPCQ
587	C-terminal tail	EIEKPSQ
588	C-terminal tail	EIEKP
589	C-terminal tail	EIEKPS
590	C-terminal tail	EIEKPC
591	C-terminal tail	EIDK
592	C-terminal tail	EIDKPCQ
593	C-terminal tail	EIDKPSQ
594	C-terminal tail	EIEPKSS

TABLE 3-continued

SEQUENCE LISTING

SEQ ID	DESCRIPTION	SEQUENCE
595	C-terminal tail	EIDKPC
596	C-terminal tail	EIDKP
597	C-terminal tail	EIDKPS
598	C-terminal tail	EIDKPSQLE
599	C-terminal tail	EIEDEDEDEDED
600	C-terminal tail	EGSGS
601	C-terminal tail	EIDKPCQLE
602	C-terminal tail	EIDKPSQHHHHHH
603	C-terminal tail	GSGCHHHHHH
604	C-terminal tail	EGSGCHHHHHH
605	C-terminal tail	PIDK
606	C-terminal tail	PIEK
607	C-terminal tail	PIDKP
608	C-terminal tail	PIEKP
609	C-terminal tail	PIDKPS
610	C-terminal tail	PIEKPS
611	C-terminal tail	PIDKPC
612	C-terminal tail	PIEKPC
613	C-terminal tail	PIDKPSQ
614	C-terminal tail	PIEKPSQ
615	C-terminal tail	PIDKPCQ
616	C-terminal tail	PIEKPCQ
617	C-terminal tail	PHHHHHH
618	C-terminal tail	PCHHHHHH
619	6X-His tag	HHHHHH
620	Human IgG1 Fc domain	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
621	Core hinge region of Fc	DKTHTCPPCPAPELLG
622	Exemplary hinge sequence	EPKSSDKTHTCPPCPAPELLGGPS
623	Exemplary hinge sequence	EPKSSDKTHTCPPCPAPELLGGSS
624	Exemplary hinge sequence	EPKSSGSTHTCPPCPAPELLGGSS
625	Exemplary hinge sequence	DKTHTCPPCPAPELLGGPS
626	Exemplary hinge sequence	DKTHTCPPCPAPELLGGSS

TABLE 3-continued

SEQUENCE LISTING

SEQ ID	DESCRIPTION	SEQUENCE
627	Fc with CH2 and CH3 regions of IgG1 for Adnectin-hinge-Fc construct	VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK
628	Fc with CH2 and CH3 regions of IgG1 for Fc-hinge-Adnectin construct	VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSP
629	Linker 1	GAGGGGSG
630	Linker 2	EPKSSD
631	Linker 3	PVGVV
632	Linker 4	ESPKAQASSVPTAQPQAEGLA
633	Linker 5	ELQLEESAAEAQDGELD
634	Linker 6	GQPDEPGGS
635	Linker 7	GGSGSGSGSGSGS
636	Linker 8	ELQLEESAAEAQEGELE
637	Linker 9	GSGSG
638	Linker 10	GSGC
639	Linker 11	AGGGGSG
640	Linker 12	GSGS
641	Linker 13	QPDEPGGS
642	Linker 14	GSGSGS
643	Linker 15	TVAAPS
644	Linker 16	KAGGGGSG
645	Linker 17	KGSGSGSGSGSGS
646	Linker 18	KQPDEPGGS
647	Linker 19	KELQLEESAAEAQDGELD
648	Linker 20	KTVAAPS
649	Linker 21	KAGGGGSGG
650	Linker 22	KGSGSGSGSGSGSG
651	Linker 23	KQPDEPGGSG
652	Linker 24	KELQLEESAAEAQDGELDG
653	Linker 25	KTVAAPSG
654	Linker 26	AGGGGSGG
655	Linker 27	AGGGGSG
656	Linker 28	GSGSGSGSGSGSG
657	Linker 29	QPDEPGGSG
658	Linker 30	TVAAPSG

TABLE 3-continued

SEQUENCE LISTING		
SEQ ID	DESCRIPTION	SEQUENCE
659	Linker 31	PSTSTST
660	Linker 32	EIDKPSQ
661	Linker 33	GSGSGSGS
662	Linker 34	GSGSGSGSGS
663	Linker 35	GSGSGSGSGSGS
664	Linker 36	GSGSGSGSGSGSGS
665	Linker 37	GGSGSGSGSGSGS
666	Linker 38	GGSGSGSGSGSGSGSG
667	Linker 39	GSEGSEGSEGSEGSE
668	Linker 40	GGSEGGSE
669	Linker 41	GGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGS
670	Linker 42	GGGGSGGGGSGGGGSGGGGSGGGGS
671	Linker 43	GGGGSGGGGSGGGGSG
672	Linker 44	GPGPGPG
673	Linker 45	GPGPGPGPGPG
674	Linker 46	PAPAPA
675	Linker 47	PAPAPAPAPAPA
676	Linker 48	PAPAPAPAPAPAPAPAPA
677	Linker 49	GSGSGSGSGSGSGSGSGSGS
678	Linker 50	GGGGSGGGGSGGGGSGGGGS

EQUIVALENTS

[0498] Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents of the specific embodiments described herein. Such equivalents are intended to be encompassed by the following claims.

SEQUENCE LISTING

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<160> NUMBER OF SEQ ID NOS: 678

<210> SEQ ID NO 1
<211> LENGTH: 94
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Full length wild-type human 10Fn3 domain

<400> SEQUENCE: 1

Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr
1               5                   10                  15

Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
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-continued

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        35                  40                  45

Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys Pro
    50                  55                  60

Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg Gly Asp
65                  70                  75                  80

Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg Thr
                85                  90


<210> SEQ ID NO 2
<211> LENGTH: 86
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Core wild-type human 10Fn3 domain

<400> SEQUENCE: 2

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala
1               5                   10                  15

Pro Ala Val Thr Val Arg Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
            20                  25                  30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Gly Ser Lys Ser Thr
        35                  40                  45

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

Tyr Ala Val Thr Gly Arg Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile
65                  70                  75                  80

Ser Ile Asn Tyr Arg Thr
                85


<210> SEQ ID NO 3
<211> LENGTH: 128
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Core 10Fn3-based scaffold with
      variable AB, BC, CD, DE, EF, and FG loops
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (6)..(20)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid;
      at least one amino acid must be present, the rest may be present
      or absent
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (26)..(40)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid;
      at least two amino acids must be present, the rest may be present
      or absent
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (46)..(60)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid;
      at least two amino acids must be present, the rest may be present
      or absent
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (64)..(78)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid;
      at least two amino acids must be present, the rest may be present
      or absent
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (85)..(99)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid;
```

-continued

at least two amino acids must be present, the rest may be present or absent
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (107)..(121)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid; at least two amino acids must be present, the rest may be present or absent

<400> SEQUENCE: 3

```
Glu Val Val Ala Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1               5                   10                  15

Xaa Xaa Xaa Xaa Leu Leu Ile Ser Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20                  25                  30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Arg Ile Thr Tyr Xaa Xaa Xaa
        35                  40                  45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Thr Val Xaa
    50                  55                  60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala Thr
65                  70                  75                  80

Ile Ser Gly Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                85                  90                  95

Xaa Xaa Xaa Tyr Thr Ile Thr Val Tyr Ala Xaa Xaa Xaa Xaa Xaa Xaa
            100                 105                 110

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile Ser Ile Asn Tyr Arg Thr
        115                 120                 125
```

<210> SEQ ID NO 4
<211> LENGTH: 103
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Core 10Fn3-based scaffold with variable BC, DE, and FG loops
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (15)..(29)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid; at least two amino acids must be present, the rest may be present or absent
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (49)..(63)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid; at least two amino acids must be present, the rest may be present or absent
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (82)..(96)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid; at least two amino acids must be present, the rest may be present or absent

<400> SEQUENCE: 4

```
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Xaa Xaa
1               5                   10                  15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Arg Ile
            20                  25                  30

Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val
        35                  40                  45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala
    50                  55                  60
```

-continued

```
Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr
65                  70                  75                  80

Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                85                  90                  95

Ile Ser Ile Asn Tyr Arg Thr
            100


<210> SEQ ID NO 5
<211> LENGTH: 86
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-968 core (aka ADX_1760_C01)

<400> SEQUENCE: 5

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Ile Ala
1               5                   10                  15

Pro Phe Tyr Asn Val Ile Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
            20                  25                  30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Gly Thr Gly Tyr Thr
        35                  40                  45

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

Tyr Ala Val Thr Asp Gly Ala Ser Ile Ala Ser Tyr Ala Phe Pro Ile
65                  70                  75                  80

Ser Ile Asn Tyr Arg Thr
                85


<210> SEQ ID NO 6
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-968 BC loop

<400> SEQUENCE: 6

Ile Ala Pro Phe Tyr Asn Val Ile Tyr
1               5


<210> SEQ ID NO 7
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-968 DE loop

<400> SEQUENCE: 7

Pro Gly Thr Gly Tyr Thr
1               5


<210> SEQ ID NO 8
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-968 FG loop

<400> SEQUENCE: 8

Val Thr Asp Gly Ala Ser Ile Ala Ser Tyr Ala Phe Pro
1               5                   10
```

-continued

```
<210> SEQ ID NO 9
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-968 w/ N leader

<400> SEQUENCE: 9

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Phe Tyr Asn Val Ile Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

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

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Asp Gly Ala
65                  70                  75                  80

Ser Ile Ala Ser Tyr Ala Phe Pro Ile Ser Ile Asn Tyr Arg Thr
                85                  90                  95


<210> SEQ ID NO 10
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-968 w/ N leader + his tag

<400> SEQUENCE: 10

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Phe Tyr Asn Val Ile Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

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

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Asp Gly Ala
65                  70                  75                  80

Ser Ile Ala Ser Tyr Ala Phe Pro Ile Ser Ile Asn Tyr Arg Thr His
                85                  90                  95

His His His His His
            100


<210> SEQ ID NO 11
<211> LENGTH: 102
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-968 w/ N leader and C tail

<400> SEQUENCE: 11

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Phe Tyr Asn Val Ile Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
```

-continued

```
        35                  40                  45

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

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Asp Gly Ala
65                  70                  75                  80

Ser Ile Ala Ser Tyr Ala Phe Pro Ile Ser Ile Asn Tyr Arg Thr Glu
                85                  90                  95

Ile Asp Lys Pro Ser Gln
            100


<210> SEQ ID NO 12
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-968 w/ N leader and C tail + his
      tag

<400> SEQUENCE: 12

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Phe Tyr Asn Val Ile Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

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

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Asp Gly Ala
65                  70                  75                  80

Ser Ile Ala Ser Tyr Ala Phe Pro Ile Ser Ile Asn Tyr Arg Thr Glu
                85                  90                  95

Ile Asp Lys Pro Ser Gln His His His His His His
            100                 105


<210> SEQ ID NO 13
<211> LENGTH: 97
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-968 w/ N leader and modified
      C-terminus including PC

<400> SEQUENCE: 13

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Phe Tyr Asn Val Ile Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

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

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Asp Gly Ala
65                  70                  75                  80

Ser Ile Ala Ser Tyr Ala Phe Pro Ile Ser Ile Asn Tyr Arg Thr Pro
                85                  90                  95

Cys
```

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<210> SEQ ID NO 14
<211> LENGTH: 103
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-968 w/ N leader and modified C-terminus including PC + his tag

<400> SEQUENCE: 14

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Phe Tyr Asn Val Ile Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

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

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Asp Gly Ala
65                  70                  75                  80

Ser Ile Ala Ser Tyr Ala Phe Pro Ile Ser Ile Asn Tyr Arg Thr Pro
                85                  90                  95

Cys His His His His His His
            100
```

<210> SEQ ID NO 15
<211> LENGTH: 109
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-968 full length

<400> SEQUENCE: 15

```
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Phe Tyr Asn Val Ile
            20                  25                  30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
        35                  40                  45

Glu Phe Thr Val Pro Gly Thr Gly Tyr Thr Ala Thr Ile Ser Gly Leu
    50                  55                  60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Asp Gly
65                  70                  75                  80

Ala Ser Ile Ala Ser Tyr Ala Phe Pro Ile Ser Ile Asn Tyr Arg Thr
                85                  90                  95

Glu Ile Asp Lys Pro Ser Gln His His His His His His
            100                 105
```

<210> SEQ ID NO 16
<211> LENGTH: 258
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-968 core (nucleotide sequence)

<400> SEQUENCE: 16

```
gaagtggttg ctgccacccc caccagcctg ctgatcagct ggatcgctcc gttctacaat     60
```

-continued

```
gtcatctatt accgcatcac ttacggcgaa acaggaggca atagccctgt ccaggagttc    120

actgtgcctg gtactggtta tacagctaca atcagcggcc ttaaacctgg cgttgattat    180

accatcactg tgtatgctgt cactgatgga gcatccattg cttcatacgc gtttccaatt    240

tccattaatt accgcaca                                                  258
```

```
<210> SEQ ID NO 17
<211> LENGTH: 288
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-968 w/ N leader (nucleotide
      sequence with N-terminal methionine)

<400> SEQUENCE: 17

atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg     60

ctgatcagct ggatcgctcc gttctacaat gtcatctatt accgcatcac ttacggcgaa    120

acaggaggca atagccctgt ccaggagttc actgtgcctg gtactggtta tacagctaca    180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cactgatgga    240

gcatccattg cttcatacgc gtttccaatt tccattaatt accgcaca                 288
```

```
<210> SEQ ID NO 18
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-968 w/ N leader and modified
      C-terminus including PC (nucleotide sequence with N-terminal
      methionine)

<400> SEQUENCE: 18

atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg     60

ctgatcagct ggatcgctcc gttctacaat gtcatctatt accgcatcac ttacggcgaa    120

acaggaggca atagccctgt ccaggagttc actgtgcctg gtactggtta tacagctaca    180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cactgatgga    240

gcatccattg cttcatacgc gtttccaatt tccattaatt accgcacacc gtgc          294
```

```
<210> SEQ ID NO 19
<211> LENGTH: 330
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-968 w/ N leader and C tail + his
      tag (nucleotide sequence with N-terminal methionine)

<400> SEQUENCE: 19

atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg     60

ctgatcagct ggatcgctcc gttctacaat gtcatctatt accgcatcac ttacggcgaa    120

acaggaggca atagccctgt ccaggagttc actgtgcctg gtactggtta tacagctaca    180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cactgatgga    240

gcatccattg cttcatacgc gtttccaatt tccattaatt accgcacaga aattgacaaa    300

ccatcccagc accatcacca ccaccactga                                     330
```

```
<210> SEQ ID NO 20
```

-continued

<211> LENGTH: 86
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-964 core (parent of
ADX_5322_A02)

<400> SEQUENCE: 20

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Ser Tyr
1   5   10   15

Asp Gly Ser Ile Glu Arg Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
            20   25   30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Pro Asp Gln Lys Thr
        35   40   45

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

Tyr Ala Val Arg Leu Glu Glu Ala His Tyr Tyr Arg Glu Ser Pro Ile
65   70   75   80

Ser Ile Asn Tyr Arg Thr
                85

<210> SEQ ID NO 21
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-964 BC loop

<400> SEQUENCE: 21

Ser Tyr Asp Gly Ser Ile Glu Arg Tyr
1   5

<210> SEQ ID NO 22
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-964 DE loop

<400> SEQUENCE: 22

Pro Pro Asp Gln Lys Thr
1   5

<210> SEQ ID NO 23
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-964 FG loop

<400> SEQUENCE: 23

Val Arg Leu Glu Glu Ala His Tyr Tyr Arg Glu Ser Pro
1   5   10

<210> SEQ ID NO 24
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-964 w/ N leader

<400> SEQUENCE: 24

-continued

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ser Tyr Asp Gly Ser Ile Glu Arg Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Pro Asp Gln Lys Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Arg Leu Glu Glu
65                  70                  75                  80

Ala His Tyr Tyr Arg Glu Ser Pro Ile Ser Ile Asn Tyr Arg Thr
                85                  90                  95


<210> SEQ ID NO 25
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-964 w/ N leader + his tag

<400> SEQUENCE: 25

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ser Tyr Asp Gly Ser Ile Glu Arg Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Pro Asp Gln Lys Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Arg Leu Glu Glu
65                  70                  75                  80

Ala His Tyr Tyr Arg Glu Ser Pro Ile Ser Ile Asn Tyr Arg Thr His
                85                  90                  95

His His His His His
            100


<210> SEQ ID NO 26
<211> LENGTH: 102
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-964 w/ N leader and C tail

<400> SEQUENCE: 26

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ser Tyr Asp Gly Ser Ile Glu Arg Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Pro Asp Gln Lys Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Arg Leu Glu Glu
65                  70                  75                  80

Ala His Tyr Tyr Arg Glu Ser Pro Ile Ser Ile Asn Tyr Arg Thr Glu
                85                  90                  95
```

-continued

```
Ile Asp Lys Pro Ser Gln
            100


<210> SEQ ID NO 27
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-964 w/ N leader and C tail + his
      tag

<400> SEQUENCE: 27

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ser Tyr Asp Gly Ser Ile Glu Arg Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Pro Asp Gln Lys Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Arg Leu Glu Glu
65                  70                  75                  80

Ala His Tyr Tyr Arg Glu Ser Pro Ile Ser Ile Asn Tyr Arg Thr Glu
                85                  90                  95

Ile Asp Lys Pro Ser Gln His His His His His His
            100                 105


<210> SEQ ID NO 28
<211> LENGTH: 97
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-964 w/ N leader and modified
      C-terminus including PC

<400> SEQUENCE: 28

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ser Tyr Asp Gly Ser Ile Glu Arg Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Pro Asp Gln Lys Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Arg Leu Glu Glu
65                  70                  75                  80

Ala His Tyr Tyr Arg Glu Ser Pro Ile Ser Ile Asn Tyr Arg Thr Pro
                85                  90                  95

Cys


<210> SEQ ID NO 29
<211> LENGTH: 103
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-964 w/ N leader and modified
      C-terminus including PC + his tag
```

-continued

<400> SEQUENCE: 29

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Ser Tyr Asp Gly Ser Ile Glu Arg Tyr
            20   25   30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35   40   45

Phe Thr Val Pro Pro Asp Gln Lys Thr Ala Thr Ile Ser Gly Leu Lys
    50   55   60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Arg Leu Glu Glu
65   70   75   80

Ala His Tyr Tyr Arg Glu Ser Pro Ile Ser Ile Asn Tyr Arg Thr Pro
                85   90   95

Cys His His His His His His
            100

<210> SEQ ID NO 30
<211> LENGTH: 109
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-964 full length

<400> SEQUENCE: 30

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1   5   10   15

Pro Thr Ser Leu Leu Ile Ser Trp Ser Tyr Asp Gly Ser Ile Glu Arg
            20   25   30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
        35   40   45

Glu Phe Thr Val Pro Pro Asp Gln Lys Thr Ala Thr Ile Ser Gly Leu
    50   55   60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Arg Leu Glu
65   70   75   80

Glu Ala His Tyr Tyr Arg Glu Ser Pro Ile Ser Ile Asn Tyr Arg Thr
                85   90   95

Glu Ile Asp Lys Pro Ser Gln His His His His His His
            100   105

<210> SEQ ID NO 31
<211> LENGTH: 258
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-964 core (nucleotide sequence)

<400> SEQUENCE: 31

gaagtggttg ctgccacccc caccagcctg ctgatcagct ggtcttacga cggttcgatt 60

gaacgttatt accgcatcac ttacggcgaa acaggaggca atagccctgt ccaggagttc 120

actgtgcctc cggatcagaa gacagctacc atcagcggcc ttaaacctgg cgttgattat 180

accatcactg tgtatgctgt caggctggaa gaagctcatt actatcgaga gtctccaatt 240

tccattaatt accgcaca 258

<210> SEQ ID NO 32

-continued

<211> LENGTH: 288
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-964 w/ N leader (nucleotide
      sequence with N-terminal methionine)

<400> SEQUENCE: 32

atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg   60

ctgatcagct ggtcttacga cggttcgatt gaacgttatt accgcatcac ttacggcgaa   120

acaggaggca atagccctgt ccaggagttc actgtgcctc cggatcagaa gacagctacc   180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt caggctggaa   240

gaagctcatt actatcgaga gtctccaatt tccattaatt accgcaca   288

<210> SEQ ID NO 33
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-964 w/ N leader and modified
      C-terminus including PC (nucleotide sequence with N-terminal
      methionine)

<400> SEQUENCE: 33

atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg   60

ctgatcagct ggtcttacga cggttcgatt gaacgttatt accgcatcac ttacggcgaa   120

acaggaggca atagccctgt ccaggagttc actgtgcctc cggatcagaa gacagctacc   180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt caggctggaa   240

gaagctcatt actatcgaga gtctccaatt tccattaatt accgcacacc gtgc   294

<210> SEQ ID NO 34
<211> LENGTH: 330
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-964 w/ N leader and C tail + his
      tag (nucleotide sequence with N-terminal methionine)

<400> SEQUENCE: 34

atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg   60

ctgatcagct ggtcttacga cggttcgatt gaacgttatt accgcatcac ttacggcgaa   120

acaggaggca atagccctgt ccaggagttc actgtgcctc cggatcagaa gacagctacc   180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt caggctggaa   240

gaagctcatt actatcgaga gtctccaatt tccattaatt accgcacaga aattgacaaa   300

ccatcccagc accatcacca ccaccactga   330

<210> SEQ ID NO 35
<211> LENGTH: 86
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-965 core

<400> SEQUENCE: 35

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Thr Ala
1   5   10   15

-continued

```
Tyr Asp Ser Val Asp Lys Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
            20                  25                  30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Gly Pro Arg His His Thr
        35                  40                  45

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

Tyr Ala Val Tyr His Thr Glu Pro Gly Tyr His Ala His Met Pro Ile
65                  70                  75                  80

Ser Ile Asn Tyr Arg Thr
                85


<210> SEQ ID NO 36
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-965 BC loop

<400> SEQUENCE: 36

Thr Ala Tyr Asp Ser Val Asp Lys Tyr
1               5


<210> SEQ ID NO 37
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-965 DE loop

<400> SEQUENCE: 37

Gly Pro Arg His His Thr
1               5


<210> SEQ ID NO 38
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-965 FG loop

<400> SEQUENCE: 38

Val Tyr His Thr Glu Pro Gly Tyr His Ala His Met Pro
1               5                   10


<210> SEQ ID NO 39
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-965 w/ N leader

<400> SEQUENCE: 39

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Thr Ala Tyr Asp Ser Val Asp Lys Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Gly Pro Arg His His Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60
```

-continued

```
Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Tyr His Thr Glu
65                  70                  75                  80

Pro Gly Tyr His Ala His Met Pro Ile Ser Ile Asn Tyr Arg Thr
                85                  90                  95


<210> SEQ ID NO 40
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-965 w/ N leader + his tag

<400> SEQUENCE: 40

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Thr Ala Tyr Asp Ser Val Asp Lys Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Gly Pro Arg His His Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Tyr His Thr Glu
65                  70                  75                  80

Pro Gly Tyr His Ala His Met Pro Ile Ser Ile Asn Tyr Arg Thr His
                85                  90                  95

His His His His His
            100


<210> SEQ ID NO 41
<211> LENGTH: 102
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-965 w/ N leader and C tail

<400> SEQUENCE: 41

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Thr Ala Tyr Asp Ser Val Asp Lys Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Gly Pro Arg His His Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Tyr His Thr Glu
65                  70                  75                  80

Pro Gly Tyr His Ala His Met Pro Ile Ser Ile Asn Tyr Arg Thr Glu
                85                  90                  95

Ile Asp Lys Pro Ser Gln
            100


<210> SEQ ID NO 42
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-965 w/ N leader and C tail + his
```

-continued

tag

<400> SEQUENCE: 42

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Thr Ala Tyr Asp Ser Val Asp Lys Tyr
            20   25   30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35   40   45

Phe Thr Val Gly Pro Arg His His Thr Ala Thr Ile Ser Gly Leu Lys
    50   55   60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Tyr His Thr Glu
65   70   75   80

Pro Gly Tyr His Ala His Met Pro Ile Ser Ile Asn Tyr Arg Thr Glu
                85   90   95

Ile Asp Lys Pro Ser Gln His His His His His His
            100   105

<210> SEQ ID NO 43
<211> LENGTH: 97
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-965 w/ N leader and modified
      C-terminus including PC

<400> SEQUENCE: 43

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Thr Ala Tyr Asp Ser Val Asp Lys Tyr
            20   25   30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35   40   45

Phe Thr Val Gly Pro Arg His His Thr Ala Thr Ile Ser Gly Leu Lys
    50   55   60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Tyr His Thr Glu
65   70   75   80

Pro Gly Tyr His Ala His Met Pro Ile Ser Ile Asn Tyr Arg Thr Pro
                85   90   95

Cys

<210> SEQ ID NO 44
<211> LENGTH: 103
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-965 w/ N leader and modified
      C-terminus including PC + his tag

<400> SEQUENCE: 44

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Thr Ala Tyr Asp Ser Val Asp Lys Tyr
            20   25   30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35   40   45

-continued

```
Phe Thr Val Gly Pro Arg His His Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Tyr His Thr Glu
65                  70                  75                  80

Pro Gly Tyr His Ala His Met Pro Ile Ser Ile Asn Tyr Arg Thr Pro
                85                  90                  95

Cys His His His His His His
            100


<210> SEQ ID NO 45
<211> LENGTH: 109
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-965  full length

<400> SEQUENCE: 45

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp Thr Ala Tyr Asp Ser Val Asp Lys
            20                  25                  30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
        35                  40                  45

Glu Phe Thr Val Gly Pro Arg His His Thr Ala Thr Ile Ser Gly Leu
    50                  55                  60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Tyr His Thr
65                  70                  75                  80

Glu Pro Gly Tyr His Ala His Met Pro Ile Ser Ile Asn Tyr Arg Thr
                85                  90                  95

Glu Ile Asp Lys Pro Ser Gln His His His His His His
            100                 105


<210> SEQ ID NO 46
<211> LENGTH: 258
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-965  core (nucleotide sequence)

<400> SEQUENCE: 46

gaagtggttg ctgccacccc caccagcctg ctgatcagct ggactgcata cgactctgtt     60

gacaaatatt accgcatcac ttacggcgaa acaggaggca atagccctgt ccaggagttc    120

actgtgggcc ctagacatca cacagctacc atcagcggcc ttaaacctgg cgttgattat    180

accatcactg tgtatgctgt ctatcacact gaaccgggct atcatgctca tatgccaatt    240

tccattaatt accgcaca                                                  258


<210> SEQ ID NO 47
<211> LENGTH: 288
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-965 w/ N leader (nucleotide
      sequence with N-terminal methionine)

<400> SEQUENCE: 47

atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg     60
```

-continued

ctgatcagct ggactgcata cgactctgtt gacaaatatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgggcc ctagacatca cacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt ctatcacact 240

gaaccgggct atcatgctca tatgccaatt tccattaatt accgcaca 288

<210> SEQ ID NO 48
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-965 w/ N leader and modified C-terminus including PC (nucleotide sequence with N-terminal methionine)

<400> SEQUENCE: 48

atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct ggactgcata cgactctgtt gacaaatatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgggcc ctagacatca cacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt ctatcacact 240

gaaccgggct atcatgctca tatgccaatt tccattaatt accgcacacc gtgc 294

<210> SEQ ID NO 49
<211> LENGTH: 330
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-965 w/ N leader and C tail + his tag (nucleotide sequence with N-terminal methionine)

<400> SEQUENCE: 49

atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct ggactgcata cgactctgtt gacaaatatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgggcc ctagacatca cacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt ctatcacact 240

gaaccgggct atcatgctca tatgccaatt tccattaatt accgcacaga aattgacaaa 300

ccatcccagc accatcacca ccaccactga 330

<210> SEQ ID NO 50
<211> LENGTH: 82
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-966 core

<400> SEQUENCE: 50

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp His Arg
1 5 10 15

Phe Ser Ser Ile Met Ala Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
20 25 30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Ala Gly Ser Val Asn Thr
35 40 45

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

Tyr Ala Val Thr Ile His Asn Val Ser Phe Pro Ile Ser Ile Asn Tyr

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```
65                  70                  75                  80

Arg Thr


&lt;210&gt; SEQ ID NO 51
&lt;211&gt; LENGTH: 9
&lt;212&gt; TYPE: PRT
&lt;213&gt; ORGANISM: Artificial Sequence
&lt;220&gt; FEATURE:
&lt;223&gt; OTHER INFORMATION: Synthetic: ATI-966 BC loop

&lt;400&gt; SEQUENCE: 51

His Arg Phe Ser Ser Ile Met Ala Tyr
1               5


&lt;210&gt; SEQ ID NO 52
&lt;211&gt; LENGTH: 6
&lt;212&gt; TYPE: PRT
&lt;213&gt; ORGANISM: Artificial Sequence
&lt;220&gt; FEATURE:
&lt;223&gt; OTHER INFORMATION: Synthetic: ATI-966 DE loop

&lt;400&gt; SEQUENCE: 52

Ala Gly Ser Val Asn Thr
1               5


&lt;210&gt; SEQ ID NO 53
&lt;211&gt; LENGTH: 9
&lt;212&gt; TYPE: PRT
&lt;213&gt; ORGANISM: Artificial Sequence
&lt;220&gt; FEATURE:
&lt;223&gt; OTHER INFORMATION: Synthetic: ATI-966 FG loop

&lt;400&gt; SEQUENCE: 53

Val Thr Ile His Asn Val Ser Phe Pro
1               5


&lt;210&gt; SEQ ID NO 54
&lt;211&gt; LENGTH: 91
&lt;212&gt; TYPE: PRT
&lt;213&gt; ORGANISM: Artificial Sequence
&lt;220&gt; FEATURE:
&lt;223&gt; OTHER INFORMATION: Synthetic: ATI-966 w/ N leader

&lt;400&gt; SEQUENCE: 54

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp His Arg Phe Ser Ser Ile Met Ala Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Ala Gly Ser Val Asn Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Ile His Asn
65                  70                  75                  80

Val Ser Phe Pro Ile Ser Ile Asn Tyr Arg Thr
                85                  90


&lt;210&gt; SEQ ID NO 55
&lt;211&gt; LENGTH: 97
&lt;212&gt; TYPE: PRT
&lt;213&gt; ORGANISM: Artificial Sequence
```

-continued

```
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-966 w/ N leader + his tag

<400> SEQUENCE: 55

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp His Arg Phe Ser Ser Ile Met Ala Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Ala Gly Ser Val Asn Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Ile His Asn
65                  70                  75                  80

Val Ser Phe Pro Ile Ser Ile Asn Tyr Arg Thr His His His His His
                85                  90                  95

His


<210> SEQ ID NO 56
<211> LENGTH: 98
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-966 w/ N leader and C tail

<400> SEQUENCE: 56

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp His Arg Phe Ser Ser Ile Met Ala Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Ala Gly Ser Val Asn Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Ile His Asn
65                  70                  75                  80

Val Ser Phe Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro
                85                  90                  95

Ser Gln


<210> SEQ ID NO 57
<211> LENGTH: 104
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-966 w/ N leader and C tail + his
      tag

<400> SEQUENCE: 57

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp His Arg Phe Ser Ser Ile Met Ala Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Ala Gly Ser Val Asn Thr Ala Thr Ile Ser Gly Leu Lys
```

-continued

```
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Ile His Asn
65                  70                  75                  80

Val Ser Phe Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro
                85                  90                  95

Ser Gln His His His His His His
            100


<210> SEQ ID NO 58
<211> LENGTH: 93
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-966 w/ N leader and modified
      C-terminus including PC

<400> SEQUENCE: 58

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp His Arg Phe Ser Ser Ile Met Ala Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Ala Gly Ser Val Asn Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Ile His Asn
65                  70                  75                  80

Val Ser Phe Pro Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90


<210> SEQ ID NO 59
<211> LENGTH: 99
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-966 w/ N leader and modified
      C-terminus including PC + his tag

<400> SEQUENCE: 59

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp His Arg Phe Ser Ser Ile Met Ala Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Ala Gly Ser Val Asn Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Ile His Asn
65                  70                  75                  80

Val Ser Phe Pro Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His
                85                  90                  95

His His His


<210> SEQ ID NO 60
<211> LENGTH: 105
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
```

-continued

<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-966 full length

<400> SEQUENCE: 60

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp His Arg Phe Ser Ser Ile Met Ala
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Ala Gly Ser Val Asn Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Ile His
65 70 75 80

Asn Val Ser Phe Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys
85 90 95

Pro Ser Gln His His His His His His
100 105

<210> SEQ ID NO 61
<211> LENGTH: 246
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-966 core (nucleotide sequence)

<400> SEQUENCE: 61

gaagtggttg ctgccacccc caccagcctg ctgatcagct ggcataggtt ctcttctatc 60

atggcgtatt accgcatcac ttacggcgaa acaggaggca atagccctgt ccaggagttc 120

actgtggctg gctctgttaa cacagctacc atcagcggcc ttaaacctgg cgttgattat 180

accatcactg tgtatgctgt cacgatccat aacgtttctt tcccaatttc cattaattac 240

cgcaca 246

<210> SEQ ID NO 62
<211> LENGTH: 276
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-966w/ N leader (nucleotide
sequence with N-terminal methionine)

<400> SEQUENCE: 62

atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct ggcataggtt ctcttctatc atggcgtatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtggctg gctctgttaa cacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cacgatccat 240

aacgtttctt tcccaatttc cattaattac cgcaca 276

<210> SEQ ID NO 63
<211> LENGTH: 282
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-966 w/ N leader and modified
C-terminus including PC (nucleotide sequence with N-terminal
methionine)

-continued

<400> SEQUENCE: 63

```
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg     60

ctgatcagct ggcataggtt ctcttctatc atggcgtatt accgcatcac ttacggcgaa    120

acaggaggca atagccctgt ccaggagttc actgtggctg gctctgttaa cacagctacc    180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cacgatccat    240

aacgtttctt tcccaatttc cattaattac cgcacaccgt gc                       282
```

<210> SEQ ID NO 64
<211> LENGTH: 318
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-966 w/ N leader and C tail + his tag (nucleotide sequence with N-terminal methionine)

<400> SEQUENCE: 64

```
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg     60

ctgatcagct ggcataggtt ctcttctatc atggcgtatt accgcatcac ttacggcgaa    120

acaggaggca atagccctgt ccaggagttc actgtggctg gctctgttaa cacagctacc    180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cacgatccat    240

aacgtttctt tcccaatttc cattaattac cgcacagaaa ttgacaaacc atcccagcac    300

catcaccacc accactga                                                  318
```

<210> SEQ ID NO 65
<211> LENGTH: 84
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-967 core (parent of ADX_5417_E01)

<400> SEQUENCE: 65

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

Gln Leu Ser Pro Ser Phe Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
            20                  25                  30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Ala Ser Gly Thr
        35                  40                  45

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

Tyr Ala Val Thr Ser His Gly Ile Tyr Phe Tyr Ala Pro Ile Ser Ile
65                  70                  75                  80

Asn Tyr Arg Thr
```

<210> SEQ ID NO 66
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-967 BC loop

<400> SEQUENCE: 66

```
Gln Gly Gln Leu Ser Pro Ser Phe Tyr
1               5
```

-continued

```
<210> SEQ ID NO 67
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-967 DE loop

<400> SEQUENCE: 67

Pro Val Ala Ser Gly Thr
1               5


<210> SEQ ID NO 68
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-967 FG loop

<400> SEQUENCE: 68

Val Thr Ser His Gly Ile Tyr Phe Tyr Ala Pro
1               5                   10


<210> SEQ ID NO 69
<211> LENGTH: 93
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-967 w/ N leader

<400> SEQUENCE: 69

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Gln Gly Gln Leu Ser Pro Ser Phe Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Val Ala Ser Gly Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Ser His Gly
65                  70                  75                  80

Ile Tyr Phe Tyr Ala Pro Ile Ser Ile Asn Tyr Arg Thr
                85                  90


<210> SEQ ID NO 70
<211> LENGTH: 99
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-967 w/ N leader + his tag

<400> SEQUENCE: 70

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Gln Gly Gln Leu Ser Pro Ser Phe Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Val Ala Ser Gly Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60
```

-continued

```
Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Ser His Gly
65                  70                  75                  80

Ile Tyr Phe Tyr Ala Pro Ile Ser Ile Asn Tyr Arg Thr His His His
                85                  90                  95

His His His


<210> SEQ ID NO 71
<211> LENGTH: 100
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-967 w/ N leader and C tail

<400> SEQUENCE: 71

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Gln Gly Gln Leu Ser Pro Ser Phe Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Val Ala Ser Gly Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Ser His Gly
65                  70                  75                  80

Ile Tyr Phe Tyr Ala Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp
                85                  90                  95

Lys Pro Ser Gln
            100


<210> SEQ ID NO 72
<211> LENGTH: 106
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-967 w/ N leader and C tail + his
      tag

<400> SEQUENCE: 72

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Gln Gly Gln Leu Ser Pro Ser Phe Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Val Ala Ser Gly Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Ser His Gly
65                  70                  75                  80

Ile Tyr Phe Tyr Ala Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp
                85                  90                  95

Lys Pro Ser Gln His His His His His His
            100                 105


<210> SEQ ID NO 73
<211> LENGTH: 95
<212> TYPE: PRT
```

-continued

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-967 w/ N leader and modified
C-terminus including PC

<400> SEQUENCE: 73

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Gln Gly Gln Leu Ser Pro Ser Phe Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Val Ala Ser Gly Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Ser His Gly
65                  70                  75                  80

Ile Tyr Phe Tyr Ala Pro Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90                  95
```

<210> SEQ ID NO 74
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-967 w/ N leader and modified
C-terminus including PC + his tag

<400> SEQUENCE: 74

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Gln Gly Gln Leu Ser Pro Ser Phe Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Val Ala Ser Gly Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Ser His Gly
65                  70                  75                  80

Ile Tyr Phe Tyr Ala Pro Ile Ser Ile Asn Tyr Arg Thr Pro Cys His
                85                  90                  95

His His His His His
            100
```

<210> SEQ ID NO 75
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-967 full length

<400> SEQUENCE: 75

```
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp Gln Gly Gln Leu Ser Pro Ser Phe
            20                  25                  30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
        35                  40                  45
```

-continued

```
Glu Phe Thr Val Pro Val Ala Ser Gly Thr Ala Thr Ile Ser Gly Leu
    50                  55                  60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Ser His
65                  70                  75                  80

Gly Ile Tyr Phe Tyr Ala Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile
                85                  90                  95

Asp Lys Pro Ser Gln His His His His His His
            100                 105
```

<210> SEQ ID NO 76
<211> LENGTH: 252
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-967 core (nucleotide sequence)

<400> SEQUENCE: 76

```
gaagtggttg ctgccacccc caccagcctg ctgatcagct ggcagggaca gctgtctccg     60

tctttctatt accgaatcac ttacggcgaa acaggaggca atagccctgt ccaggagttc    120

actgtgcctg ttgctagtgg gacagctacc atcagcggcc ttaaacctgg cgttgattat    180

accatcactg tgtatgctgt cacttctcat ggcatatact tctacgctcc aatttccatt    240

aattaccgca ca                                                        252
```

<210> SEQ ID NO 77
<211> LENGTH: 282
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-967 w/ N leader (nucleotide sequence with N-terminal methionine)

<400> SEQUENCE: 77

```
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg     60

ctgatcagct ggcagggaca gctgtctccg tctttctatt accgaatcac ttacggcgaa    120

acaggaggca atagccctgt ccaggagttc actgtgcctg ttgctagtgg gacagctacc    180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cacttctcat    240

ggcatatact tctacgctcc aatttccatt aattaccgca ca                       282
```

<210> SEQ ID NO 78
<211> LENGTH: 288
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-967 w/ N leader and modified C-terminus including PC (nucleotide sequence with N-terminal methionine)

<400> SEQUENCE: 78

```
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg     60

ctgatcagct ggcagggaca gctgtctccg tctttctatt accgaatcac ttacggcgaa    120

acaggaggca atagccctgt ccaggagttc actgtgcctg ttgctagtgg gacagctacc    180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cacttctcat    240

ggcatatact tctacgctcc aatttccatt aattaccgca caccgtgc                 288
```

-continued

<210> SEQ ID NO 79
<211> LENGTH: 325
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI-967 w/ N leader and C tail + his tag (nucleotide sequence with N-terminal methionine)

<400> SEQUENCE: 79

atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct ggcagggaca gctgtctccg tctttctatt accgaatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgcctg ttgctagtgg gacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cacttctcat 240

ggcatatact tctacgctcc aatttccatt aattaccgca cagaaattga caaaccatcc 300

cagcaccatc accaccacca ctgat 325

<210> SEQ ID NO 80
<211> LENGTH: 86
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ADX_5322_A02 core

<400> SEQUENCE: 80

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Ser Tyr
1 5 10 15

Asp Gly Pro Ile Asp Arg Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
20 25 30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Pro Asp Gln Lys Thr
35 40 45

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

Tyr Ala Val Arg Leu Glu Glu Ala His Tyr Asn Arg Glu Phe Pro Ile
65 70 75 80

Ser Ile Asn Tyr Arg Thr
85

<210> SEQ ID NO 81
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ADX_5322_A02 BC loop

<400> SEQUENCE: 81

Ser Tyr Asp Gly Pro Ile Asp Arg Tyr
1 5

<210> SEQ ID NO 82
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ADX_5322_A02 DE loop

<400> SEQUENCE: 82

Pro Pro Asp Gln Lys Thr
1 5

-continued

<210> SEQ ID NO 83
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ADX_5322_A02 FG loop

<400> SEQUENCE: 83

Val Arg Leu Glu Glu Ala His Tyr Asn Arg Glu Phe Pro
1 5 10

<210> SEQ ID NO 84
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ADX_5322_A02 w/ N leader

<400> SEQUENCE: 84

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Ser Tyr Asp Gly Pro Ile Asp Arg Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

Phe Thr Val Pro Pro Asp Gln Lys Thr Ala Thr Ile Ser Gly Leu Lys
50 55 60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Arg Leu Glu Glu
65 70 75 80

Ala His Tyr Asn Arg Glu Phe Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

<210> SEQ ID NO 85
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ADX_5322_A02 w/ N leader + his tag

<400> SEQUENCE: 85

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Ser Tyr Asp Gly Pro Ile Asp Arg Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

Phe Thr Val Pro Pro Asp Gln Lys Thr Ala Thr Ile Ser Gly Leu Lys
50 55 60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Arg Leu Glu Glu
65 70 75 80

Ala His Tyr Asn Arg Glu Phe Pro Ile Ser Ile Asn Tyr Arg Thr His
85 90 95

His His His His His
100

<210> SEQ ID NO 86
<211> LENGTH: 102
<212> TYPE: PRT

-continued

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ADX_5322_A02 w/ N leader and C tail

<400> SEQUENCE: 86

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Ser Tyr Asp Gly Pro Ile Asp Arg Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

Phe Thr Val Pro Pro Asp Gln Lys Thr Ala Thr Ile Ser Gly Leu Lys
50 55 60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Arg Leu Glu Glu
65 70 75 80

Ala His Tyr Asn Arg Glu Phe Pro Ile Ser Ile Asn Tyr Arg Thr Glu
85 90 95

Ile Asp Lys Pro Ser Gln
100

<210> SEQ ID NO 87
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ADX_5322_A02 w/ N leader and C tail + his tag

<400> SEQUENCE: 87

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Ser Tyr Asp Gly Pro Ile Asp Arg Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

Phe Thr Val Pro Pro Asp Gln Lys Thr Ala Thr Ile Ser Gly Leu Lys
50 55 60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Arg Leu Glu Glu
65 70 75 80

Ala His Tyr Asn Arg Glu Phe Pro Ile Ser Ile Asn Tyr Arg Thr Glu
85 90 95

Ile Asp Lys Pro Ser Gln His His His His His His
100 105

<210> SEQ ID NO 88
<211> LENGTH: 97
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ADX_5322_A02 w/ N leader and modified C-terminus including PC

<400> SEQUENCE: 88

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Ser Tyr Asp Gly Pro Ile Asp Arg Tyr
20 25 30

-continued

```
Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Pro Asp Gln Lys Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Arg Leu Glu Glu
65                  70                  75                  80

Ala His Tyr Asn Arg Glu Phe Pro Ile Ser Ile Asn Tyr Arg Thr Pro
                85                  90                  95

Cys


<210> SEQ ID NO 89
<211> LENGTH: 103
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ADX_5322_A02  w/ N leader and
      modified C-terminus including PC + his tag

<400> SEQUENCE: 89

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ser Tyr Asp Gly Pro Ile Asp Arg Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Pro Asp Gln Lys Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Arg Leu Glu Glu
65                  70                  75                  80

Ala His Tyr Asn Arg Glu Phe Pro Ile Ser Ile Asn Tyr Arg Thr Pro
                85                  90                  95

Cys His His His His His His
            100


<210> SEQ ID NO 90
<211> LENGTH: 97
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ADX_5322_A02-Mal-DBCO-FFPF18

<400> SEQUENCE: 90

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ser Tyr Asp Gly Pro Ile Asp Arg Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Pro Asp Gln Lys Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Arg Leu Glu Glu
65                  70                  75                  80

Ala His Tyr Asn Arg Glu Phe Pro Ile Ser Ile Asn Tyr Arg Thr Pro
                85                  90                  95

Cys
```

-continued

<210> SEQ ID NO 91
<211> LENGTH: 104
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ADX_5322_A02 full length

<400> SEQUENCE: 91

```
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp Ser Tyr Asp Gly Pro Ile Asp Arg
            20                  25                  30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
        35                  40                  45

Glu Phe Thr Val Pro Pro Asp Gln Lys Thr Ala Thr Ile Ser Gly Leu
    50                  55                  60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Arg Leu Glu
65                  70                  75                  80

Glu Ala His Tyr Asn Arg Glu Phe Pro Ile Ser Ile Asn Tyr Arg Thr
                85                  90                  95

Pro Cys His His His His His His
            100
```

<210> SEQ ID NO 92
<211> LENGTH: 258
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ADX_5322_A02 core (nucleotide sequence)

<400> SEQUENCE: 92

```
gaagtggttg ctgccacccc caccagcctg ctgatcagct ggtcttacga tggcccaatt     60

gaccggtatt accgcatcac ttacggcgaa acaggaggca atagccctgt ccaggagttc    120

actgtgcctc cggatcagaa gacagctacc atcagcggcc ttaaacctgg cgttgattat    180

accatcactg tgtatgctgt ccggctggaa gaagctcatt acaatcgaga gtttccaatt    240

tccattaatt accgcaca                                                  258
```

<210> SEQ ID NO 93
<211> LENGTH: 288
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ADX_5322_A02 w/ N leader (nucleotide sequence with N-terminal methionine)

<400> SEQUENCE: 93

```
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg     60

ctgatcagct ggtcttacga tggcccaatt gaccggtatt accgcatcac ttacggcgaa    120

acaggaggca atagccctgt ccaggagttc actgtgcctc cggatcagaa gacagctacc    180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt ccggctggaa    240

gaagctcatt acaatcgaga gtttccaatt tccattaatt accgcaca                 288
```

<210> SEQ ID NO 94
<211> LENGTH: 294

-continued

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ADX_5322_A02 w/ N leader and modified C-terminus including PC (nucleotide sequence with N-terminal methionine)

<400> SEQUENCE: 94

```
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg     60

ctgatcagct ggtcttacga tggcccaatt gaccggtatt accgcatcac ttacggcgaa    120

acaggaggca atagccctgt ccaggagttc actgtgcctc cggatcagaa gacagctacc    180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt ccggctggaa    240

gaagctcatt acaatcgaga gtttccaatt tccattaatt accgcacacc gtgc          294
```

<210> SEQ ID NO 95
<211> LENGTH: 315
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ADX_5322_A02 w/ N leader and C tail + his tag (nucleotide sequence with N-terminal methionine)

<400> SEQUENCE: 95

```
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg     60

ctgatcagct ggtcttacga tggcccaatt gaccggtatt accgcatcac ttacggcgaa    120

acaggaggca atagccctgt ccaggagttc actgtgcctc cggatcagaa gacagctacc    180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt ccggctggaa    240

gaagctcatt acaatcgaga gtttccaatt tccattaatt accgcacacc gtgccaccat    300

caccaccacc actga                                                     315
```

<210> SEQ ID NO 96
<211> LENGTH: 84
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ADX_5417_E01 core

<400> SEQUENCE: 96

```
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Arg Ala
1               5                   10                  15

Gln Leu Ser Pro Ser Phe Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
            20                  25                  30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Asn Asp Val Met Thr
        35                  40                  45

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

Tyr Ala Val Thr Thr His Gly Val Tyr Phe Tyr Ser Pro Ile Ser Ile
65                  70                  75                  80

Asn Tyr Arg Thr
```

<210> SEQ ID NO 97
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ADX_5417_E01 BC loop

-continued

<400> SEQUENCE: 97

Arg Ala Gln Leu Ser Pro Ser Phe Tyr
1   5

<210> SEQ ID NO 98
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ADX_5417_E01 DE loop

<400> SEQUENCE: 98

Pro Asn Asp Val Met Thr
1   5

<210> SEQ ID NO 99
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ADX_5417_E01 FG loop

<400> SEQUENCE: 99

Val Thr Thr His Gly Val Tyr Phe Tyr Ser Pro
1   5   10

<210> SEQ ID NO 100
<211> LENGTH: 93
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ADX_5417_E01 w/ N leader

<400> SEQUENCE: 100

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Arg Ala Gln Leu Ser Pro Ser Phe Tyr
            20   25   30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35   40   45

Phe Thr Val Pro Asn Asp Val Met Thr Ala Thr Ile Ser Gly Leu Lys
    50   55   60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Thr His Gly
65   70   75   80

Val Tyr Phe Tyr Ser Pro Ile Ser Ile Asn Tyr Arg Thr
                85   90

<210> SEQ ID NO 101
<211> LENGTH: 99
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ADX_5417_E01 w/ N leader + his tag

<400> SEQUENCE: 101

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Arg Ala Gln Leu Ser Pro Ser Phe Tyr
            20   25   30

-continued

```
Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Asn Asp Val Met Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Thr His Gly
65                  70                  75                  80

Val Tyr Phe Tyr Ser Pro Ile Ser Ile Asn Tyr Arg Thr His His His
                85                  90                  95

His His His
```

<210> SEQ ID NO 102
<211> LENGTH: 100
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ADX_5417_E01 w/ N leader and C tail

<400> SEQUENCE: 102

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Arg Ala Gln Leu Ser Pro Ser Phe Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Asn Asp Val Met Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Thr His Gly
65                  70                  75                  80

Val Tyr Phe Tyr Ser Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp
                85                  90                  95

Lys Pro Ser Gln
            100
```

<210> SEQ ID NO 103
<211> LENGTH: 106
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ADX_5417_E01 w/ N leader and C tail + his tag

<400> SEQUENCE: 103

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Arg Ala Gln Leu Ser Pro Ser Phe Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Asn Asp Val Met Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Thr His Gly
65                  70                  75                  80

Val Tyr Phe Tyr Ser Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp
                85                  90                  95

Lys Pro Ser Gln His His His His His His
            100                 105
```

-continued

```
<210> SEQ ID NO 104
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ADX_5417_E01 w/ N leader and
      modified C-terminus including PC

<400> SEQUENCE: 104

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Arg Ala Gln Leu Ser Pro Ser Phe Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Asn Asp Val Met Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Thr His Gly
65                  70                  75                  80

Val Tyr Phe Tyr Ser Pro Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90                  95


<210> SEQ ID NO 105
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ADX_5417_E01 w/ N leader and
      modified C-terminus including PC + his tag

<400> SEQUENCE: 105

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Arg Ala Gln Leu Ser Pro Ser Phe Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Asn Asp Val Met Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Thr His Gly
65                  70                  75                  80

Val Tyr Phe Tyr Ser Pro Ile Ser Ile Asn Tyr Arg Thr Pro Cys His
                85                  90                  95

His His His His His
            100


<210> SEQ ID NO 106
<211> LENGTH: 97
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ADX-5417_E01 Mal-DBCO-FFPF18

<400> SEQUENCE: 106

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ser Tyr Asp Gly Pro Ile Asp Arg Tyr
```

-continued

```
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Pro Asp Gln Lys Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Arg Leu Glu Glu
65                  70                  75                  80

Ala His Tyr Asn Arg Glu Phe Pro Ile Ser Ile Asn Tyr Arg Thr Pro
                85                  90                  95

Cys
```

<210> SEQ ID NO 107
<211> LENGTH: 102
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ADX-5417_E01 full length

<400> SEQUENCE: 107

```
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp Arg Ala Gln Leu Ser Pro Ser Phe
            20                  25                  30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
        35                  40                  45

Glu Phe Thr Val Pro Asn Asp Val Met Thr Ala Thr Ile Ser Gly Leu
    50                  55                  60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Thr His
65                  70                  75                  80

Gly Val Tyr Phe Tyr Ser Pro Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90                  95

His His His His His His
            100
```

<210> SEQ ID NO 108
<211> LENGTH: 252
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ADX-5417_E01 core (nucleotide sequence)

<400> SEQUENCE: 108

```
gaagtggttg ctgccacccc caccagcctg ctgatcagct ggagggctca gctgtctccg     60

tctttctatt accgcatcac ttacggcgaa acaggaggca atagccctgt ccaggagttc    120

actgtgccta atgatgtaat gacagctacc atcagcggcc ttaaacctgg cgttgattat    180

accatcactg tgtatgctgt cactactcat ggtgtttatt tctactcacc aatttccatt    240

aattaccgca ca                                                        252
```

<210> SEQ ID NO 109
<211> LENGTH: 282
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ADX_5417_E01 w/ N leader (nucleotide sequence with N-terminal methionine)

-continued

<400> SEQUENCE: 109

atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct ggagggctca gctgtctccg tctttctatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgccta atgatgtaat gacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cactactcat 240

ggtgtttatt tctactcacc aatttccatt aattaccgca ca 282

<210> SEQ ID NO 110
<211> LENGTH: 288
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ADX_5417_E01 w/ N leader and modified C-terminus including PC (nucleotide sequence with N-terminal methionine)

<400> SEQUENCE: 110

atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct ggagggctca gctgtctccg tctttctatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgccta atgatgtaat gacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cactactcat 240

ggtgtttatt tctactcacc aatttccatt aattaccgca caccgtgc 288

<210> SEQ ID NO 111
<211> LENGTH: 309
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ADX_5417_E01 w/ N leader and C tail + his tag (nucleotide sequence with N-terminal methionine)

<400> SEQUENCE: 111

atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct ggagggctca gctgtctccg tctttctatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgccta atgatgtaat gacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cactactcat 240

ggtgtttatt tctactcacc aatttccatt aattaccgca caccgtgcca ccatcaccac 300

caccactga 309

<210> SEQ ID NO 112
<211> LENGTH: 80
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_A10 core

<400> SEQUENCE: 112

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Pro Tyr
1 5 10 15

Pro Ser Tyr Tyr Ile Glu Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly
20 25 30

Asn Ser Pro Val Gln Glu Phe Thr Val Gln Ser Met Lys Ala Thr Ile
35 40 45

-continued

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

Arg His Pro Gly Met Leu Glu Phe Gly Ile Ser Ile Asn Tyr Arg Thr
65                  70                  75                  80


<210> SEQ ID NO 113
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_A10 BC loop

<400> SEQUENCE: 113

Pro Tyr Pro Ser Tyr Tyr Ile Glu
1               5


<210> SEQ ID NO 114
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_A10 DE loop

<400> SEQUENCE: 114

Ile Arg His Pro Gly Met Leu Glu Phe Gly
1               5                   10


<210> SEQ ID NO 115
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_A10 FG loop

<400> SEQUENCE: 115

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


<210> SEQ ID NO 116
<211> LENGTH: 89
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_A10 w/ N leader

<400> SEQUENCE: 116

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Pro Tyr Pro Ser Tyr Tyr Ile Glu Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

Thr Val Gln Ser Met Lys Ala Thr Ile Ser Gly Leu Lys Pro Gly Val
    50                  55                  60

Asp Tyr Thr Ile Thr Val Tyr Ala Ile Arg His Pro Gly Met Leu Glu
65                  70                  75                  80

Phe Gly Ile Ser Ile Asn Tyr Arg Thr
                85


<210> SEQ ID NO 117
```

-continued

```
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_A10 w/ N leader + his tag

<400> SEQUENCE: 117

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Pro Tyr Pro Ser Tyr Tyr Ile Glu Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

Thr Val Gln Ser Met Lys Ala Thr Ile Ser Gly Leu Lys Pro Gly Val
    50                  55                  60

Asp Tyr Thr Ile Thr Val Tyr Ala Ile Arg His Pro Gly Met Leu Glu
65                  70                  75                  80

Phe Gly Ile Ser Ile Asn Tyr Arg Thr His His His His His His
                85                  90                  95


<210> SEQ ID NO 118
<211> LENGTH: 96
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_A10 w/ N leader and C tail

<400> SEQUENCE: 118

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Pro Tyr Pro Ser Tyr Tyr Ile Glu Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

Thr Val Gln Ser Met Lys Ala Thr Ile Ser Gly Leu Lys Pro Gly Val
    50                  55                  60

Asp Tyr Thr Ile Thr Val Tyr Ala Ile Arg His Pro Gly Met Leu Glu
65                  70                  75                  80

Phe Gly Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95


<210> SEQ ID NO 119
<211> LENGTH: 102
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_A10w/ N leader and C
      tail + his tag

<400> SEQUENCE: 119

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Pro Tyr Pro Ser Tyr Tyr Ile Glu Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

Thr Val Gln Ser Met Lys Ala Thr Ile Ser Gly Leu Lys Pro Gly Val
    50                  55                  60
```

-continued

```
Asp Tyr Thr Ile Thr Val Tyr Ala Ile Arg His Pro Gly Met Leu Glu
65                  70                  75                  80

Phe Gly Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95

His His His His His His
            100


<210> SEQ ID NO 120
<211> LENGTH: 91
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_A10w/ N leader and modified
      C-terminus including PC

<400> SEQUENCE: 120

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Pro Tyr Pro Ser Tyr Tyr Ile Glu Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

Thr Val Gln Ser Met Lys Ala Thr Ile Ser Gly Leu Lys Pro Gly Val
    50                  55                  60

Asp Tyr Thr Ile Thr Val Tyr Ala Ile Arg His Pro Gly Met Leu Glu
65                  70                  75                  80

Phe Gly Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90


<210> SEQ ID NO 121
<211> LENGTH: 97
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_A10 w/ N leader and
      modified C-terminus including PC + his tag

<400> SEQUENCE: 121

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Pro Tyr Pro Ser Tyr Tyr Ile Glu Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

Thr Val Gln Ser Met Lys Ala Thr Ile Ser Gly Leu Lys Pro Gly Val
    50                  55                  60

Asp Tyr Thr Ile Thr Val Tyr Ala Ile Arg His Pro Gly Met Leu Glu
65                  70                  75                  80

Phe Gly Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His His His
                85                  90                  95

His


<210> SEQ ID NO 122
<211> LENGTH: 103
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
```

-continued

<223> OTHER INFORMATION: Synthetic: ATI_1420_A10 full length

<400> SEQUENCE: 122

```
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp Pro Tyr Pro Ser Tyr Tyr Ile Glu
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Gln Ser Met Lys Ala Thr Ile Ser Gly Leu Lys Pro Gly
    50                  55                  60

Val Asp Tyr Thr Ile Thr Val Tyr Ala Ile Arg His Pro Gly Met Leu
65                  70                  75                  80

Glu Phe Gly Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser
                85                  90                  95

Gln His His His His His His
            100
```

<210> SEQ ID NO 123
<211> LENGTH: 76
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_B09 core

<400> SEQUENCE: 123

```
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp His Lys
1               5                   10                  15

Phe Ser Ser Leu Met Ser Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly
            20                  25                  30

Asn Ser Pro Val Gln Glu Phe Thr Val Gly Ser Val Asn Ala Thr Ile
        35                  40                  45

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

His Asn Val Gly Phe Ile Ser Ile Asn Tyr Arg Thr
65                  70                  75
```

<210> SEQ ID NO 124
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_B09 BC loop

<400> SEQUENCE: 124

```
His Lys Phe Ser Ser Leu Met Ser
1               5
```

<210> SEQ ID NO 125
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_B09 DE loop

<400> SEQUENCE: 125

```
Gly Ser Val Asn
1
```

-continued

<210> SEQ ID NO 126
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_B09 FG loop

<400> SEQUENCE: 126

Ile His Asn Val Gly Phe
1 5

<210> SEQ ID NO 127
<211> LENGTH: 85
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_B09 w/ N leader

<400> SEQUENCE: 127

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp His Lys Phe Ser Ser Leu Met Ser Tyr
20 25 30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
35 40 45

Thr Val Gly Ser Val Asn Ala Thr Ile Ser Gly Leu Lys Pro Gly Val
50 55 60

Asp Tyr Thr Ile Thr Val Tyr Ala Ile His Asn Val Gly Phe Ile Ser
65 70 75 80

Ile Asn Tyr Arg Thr
85

<210> SEQ ID NO 128
<211> LENGTH: 91
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_B09 w/ N leader + his tag

<400> SEQUENCE: 128

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp His Lys Phe Ser Ser Leu Met Ser Tyr
20 25 30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
35 40 45

Thr Val Gly Ser Val Asn Ala Thr Ile Ser Gly Leu Lys Pro Gly Val
50 55 60

Asp Tyr Thr Ile Thr Val Tyr Ala Ile His Asn Val Gly Phe Ile Ser
65 70 75 80

Ile Asn Tyr Arg Thr His His His His His His
85 90

<210> SEQ ID NO 129
<211> LENGTH: 92
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: AATI_1420_B09 w/ N leader and C tail

-continued

<400> SEQUENCE: 129

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp His Lys Phe Ser Ser Leu Met Ser Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

Thr Val Gly Ser Val Asn Ala Thr Ile Ser Gly Leu Lys Pro Gly Val
    50                  55                  60

Asp Tyr Thr Ile Thr Val Tyr Ala Ile His Asn Val Gly Phe Ile Ser
65                  70                  75                  80

Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90
```

<210> SEQ ID NO 130
<211> LENGTH: 98
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_B09 w/ N leader and C tail + his tag

<400> SEQUENCE: 130

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp His Lys Phe Ser Ser Leu Met Ser Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

Thr Val Gly Ser Val Asn Ala Thr Ile Ser Gly Leu Lys Pro Gly Val
    50                  55                  60

Asp Tyr Thr Ile Thr Val Tyr Ala Ile His Asn Val Gly Phe Ile Ser
65                  70                  75                  80

Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His
                85                  90                  95

His His
```

<210> SEQ ID NO 131
<211> LENGTH: 87
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_B09 w/ N leader and modified C-terminus including PC

<400> SEQUENCE: 131

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp His Lys Phe Ser Ser Leu Met Ser Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

Thr Val Gly Ser Val Asn Ala Thr Ile Ser Gly Leu Lys Pro Gly Val
    50                  55                  60

Asp Tyr Thr Ile Thr Val Tyr Ala Ile His Asn Val Gly Phe Ile Ser
```

-continued

```
65                  70                  75                  80

Ile Asn Tyr Arg Thr Pro Cys
                85


<210> SEQ ID NO 132
<211> LENGTH: 93
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_B09 w/ N leader and
      modified C-terminus including PC + his tag

<400> SEQUENCE: 132

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp His Lys Phe Ser Ser Leu Met Ser Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

Thr Val Gly Ser Val Asn Ala Thr Ile Ser Gly Leu Lys Pro Gly Val
    50                  55                  60

Asp Tyr Thr Ile Thr Val Tyr Ala Ile His Asn Val Gly Phe Ile Ser
65                  70                  75                  80

Ile Asn Tyr Arg Thr Pro Cys His His His His His His
                85                  90


<210> SEQ ID NO 133
<211> LENGTH: 99
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_B09 full length

<400> SEQUENCE: 133

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp His Lys Phe Ser Ser Leu Met Ser
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Gly Ser Val Asn Ala Thr Ile Ser Gly Leu Lys Pro Gly
    50                  55                  60

Val Asp Tyr Thr Ile Thr Val Tyr Ala Ile His Asn Val Gly Phe Ile
65                  70                  75                  80

Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His
                85                  90                  95

His His His


<210> SEQ ID NO 134
<211> LENGTH: 79
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_C02 core

<400> SEQUENCE: 134

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Arg Ile
1               5                   10                  15
```

-continued

```
Lys Ser Tyr Tyr Ala Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn
            20                  25                  30

Ser Pro Val Gln Glu Phe Thr Val Arg Gln His Val Ala Thr Ile Ser
        35                  40                  45

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

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


<210> SEQ ID NO 135
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_C02 BC loop

<400> SEQUENCE: 135

Arg Ile Lys Ser Tyr Tyr Ala
1               5


<210> SEQ ID NO 136
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_C02 DE loop

<400> SEQUENCE: 136

Arg Gln His Val
1


<210> SEQ ID NO 137
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_C02 FG loop

<400> SEQUENCE: 137

Arg Leu Gly Asp Val Glu Leu Val Tyr Glu
1               5                   10


<210> SEQ ID NO 138
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_C02 w/ N leader

<400> SEQUENCE: 138

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Arg Ile Lys Ser Tyr Tyr Ala Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

Val Arg Gln His Val Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50                  55                  60

Tyr Thr Ile Thr Val Tyr Ala Arg Leu Gly Asp Val Glu Leu Val Tyr
65                  70                  75                  80
```

-continued

Glu Ile Ser Ile Asn Tyr Arg Thr
                85

<210> SEQ ID NO 139
<211> LENGTH: 91
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_C02 w/ N leader + his tag

<400> SEQUENCE: 139

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp His Lys Phe Ser Ser Leu Met Ser Tyr
            20   25   30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35   40   45

Thr Val Gly Ser Val Asn Ala Thr Ile Ser Gly Leu Lys Pro Gly Val
    50   55   60

Asp Tyr Thr Ile Thr Val Tyr Ala Ile His Asn Val Gly Phe Ile Ser
65   70   75   80

Ile Asn Tyr Arg Thr His His His His His His
                85   90

<210> SEQ ID NO 140
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_C02 w/ N leader and C tail

<400> SEQUENCE: 140

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Arg Ile Lys Ser Tyr Tyr Ala Tyr Arg
            20   25   30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35   40   45

Val Arg Gln His Val Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50   55   60

Tyr Thr Ile Thr Val Tyr Ala Arg Leu Gly Asp Val Glu Leu Val Tyr
65   70   75   80

Glu Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85   90   95

<210> SEQ ID NO 141
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_C02 w/ N leader and C
      tail + his tag

<400> SEQUENCE: 141

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Arg Ile Lys Ser Tyr Tyr Ala Tyr Arg
            20   25   30

-continued

```
Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

Val Arg Gln His Val Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50                  55                  60

Tyr Thr Ile Thr Val Tyr Ala Arg Leu Gly Asp Val Glu Leu Val Tyr
65                  70                  75                  80

Glu Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His
                85                  90                  95

His His His His His
            100


<210> SEQ ID NO 142
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_C02 w/ N leader and
      modified C-terminus including PC

<400> SEQUENCE: 142

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Arg Ile Lys Ser Tyr Tyr Ala Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

Val Arg Gln His Val Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50                  55                  60

Tyr Thr Ile Thr Val Tyr Ala Arg Leu Gly Asp Val Glu Leu Val Tyr
65                  70                  75                  80

Glu Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90


<210> SEQ ID NO 143
<211> LENGTH: 93
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_C02 w/ N leader and
      modified C-terminus including PC + his tag

<400> SEQUENCE: 143

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp His Lys Phe Ser Ser Leu Met Ser Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

Thr Val Gly Ser Val Asn Ala Thr Ile Ser Gly Leu Lys Pro Gly Val
    50                  55                  60

Asp Tyr Thr Ile Thr Val Tyr Ala Ile His Asn Val Gly Phe Ile Ser
65                  70                  75                  80

Ile Asn Tyr Arg Thr Pro Cys His His His His His His
                85                  90


<210> SEQ ID NO 144
```

-continued

<211> LENGTH: 102
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_C02 full length

<400> SEQUENCE: 144

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Arg Ile Lys Ser Tyr Tyr Ala Tyr
20 25 30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
35 40 45

Thr Val Arg Gln His Val Ala Thr Ile Ser Gly Leu Lys Pro Gly Val
50 55 60

Asp Tyr Thr Ile Thr Val Tyr Ala Arg Leu Gly Asp Val Glu Leu Val
65 70 75 80

Tyr Glu Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
85 90 95

His His His His His His
100

<210> SEQ ID NO 145
<211> LENGTH: 80
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_C11 core

<400> SEQUENCE: 145

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Met Tyr
1 5 10 15

Pro Leu Lys Ser Val Pro Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly
20 25 30

Asn Ser Pro Val Gln Glu Phe Thr Val Tyr Ser Ser Gly Ala Thr Ile
35 40 45

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

Ser Tyr Ser Thr Tyr His Ala Phe Met Ile Ser Ile Asn Tyr Arg Thr
65 70 75 80

<210> SEQ ID NO 146
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_C11 BC loop

<400> SEQUENCE: 146

Met Tyr Pro Leu Lys Ser Val Pro
1 5

<210> SEQ ID NO 147
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_C11 DE loop

<400> SEQUENCE: 147

-continued

Tyr Ser Ser Gly
1

<210> SEQ ID NO 148
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_C11 FG loop

<400> SEQUENCE: 148

```
Met Ser Tyr Ser Thr Tyr His Ala Phe Met
1               5                   10
```

<210> SEQ ID NO 149
<211> LENGTH: 89
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_C11 w/ N leader

<400> SEQUENCE: 149

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Met Tyr Pro Leu Lys Ser Val Pro Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Met Ser Tyr Ser Thr Tyr His Ala
65                  70                  75                  80

Phe Met Ile Ser Ile Asn Tyr Arg Thr
                85
```

<210> SEQ ID NO 150
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_C11 w/ N leader + his tag

<400> SEQUENCE: 150

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Met Tyr Pro Leu Lys Ser Val Pro Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Met Ser Tyr Ser Thr Tyr His Ala
65                  70                  75                  80

Phe Met Ile Ser Ile Asn Tyr Arg Thr His His His His His His
                85                  90                  95
```

<210> SEQ ID NO 151
<211> LENGTH: 96

-continued

<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_C11 w/ N leader and C tail

<400> SEQUENCE: 151

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Met Tyr Pro Leu Lys Ser Val Pro Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Met Ser Tyr Ser Thr Tyr His Ala
65                  70                  75                  80

Phe Met Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95
```

<210> SEQ ID NO 152
<211> LENGTH: 102
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_C11 w/ N leader and C tail + his tag

<400> SEQUENCE: 152

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Met Tyr Pro Leu Lys Ser Val Pro Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Met Ser Tyr Ser Thr Tyr His Ala
65                  70                  75                  80

Phe Met Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95

His His His His His His
            100
```

<210> SEQ ID NO 153
<211> LENGTH: 91
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_C11 w/ N leader and modified C-terminus including PC

<400> SEQUENCE: 153

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Met Tyr Pro Leu Lys Ser Val Pro Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45
```

-continued

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

Asp Tyr Thr Ile Thr Val Tyr Ala Met Ser Tyr Ser Thr Tyr His Ala
65                  70                  75                  80

Phe Met Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90


<210> SEQ ID NO 154
<211> LENGTH: 97
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_C11 w/ N leader and
      modified C-terminus including PC + his tag

<400> SEQUENCE: 154

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Met Tyr Pro Leu Lys Ser Val Pro Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Met Ser Tyr Ser Thr Tyr His Ala
65                  70                  75                  80

Phe Met Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His His His
                85                  90                  95

His


<210> SEQ ID NO 155
<211> LENGTH: 103
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: AATI_1420_C11 full length

<400> SEQUENCE: 155

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp Met Tyr Pro Leu Lys Ser Val Pro
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Met Ser Tyr Ser Thr Tyr His
65                  70                  75                  80

Ala Phe Met Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser
                85                  90                  95

Gln His His His His His His
            100


<210> SEQ ID NO 156
<211> LENGTH: 79
<212> TYPE: PRT
```

-continued

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_D01 core

<400> SEQUENCE: 156

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Arg Thr
1   5   10   15

Val Pro Glu Thr Asp Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn
            20   25   30

Ser Pro Val Gln Glu Phe Thr Val Pro Asp Asn Thr Ala Thr Ile Ser
        35   40   45

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

Thr Ala His Tyr Asn Arg Asp Tyr Ile Ser Ile Asn Tyr Arg Thr
65   70   75

<210> SEQ ID NO 157
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_D01 BC loop

<400> SEQUENCE: 157

Arg Thr Val Pro Glu Thr Asp
1   5

<210> SEQ ID NO 158
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_D01 DE loop

<400> SEQUENCE: 158

Pro Asp Asn Thr
1

<210> SEQ ID NO 159
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_D01 FG loop

<400> SEQUENCE: 159

Leu Glu Thr Ala His Tyr Asn Arg Asp Tyr
1   5   10

<210> SEQ ID NO 160
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_D01 w/ N leader

<400> SEQUENCE: 160

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Arg Thr Val Pro Glu Thr Asp Tyr Arg
            20   25   30

-continued

```
Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Thr Ala His Tyr Asn Arg Asp
65                  70                  75                  80

Tyr Ile Ser Ile Asn Tyr Arg Thr
                85
```

<210> SEQ ID NO 161
<211> LENGTH: 94
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_D01 w/ N leader + his tag

<400> SEQUENCE: 161

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Arg Thr Val Pro Glu Thr Asp Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Thr Ala His Tyr Asn Arg Asp
65                  70                  75                  80

Tyr Ile Ser Ile Asn Tyr Arg Thr His His His His His His
                85                  90
```

<210> SEQ ID NO 162
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_D01 w/ N leader and C tail

<400> SEQUENCE: 162

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Arg Thr Val Pro Glu Thr Asp Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Thr Ala His Tyr Asn Arg Asp
65                  70                  75                  80

Tyr Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95
```

<210> SEQ ID NO 163
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_D01 w/ N leader and C
      tail + his tag

-continued

<400> SEQUENCE: 163

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Arg Thr Val Pro Glu Thr Asp Tyr Arg
            20   25   30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35   40   45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Thr Ala His Tyr Asn Arg Asp
65   70   75   80

Tyr Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His
                85   90   95

His His His His His
            100

<210> SEQ ID NO 164
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_D01 w/ N leader and
      modified C-terminus including PC

<400> SEQUENCE: 164

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Arg Thr Val Pro Glu Thr Asp Tyr Arg
            20   25   30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35   40   45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Thr Ala His Tyr Asn Arg Asp
65   70   75   80

Tyr Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85   90

<210> SEQ ID NO 165
<211> LENGTH: 96
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_D01 w/ N leader and
      modified C-terminus including PC + his tag

<400> SEQUENCE: 165

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Arg Thr Val Pro Glu Thr Asp Tyr Arg
            20   25   30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35   40   45

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

-continued

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Thr Ala His Tyr Asn Arg Asp
65 70 75 80

Tyr Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His His His His
85 90 95

<210> SEQ ID NO 166
<211> LENGTH: 102
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_D01 full length

<400> SEQUENCE: 166

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Arg Thr Val Pro Glu Thr Asp Tyr
20 25 30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
35 40 45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Leu Glu Thr Ala His Tyr Asn Arg
65 70 75 80

Asp Tyr Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
85 90 95

His His His His His His
100

<210> SEQ ID NO 167
<211> LENGTH: 82
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_D05 core

<400> SEQUENCE: 167

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Thr Ala
1 5 10 15

Tyr Tyr Ser Thr Ile Lys Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly
20 25 30

Asn Ser Pro Val Gln Glu Phe Thr Val Gly Pro Lys His His Ala Thr
35 40 45

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

Tyr Asn Thr Lys Pro Gly Tyr His Ala His Gln Ile Ser Ile Asn Tyr
65 70 75 80

Arg Thr

<210> SEQ ID NO 168
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_D05 BC loop

<400> SEQUENCE: 168

Thr Ala Tyr Tyr Ser Thr Ile Lys
1 5

-continued

<210> SEQ ID NO 169
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_D05 DE loop

<400> SEQUENCE: 169

```
Gly Pro Lys His His
1               5
```

<210> SEQ ID NO 170
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_D05 FG loop

<400> SEQUENCE: 170

```
Tyr Asn Thr Lys Pro Gly Tyr His Ala His Gln
1               5                   10
```

<210> SEQ ID NO 171
<211> LENGTH: 91
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_D05 w/ N leader

<400> SEQUENCE: 171

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Thr Ala Tyr Tyr Ser Thr Ile Lys Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

Thr Val Gly Pro Lys His His Ala Thr Ile Ser Gly Leu Lys Pro Gly
    50                  55                  60

Val Asp Tyr Thr Ile Thr Val Tyr Ala Tyr Asn Thr Lys Pro Gly Tyr
65                  70                  75                  80

His Ala His Gln Ile Ser Ile Asn Tyr Arg Thr
                85                  90
```

<210> SEQ ID NO 172
<211> LENGTH: 97
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_D05 w/ N leader + his tag

<400> SEQUENCE: 172

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Thr Ala Tyr Tyr Ser Thr Ile Lys Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

Thr Val Gly Pro Lys His His Ala Thr Ile Ser Gly Leu Lys Pro Gly
    50                  55                  60
```

-continued

Val Asp Tyr Thr Ile Thr Val Tyr Ala Tyr Asn Thr Lys Pro Gly Tyr
65 70 75 80

His Ala His Gln Ile Ser Ile Asn Tyr Arg Thr His His His His His
85 90 95

His

<210> SEQ ID NO 173
<211> LENGTH: 98
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_D05 w/ N leader and C tail

<400> SEQUENCE: 173

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Thr Ala Tyr Tyr Ser Thr Ile Lys Tyr
20 25 30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
35 40 45

Thr Val Gly Pro Lys His His Ala Thr Ile Ser Gly Leu Lys Pro Gly
50 55 60

Val Asp Tyr Thr Ile Thr Val Tyr Ala Tyr Asn Thr Lys Pro Gly Tyr
65 70 75 80

His Ala His Gln Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro
85 90 95

Ser Gln

<210> SEQ ID NO 174
<211> LENGTH: 104
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_D05 w/ N leader and C
tail + his tag

<400> SEQUENCE: 174

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Thr Ala Tyr Tyr Ser Thr Ile Lys Tyr
20 25 30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
35 40 45

Thr Val Gly Pro Lys His His Ala Thr Ile Ser Gly Leu Lys Pro Gly
50 55 60

Val Asp Tyr Thr Ile Thr Val Tyr Ala Tyr Asn Thr Lys Pro Gly Tyr
65 70 75 80

His Ala His Gln Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro
85 90 95

Ser Gln His His His His His His
100

<210> SEQ ID NO 175
<211> LENGTH: 93
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

-continued

<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_D05 w/ N leader and
modified C-terminus including PC

<400> SEQUENCE: 175

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Thr Ala Tyr Tyr Ser Thr Ile Lys Tyr
20 25 30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
35 40 45

Thr Val Gly Pro Lys His His Ala Thr Ile Ser Gly Leu Lys Pro Gly
50 55 60

Val Asp Tyr Thr Ile Thr Val Tyr Ala Tyr Asn Thr Lys Pro Gly Tyr
65 70 75 80

His Ala His Gln Ile Ser Ile Asn Tyr Arg Thr Pro Cys
85 90

<210> SEQ ID NO 176
<211> LENGTH: 99
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_D05 w/ N leader and
modified C-terminus including PC + his tag

<400> SEQUENCE: 176

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Thr Ala Tyr Tyr Ser Thr Ile Lys Tyr
20 25 30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
35 40 45

Thr Val Gly Pro Lys His His Ala Thr Ile Ser Gly Leu Lys Pro Gly
50 55 60

Val Asp Tyr Thr Ile Thr Val Tyr Ala Tyr Asn Thr Lys Pro Gly Tyr
65 70 75 80

His Ala His Gln Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His
85 90 95

His His His

<210> SEQ ID NO 177
<211> LENGTH: 105
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_D05 full length

<400> SEQUENCE: 177

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Thr Ala Tyr Tyr Ser Thr Ile Lys
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

Phe Thr Val Gly Pro Lys His His Ala Thr Ile Ser Gly Leu Lys Pro
50 55 60

-continued

```
Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Tyr Asn Thr Lys Pro Gly
65                  70                  75                  80

Tyr His Ala His Gln Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys
                85                  90                  95

Pro Ser Gln His His His His His His
            100                 105


<210> SEQ ID NO 178
<211> LENGTH: 80
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_D10  core

<400> SEQUENCE: 178

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Arg Ile
1               5                   10                  15

Pro Ser Tyr His Ile Gln Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly
            20                  25                  30

Asn Ser Pro Val Gln Glu Phe Thr Val Tyr Gln Lys Tyr Ala Thr Ile
        35                  40                  45

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

Ser Pro Pro Lys Gln Leu Arg Phe Gly Ile Ser Ile Asn Tyr Arg Thr
65                  70                  75                  80


<210> SEQ ID NO 179
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_D10  BC loop

<400> SEQUENCE: 179

Arg Ile Pro Ser Tyr His Ile Gln
1               5


<210> SEQ ID NO 180
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_D10  DE loop

<400> SEQUENCE: 180

Tyr Gln Lys Tyr
1


<210> SEQ ID NO 181
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_D10  FG loop

<400> SEQUENCE: 181

Val Ser Pro Pro Lys Gln Leu Arg Phe Gly
1               5                   10


<210> SEQ ID NO 182
```

-continued

<211> LENGTH: 89
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_D10 w/ N leader

<400> SEQUENCE: 182

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Arg Ile Pro Ser Tyr His Ile Gln Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Val Ser Pro Pro Lys Gln Leu Arg
65                  70                  75                  80

Phe Gly Ile Ser Ile Asn Tyr Arg Thr
                85
```

<210> SEQ ID NO 183
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_D10 w/ N leader + his tag

<400> SEQUENCE: 183

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Arg Ile Pro Ser Tyr His Ile Gln Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Val Ser Pro Pro Lys Gln Leu Arg
65                  70                  75                  80

Phe Gly Ile Ser Ile Asn Tyr Arg Thr His His His His His His
                85                  90                  95
```

<210> SEQ ID NO 184
<211> LENGTH: 96
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_D10 w/ N leader and C tail

<400> SEQUENCE: 184

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Arg Ile Pro Ser Tyr His Ile Gln Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

Thr Val Tyr Gln Lys Tyr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val
    50                  55                  60
```

-continued

```
Asp Tyr Thr Ile Thr Val Tyr Ala Val Ser Pro Pro Lys Gln Leu Arg
65                  70                  75                  80

Phe Gly Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95


&lt;210&gt; SEQ ID NO 185
&lt;211&gt; LENGTH: 102
&lt;212&gt; TYPE: PRT
&lt;213&gt; ORGANISM: Artificial Sequence
&lt;220&gt; FEATURE:
&lt;223&gt; OTHER INFORMATION: Synthetic: ATI_1420_D10  w/ N leader and C
      tail + his tag

&lt;400&gt; SEQUENCE: 185

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Arg Ile Pro Ser Tyr His Ile Gln Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Val Ser Pro Pro Lys Gln Leu Arg
65                  70                  75                  80

Phe Gly Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95

His His His His His His
            100


&lt;210&gt; SEQ ID NO 186
&lt;211&gt; LENGTH: 91
&lt;212&gt; TYPE: PRT
&lt;213&gt; ORGANISM: Artificial Sequence
&lt;220&gt; FEATURE:
&lt;223&gt; OTHER INFORMATION: Synthetic: ATI_1420_D10  w/ N leader and
      modified C-terminus including PC

&lt;400&gt; SEQUENCE: 186

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Arg Ile Pro Ser Tyr His Ile Gln Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Val Ser Pro Pro Lys Gln Leu Arg
65                  70                  75                  80

Phe Gly Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90


&lt;210&gt; SEQ ID NO 187
&lt;211&gt; LENGTH: 97
&lt;212&gt; TYPE: PRT
&lt;213&gt; ORGANISM: Artificial Sequence
&lt;220&gt; FEATURE:
&lt;223&gt; OTHER INFORMATION: Synthetic: ATI_1420_D10  w/ N leader and
      modified C-terminus including PC + his tag
```

-continued

<400> SEQUENCE: 187

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Arg Ile Pro Ser Tyr His Ile Gln Tyr
20 25 30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
35 40 45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Val Ser Pro Pro Lys Gln Leu Arg
65 70 75 80

Phe Gly Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His His His
85 90 95

His

<210> SEQ ID NO 188
<211> LENGTH: 103
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_D010 full length

<400> SEQUENCE: 188

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Arg Ile Pro Ser Tyr His Ile Gln
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

Phe Thr Val Tyr Gln Lys Tyr Ala Thr Ile Ser Gly Leu Lys Pro Gly
50 55 60

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

Arg Phe Gly Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser
85 90 95

Gln His His His His His His
100

<210> SEQ ID NO 189
<211> LENGTH: 76
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_F10_core

<400> SEQUENCE: 189

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Pro Ala
1 5 10 15

Pro Pro Ser Tyr Val Phe Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly
20 25 30

Asn Ser Pro Val Gln Glu Phe Thr Val Tyr Pro Tyr Met Ala Thr Ile
35 40 45

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

Thr Ser Gly Phe Ser Ile Ser Ile Asn Tyr Arg Thr

-continued

```
65                  70                  75

<210> SEQ ID NO 190
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_F10  BC loop

<400> SEQUENCE: 190

Pro Ala Pro Pro Ser Tyr Val Phe
1               5


<210> SEQ ID NO 191
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_F10 DE loop

<400> SEQUENCE: 191

Tyr Pro Tyr Met
1


<210> SEQ ID NO 192
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_F10 FG loop

<400> SEQUENCE: 192

Tyr Thr Ser Gly Phe Ser
1               5


<210> SEQ ID NO 193
<211> LENGTH: 85
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_F10 w/ N leader

<400> SEQUENCE: 193

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Pro Ala Pro Pro Ser Tyr Val Phe Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Tyr Thr Ser Gly Phe Ser Ile Ser
65                  70                  75                  80

Ile Asn Tyr Arg Thr
                85


<210> SEQ ID NO 194
<211> LENGTH: 91
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_F10  w/ N leader + his tag
```

-continued

<400> SEQUENCE: 194

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Pro Ala Pro Pro Ser Tyr Val Phe Tyr
            20   25   30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35   40   45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Tyr Thr Ser Gly Phe Ser Ile Ser
65   70   75   80

Ile Asn Tyr Arg Thr His His His His His His
                85   90

<210> SEQ ID NO 195
<211> LENGTH: 92
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_F10 w/ N leader and C tail

<400> SEQUENCE: 195

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Pro Ala Pro Pro Ser Tyr Val Phe Tyr
            20   25   30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35   40   45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Tyr Thr Ser Gly Phe Ser Ile Ser
65   70   75   80

Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85   90

<210> SEQ ID NO 196
<211> LENGTH: 98
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_F10 w/ N leader and C
      tail + his tag

<400> SEQUENCE: 196

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Pro Ala Pro Pro Ser Tyr Val Phe Tyr
            20   25   30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35   40   45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Tyr Thr Ser Gly Phe Ser Ile Ser
65   70   75   80

Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His

-continued

```
                85                  90                  95

His His


<210> SEQ ID NO 197
<211> LENGTH: 87
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_F10  w/ N leader and
      modified C-terminus including PC

<400> SEQUENCE: 197

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Pro Ala Pro Pro Ser Tyr Val Phe Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Tyr Thr Ser Gly Phe Ser Ile Ser
65                  70                  75                  80

Ile Asn Tyr Arg Thr Pro Cys
                85


<210> SEQ ID NO 198
<211> LENGTH: 93
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_F10  w/ N leader and
      modified C-terminus including PC + his tag

<400> SEQUENCE: 198

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Pro Ala Pro Pro Ser Tyr Val Phe Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Tyr Thr Ser Gly Phe Ser Ile Ser
65                  70                  75                  80

Ile Asn Tyr Arg Thr Pro Cys His His His His His His
                85                  90


<210> SEQ ID NO 199
<211> LENGTH: 99
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1420_F10 full length

<400> SEQUENCE: 199

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp Pro Ala Pro Pro Ser Tyr Val Phe
```

-continued

```
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Tyr Pro Tyr Met Ala Thr Ile Ser Gly Leu Lys Pro Gly
    50                  55                  60

Val Asp Tyr Thr Ile Thr Val Tyr Ala Tyr Thr Ser Gly Phe Ser Ile
65                  70                  75                  80

Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His
                85                  90                  95

His His His


<210> SEQ ID NO 200
<211> LENGTH: 79
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_C05_core

<400> SEQUENCE: 200

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Tyr Met
1               5                   10                  15

Asp His Lys Ser Lys Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn
            20                  25                  30

Ser Pro Val Gln Glu Phe Thr Val Pro Asp Gln Arg Ala Thr Ile Ser
        35                  40                  45

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

Glu Ala His Tyr Leu Arg Asp Lys Ile Ser Ile Asn Tyr Arg Thr
65                  70                  75


<210> SEQ ID NO 201
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_C05  BC loop

<400> SEQUENCE: 201

Tyr Met Asp His Lys Ser Lys
1               5


<210> SEQ ID NO 202
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_C05 DE loop

<400> SEQUENCE: 202

Pro Asp Gln Arg
1


<210> SEQ ID NO 203
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_C05 FG loop

<400> SEQUENCE: 203
```

-continued

```
Leu Ser Glu Ala His Tyr Leu Arg Asp Lys
1               5                   10


<210> SEQ ID NO 204
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_C05 w/ N leader

<400> SEQUENCE: 204

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Tyr Met Asp His Lys Ser Lys Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

Val Pro Asp Gln Arg Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50                  55                  60

Tyr Thr Ile Thr Val Tyr Ala Leu Ser Glu Ala His Tyr Leu Arg Asp
65                  70                  75                  80

Lys Ile Ser Ile Asn Tyr Arg Thr
                85


<210> SEQ ID NO 205
<211> LENGTH: 94
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_C05  w/ N leader + his tag

<400> SEQUENCE: 205

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Tyr Met Asp His Lys Ser Lys Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

Val Pro Asp Gln Arg Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50                  55                  60

Tyr Thr Ile Thr Val Tyr Ala Leu Ser Glu Ala His Tyr Leu Arg Asp
65                  70                  75                  80

Lys Ile Ser Ile Asn Tyr Arg Thr His His His His His His
                85                  90


<210> SEQ ID NO 206
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_C05 w/ N leader and C tail

<400> SEQUENCE: 206

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Tyr Met Asp His Lys Ser Lys Tyr Arg
            20                  25                  30
```

-continued

```
Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

Val Pro Asp Gln Arg Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50                  55                  60

Tyr Thr Ile Thr Val Tyr Ala Leu Ser Glu Ala His Tyr Leu Arg Asp
65                  70                  75                  80

Lys Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95


<210> SEQ ID NO 207
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_C05  w/ N leader and C
      tail + his tag

<400> SEQUENCE: 207

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Tyr Met Asp His Lys Ser Lys Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

Val Pro Asp Gln Arg Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50                  55                  60

Tyr Thr Ile Thr Val Tyr Ala Leu Ser Glu Ala His Tyr Leu Arg Asp
65                  70                  75                  80

Lys Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His
                85                  90                  95

His His His His His
            100


<210> SEQ ID NO 208
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_C05  w/ N leader and
      modified C-terminus including PC

<400> SEQUENCE: 208

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Tyr Met Asp His Lys Ser Lys Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

Val Pro Asp Gln Arg Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50                  55                  60

Tyr Thr Ile Thr Val Tyr Ala Leu Ser Glu Ala His Tyr Leu Arg Asp
65                  70                  75                  80

Lys Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90


<210> SEQ ID NO 209
<211> LENGTH: 96
```

-continued

<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_C05 w/ N leader and modified C-terminus including PC + his tag

<400> SEQUENCE: 209

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Tyr Met Asp His Lys Ser Lys Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

Val Pro Asp Gln Arg Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50                  55                  60

Tyr Thr Ile Thr Val Tyr Ala Leu Ser Glu Ala His Tyr Leu Arg Asp
65                  70                  75                  80

Lys Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His His His His
                85                  90                  95
```

<210> SEQ ID NO 210
<211> LENGTH: 102
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_C05 full length

<400> SEQUENCE: 210

```
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp Tyr Met Asp His Lys Ser Lys Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

Thr Val Pro Asp Gln Arg Ala Thr Ile Ser Gly Leu Lys Pro Gly Val
    50                  55                  60

Asp Tyr Thr Ile Thr Val Tyr Ala Leu Ser Glu Ala His Tyr Leu Arg
65                  70                  75                  80

Asp Lys Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95

His His His His His His
            100
```

<210> SEQ ID NO 211
<211> LENGTH: 79
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_C06 core

<400> SEQUENCE: 211

```
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Glu Asn
1               5                   10                  15

Leu Ala Ser Tyr Gln Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn
            20                  25                  30

Ser Pro Val Gln Glu Phe Thr Val Pro Asp Gln Ala Ala Thr Ile Ser
        35                  40                  45
```

-continued

```
Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Leu Gln
    50                  55                  60

Thr Ala His Tyr Tyr Arg Gln His Ile Ser Ile Asn Tyr Arg Thr
65                  70                  75
```

<210> SEQ ID NO 212
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_C06 BC loop

<400> SEQUENCE: 212

```
Glu Asn Leu Ala Ser Tyr Gln
1               5
```

<210> SEQ ID NO 213
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_C06DE loop

<400> SEQUENCE: 213

```
Pro Asp Gln Ala
1
```

<210> SEQ ID NO 214
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_C06FG loop

<400> SEQUENCE: 214

```
Leu Gln Thr Ala His Tyr Tyr Arg Gln His
1               5                   10
```

<210> SEQ ID NO 215
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_C06 w/ N leader

<400> SEQUENCE: 215

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Glu Asn Leu Ala Ser Tyr Gln Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Gln Thr Ala His Tyr Tyr Arg Gln
65                  70                  75                  80

His Ile Ser Ile Asn Tyr Arg Thr
                85
```

<210> SEQ ID NO 216
<211> LENGTH: 94

-continued

<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_C06 w/ N leader + his tag

<400> SEQUENCE: 216

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Glu Asn Leu Ala Ser Tyr Gln Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Gln Thr Ala His Tyr Tyr Arg Gln
65                  70                  75                  80

His Ile Ser Ile Asn Tyr Arg Thr His His His His His His
                85                  90
```

<210> SEQ ID NO 217
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_C06w/ N leader and C tail

<400> SEQUENCE: 217

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Glu Asn Leu Ala Ser Tyr Gln Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Gln Thr Ala His Tyr Tyr Arg Gln
65                  70                  75                  80

His Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95
```

<210> SEQ ID NO 218
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_C06 w/ N leader and C
      tail + his tag

<400> SEQUENCE: 218

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Glu Asn Leu Ala Ser Tyr Gln Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

Val Pro Asp Gln Ala Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50                  55                  60
```

-continued

```
Tyr Thr Ile Thr Val Tyr Ala Leu Gln Thr Ala His Tyr Tyr Arg Gln
65                  70                  75                  80

His Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His
                85                  90                  95

His His His His His
            100


<210> SEQ ID NO 219
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_C06 w/ N leader and
      modified C-terminus including PC

<400> SEQUENCE: 219

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Glu Asn Leu Ala Ser Tyr Gln Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Gln Thr Ala His Tyr Tyr Arg Gln
65                  70                  75                  80

His Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90


<210> SEQ ID NO 220
<211> LENGTH: 96
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_C06 w/ N leader and
      modified C-terminus including PC + his tag

<400> SEQUENCE: 220

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Glu Asn Leu Ala Ser Tyr Gln Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Gln Thr Ala His Tyr Tyr Arg Gln
65                  70                  75                  80

His Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His His His His
                85                  90                  95


<210> SEQ ID NO 221
<211> LENGTH: 102
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_C06 full length

<400> SEQUENCE: 221
```

-continued

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Glu Asn Leu Ala Ser Tyr Gln Tyr
20 25 30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
35 40 45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Leu Gln Thr Ala His Tyr Tyr Arg
65 70 75 80

Gln His Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
85 90 95

His His His His His His
100

<210> SEQ ID NO 222
<211> LENGTH: 79
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI 1421_D05 core

<400> SEQUENCE: 222

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Tyr Tyr
1 5 10 15

Val Gln Tyr Asn Asp Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn
20 25 30

Ser Pro Val Gln Glu Phe Thr Val Pro Asp Gln Ser Ala Thr Ile Ser
35 40 45

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

Lys Ala His Tyr Tyr Arg Gln Asn Ile Ser Ile Asn Tyr Arg Thr
65 70 75

<210> SEQ ID NO 223
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI 1421_D05 BC loop

<400> SEQUENCE: 223

Tyr Tyr Val Gln Tyr Asn Asp
1 5

<210> SEQ ID NO 224
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI 1421_D05 DE loop

<400> SEQUENCE: 224

Pro Asp Gln Ser
1

<210> SEQ ID NO 225
<211> LENGTH: 10

-continued

<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI 1421_D05 FG loop

<400> SEQUENCE: 225

```
Leu Glu Lys Ala His Tyr Tyr Arg Gln Asn
1               5                   10
```

<210> SEQ ID NO 226
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI 1421_D05 w/ N leader

<400> SEQUENCE: 226

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Tyr Tyr Val Gln Tyr Asn Asp Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Lys Ala His Tyr Tyr Arg Gln
65                  70                  75                  80

Asn Ile Ser Ile Asn Tyr Arg Thr
                85
```

<210> SEQ ID NO 227
<211> LENGTH: 94
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI 1421_D05 w/ N leader + his tag

<400> SEQUENCE: 227

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Tyr Tyr Val Gln Tyr Asn Asp Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Lys Ala His Tyr Tyr Arg Gln
65                  70                  75                  80

Asn Ile Ser Ile Asn Tyr Arg Thr His His His His His His
                85                  90
```

<210> SEQ ID NO 228
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI 1421_D05 w/ N leader and C tail

<400> SEQUENCE: 228

-continued

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Tyr Tyr Val Gln Tyr Asn Asp Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Lys Ala His Tyr Tyr Arg Gln
65                  70                  75                  80

Asn Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95


<210> SEQ ID NO 229
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI 1421_D05 w/ N leader and C
      tail + his tag

<400> SEQUENCE: 229

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Tyr Tyr Val Gln Tyr Asn Asp Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Lys Ala His Tyr Tyr Arg Gln
65                  70                  75                  80

Asn Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His
                85                  90                  95

His His His His His
            100


<210> SEQ ID NO 230
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI 1421_D05 w/ N leader and
      modified C-terminus including PC

<400> SEQUENCE: 230

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Tyr Tyr Val Gln Tyr Asn Asp Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Lys Ala His Tyr Tyr Arg Gln
65                  70                  75                  80
```

-continued

```
Asn Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90


<210> SEQ ID NO 231
<211> LENGTH: 96
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI 1421_D05 w/ N leader and
      modified C-terminus including PC + his tag

<400> SEQUENCE: 231

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Tyr Tyr Val Gln Tyr Asn Asp Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Lys Ala His Tyr Tyr Arg Gln
65                  70                  75                  80

Asn Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His His His His
                85                  90                  95


<210> SEQ ID NO 232
<211> LENGTH: 102
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI 1421_D05  full length

<400> SEQUENCE: 232

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp Tyr Tyr Val Gln Tyr Asn Asp Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Leu Glu Lys Ala His Tyr Tyr Arg
65                  70                  75                  80

Gln Asn Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95

His His His His His His
            100


<210> SEQ ID NO 233
<211> LENGTH: 79
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_D06 core

<400> SEQUENCE: 233

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Gly His
1               5                   10                  15
```

-continued

```
Asn Tyr Asp Asp Glu Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn
            20                  25                  30

Ser Pro Val Gln Glu Phe Thr Val Pro Asp Gln Tyr Ala Thr Ile Ser
        35                  40                  45

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

Glu Ala His Val Arg Lys Asn His Ile Ser Ile Asn Tyr Arg Thr
65                  70                  75


<210> SEQ ID NO 234
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_D06 BC loop

<400> SEQUENCE: 234

Gly His Asn Tyr Asp Asp Glu
1               5


<210> SEQ ID NO 235
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_D06  DE loop

<400> SEQUENCE: 235

Pro Asp Gln Tyr
1


<210> SEQ ID NO 236
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_D06  FG loop

<400> SEQUENCE: 236

Leu Ala Glu Ala His Val Arg Lys Asn His
1               5                   10


<210> SEQ ID NO 237
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_D06 w/ N leader

<400> SEQUENCE: 237

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Gly His Asn Tyr Asp Asp Glu Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Ala Glu Ala His Val Arg Lys Asn
65                  70                  75                  80
```

-continued

```
His Ile Ser Ile Asn Tyr Arg Thr
                85


<210> SEQ ID NO 238
<211> LENGTH: 94
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_D06 w/ N leader + his tag

<400> SEQUENCE: 238

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Gly His Asn Tyr Asp Asp Glu Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Ala Glu Ala His Val Arg Lys Asn
65                  70                  75                  80

His Ile Ser Ile Asn Tyr Arg Thr His His His His His His
                85                  90


<210> SEQ ID NO 239
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_D06 w/ N leader and C tail

<400> SEQUENCE: 239

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Gly His Asn Tyr Asp Asp Glu Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Ala Glu Ala His Val Arg Lys Asn
65                  70                  75                  80

His Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95


<210> SEQ ID NO 240
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_D06 w/ N leader and C
      tail + his tag

<400> SEQUENCE: 240

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Gly His Asn Tyr Asp Asp Glu Tyr Arg
            20                  25                  30
```

-continued

```
Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Ala Glu Ala His Val Arg Lys Asn
65                  70                  75                  80

His Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His
                85                  90                  95

His His His His His
            100


<210> SEQ ID NO 241
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_D06 w/ N leader and
      modified C-terminus including PC

<400> SEQUENCE: 241

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Gly His Asn Tyr Asp Asp Glu Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Ala Glu Ala His Val Arg Lys Asn
65                  70                  75                  80

His Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90


<210> SEQ ID NO 242
<211> LENGTH: 96
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_D06 w/ N leader and
      modified C-terminus including PC + his tag

<400> SEQUENCE: 242

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Gly His Asn Tyr Asp Asp Glu Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Ala Glu Ala His Val Arg Lys Asn
65                  70                  75                  80

His Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His His His His
                85                  90                  95


<210> SEQ ID NO 243
<211> LENGTH: 102
```

-continued

<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_D06 full length

<400> SEQUENCE: 243

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1   5   10   15

Pro Thr Ser Leu Leu Ile Ser Trp Gly His Asn Tyr Asp Asp Glu Tyr
            20   25   30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35   40   45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Leu Ala Glu Ala His Val Arg Lys
65   70   75   80

Asn His Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85   90   95

His His His His His His
            100

<210> SEQ ID NO 244
<211> LENGTH: 79
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_E03 core

<400> SEQUENCE: 244

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Val Tyr
1   5   10   15

His Tyr Asp Ala Gln Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn
            20   25   30

Ser Pro Val Gln Glu Phe Thr Val Pro Asp Gln Lys Ala Thr Ile Ser
        35   40   45

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

Glu Ala His His Lys Arg Asp Ser Ile Ser Ile Asn Tyr Arg Thr
65   70   75

<210> SEQ ID NO 245
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_E03 BC loop

<400> SEQUENCE: 245

Val Tyr His Tyr Asp Ala Gln
1   5

<210> SEQ ID NO 246
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_E03 DE loop

<400> SEQUENCE: 246

-continued

```
Pro Asp Gln Lys
1


<210> SEQ ID NO 247
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_E03 FG loop

<400> SEQUENCE: 247

Leu Ser Glu Ala His His Lys Arg Asp Ser
1               5                   10


<210> SEQ ID NO 248
<211> LENGTH: 94
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_E03 w/ N leader

<400> SEQUENCE: 248

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

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

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Ser Glu Ala His His Lys Arg Asp
65                  70                  75                  80

Ser Ile Ser Ile Asn Tyr Arg Thr His His His His His His
                85                  90


<210> SEQ ID NO 249
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_E03w/ N leader + his tag

<400> SEQUENCE: 249

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

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

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Ser Glu Ala His His Lys Arg Asp
65                  70                  75                  80

Ser Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95


<210> SEQ ID NO 250
<211> LENGTH: 101
<212> TYPE: PRT
```

-continued

```
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_E03w/ N leader and C tail

<400> SEQUENCE: 250

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

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

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Ser Glu Ala His His Lys Arg Asp
65                  70                  75                  80

Ser Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His
                85                  90                  95

His His His His His
            100


<210> SEQ ID NO 251
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_E03 w/ N leader and C
      tail + his tag

<400> SEQUENCE: 251

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

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

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Ser Glu Ala His His Lys Arg Asp
65                  70                  75                  80

Ser Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90


<210> SEQ ID NO 252
<211> LENGTH: 96
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_E03 w/ N leader and
      modified C-terminus including PC

<400> SEQUENCE: 252

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

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

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45
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Val Pro Asp Gln Lys Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50   55   60

Tyr Thr Ile Thr Val Tyr Ala Leu Ser Glu Ala His His Lys Arg Asp
65   70   75   80

Ser Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His His His His
                85   90   95

<210> SEQ ID NO 253
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_E03 w/ N leader and modified C-terminus including PC + his tag

<400> SEQUENCE: 253

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

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

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35   40   45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Ser Glu Ala His His Lys Arg Asp
65   70   75   80

Ser Ile Ser Ile Asn Tyr Arg Thr
                85

<210> SEQ ID NO 254
<211> LENGTH: 102
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_E03 full length

<400> SEQUENCE: 254

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1   5   10   15

Pro Thr Ser Leu Leu Ile Ser Trp Val Tyr His Tyr Asp Ala Gln Tyr
            20   25   30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35   40   45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Leu Ser Glu Ala His His Lys Arg
65   70   75   80

Asp Ser Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85   90   95

His His His His His His
            100

<210> SEQ ID NO 255
<211> LENGTH: 79
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_E04 core

-continued

<400> SEQUENCE: 255

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Ser Tyr
1   5   10   15

Asn Gly Pro Ile Glu Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn
            20   25   30

Ser Pro Val Gln Glu Phe Thr Val Pro Asp Gln Gln Ala Thr Ile Ser
        35   40   45

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

Glu Ala His Tyr Ser Arg Gln Ser Ile Ser Ile Asn Tyr Arg Thr
65   70   75

<210> SEQ ID NO 256
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_E04 BC loop

<400> SEQUENCE: 256

Ser Tyr Asn Gly Pro Ile Glu
1   5

<210> SEQ ID NO 257
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_E04 DE loop

<400> SEQUENCE: 257

Pro Asp Gln Gln
1

<210> SEQ ID NO 258
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_E04 FG loop

<400> SEQUENCE: 258

Leu Glu Glu Ala His Tyr Ser Arg Gln Ser
1   5   10

<210> SEQ ID NO 259
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_E04 w/ N leader

<400> SEQUENCE: 259

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Ser Tyr Asn Gly Pro Ile Glu Tyr Arg
            20   25   30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35   40   45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Glu Ala His Tyr Ser Arg Gln
65   70   75   80

Ser Ile Ser Ile Asn Tyr Arg Thr
                85

<210> SEQ ID NO 260
<211> LENGTH: 94
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_E04 w/ N leader + his tag

<400> SEQUENCE: 260

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Ser Tyr Asn Gly Pro Ile Glu Tyr Arg
            20   25   30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35   40   45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Glu Ala His Tyr Ser Arg Gln
65   70   75   80

Ser Ile Ser Ile Asn Tyr Arg Thr His His His His His His
                85   90

<210> SEQ ID NO 261
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_E04 w/ N leader and C tail

<400> SEQUENCE: 261

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Ser Tyr Asn Gly Pro Ile Glu Tyr Arg
            20   25   30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35   40   45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Glu Ala His Tyr Ser Arg Gln
65   70   75   80

Ser Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85   90   95

<210> SEQ ID NO 262
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_E04 w/ N leader and C
      tail + his tag

<400> SEQUENCE: 262

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Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ser Tyr Asn Gly Pro Ile Glu Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Glu Ala His Tyr Ser Arg Gln
65                  70                  75                  80

Ser Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His
                85                  90                  95

His His His His His
            100


<210> SEQ ID NO 263
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_E04 w/ N leader and
      modified C-terminus including PC

<400> SEQUENCE: 263

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ser Tyr Asn Gly Pro Ile Glu Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Glu Ala His Tyr Ser Arg Gln
65                  70                  75                  80

Ser Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90


<210> SEQ ID NO 264
<211> LENGTH: 96
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_E04 w/ N leader and
      modified C-terminus including PC + his tag

<400> SEQUENCE: 264

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ser Tyr Asn Gly Pro Ile Glu Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Glu Ala His Tyr Ser Arg Gln
65                  70                  75                  80
```

-continued

```
Ser Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His His His His
                85                  90                  95


<210> SEQ ID NO 265
<211> LENGTH: 102
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_E04 full length

<400> SEQUENCE: 265

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp Ser Tyr Asn Gly Pro Ile Glu Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Leu Glu Glu Ala His Tyr Ser Arg
65                  70                  75                  80

Gln Ser Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95

His His His His His His
            100


<210> SEQ ID NO 266
<211> LENGTH: 79
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_F03 core

<400> SEQUENCE: 266

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Ile Ser
1               5                   10                  15

Val Gln Thr Tyr Asp Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn
            20                  25                  30

Ser Pro Val Gln Glu Phe Thr Val Pro Asp Gln Ser Ala Thr Ile Ser
        35                  40                  45

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

Lys Ala His Tyr Tyr Arg Gln Asn Ile Ser Ile Asn Tyr Arg Thr
65                  70                  75


<210> SEQ ID NO 267
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_F03 BC loop

<400> SEQUENCE: 267

Ile Ser Val Gln Thr Tyr Asp
1               5


<210> SEQ ID NO 268
<211> LENGTH: 4
<212> TYPE: PRT
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-continued

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_F03 DE loop

<400> SEQUENCE: 268

Pro Asp Gln Ser
1

<210> SEQ ID NO 269
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_F03 FG loop

<400> SEQUENCE: 269

Leu Glu Lys Ala His Tyr Tyr Arg Gln Asn
1   5   10

<210> SEQ ID NO 270
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_F03 w/ N leader

<400> SEQUENCE: 270

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

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

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35   40   45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Lys Ala His Tyr Tyr Arg Gln
65   70   75   80

Asn Ile Ser Ile Asn Tyr Arg Thr
                85

<210> SEQ ID NO 271
<211> LENGTH: 94
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_F03 w/ N leader + his tag

<400> SEQUENCE: 271

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

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

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35   40   45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Lys Ala His Tyr Tyr Arg Gln
65   70   75   80

Asn Ile Ser Ile Asn Tyr Arg Thr His His His His His His

-continued

```
                85                  90


<210> SEQ ID NO 272
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_F03 w/ N leader and C tail

<400> SEQUENCE: 272

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

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

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Lys Ala His Tyr Tyr Arg Gln
65                  70                  75                  80

Asn Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95


<210> SEQ ID NO 273
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_F03 w/ N leader and C
      tail + his tag

<400> SEQUENCE: 273

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

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

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Lys Ala His Tyr Tyr Arg Gln
65                  70                  75                  80

Asn Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His
                85                  90                  95

His His His His His
            100


<210> SEQ ID NO 274
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_F03 w/ N leader and
      modified C-terminus including PC

<400> SEQUENCE: 274

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15
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```
Thr Ser Leu Leu Ile Ser Trp Ile Ser Val Gln Thr Tyr Asp Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Lys Ala His Tyr Tyr Arg Gln
65                  70                  75                  80

Asn Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90


<210> SEQ ID NO 275
<211> LENGTH: 96
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_F03 w/ N leader and
      modified C-terminus including PC + his tag

<400> SEQUENCE: 275

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

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

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Lys Ala His Tyr Tyr Arg Gln
65                  70                  75                  80

Asn Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His His His His
                85                  90                  95


<210> SEQ ID NO 276
<211> LENGTH: 102
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_F03 full length

<400> SEQUENCE: 276

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp Ile Ser Val Gln Thr Tyr Asp Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Leu Glu Lys Ala His Tyr Tyr Arg
65                  70                  75                  80

Gln Asn Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95

His His His His His His
            100
```

-continued

<210> SEQ ID NO 277
<211> LENGTH: 79
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_F05 core

<400> SEQUENCE: 277

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Leu Ala
1   5   10   15

Arg His Asp Ala Arg Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn
            20   25   30

Ser Pro Val Gln Glu Phe Thr Val Pro Asp Arg Met Ala Thr Ile Ser
        35   40   45

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

Gln Ala His Tyr Tyr Arg Leu Tyr Ile Ser Ile Asn Tyr Arg Thr
65   70   75

<210> SEQ ID NO 278
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_F05 BC loop

<400> SEQUENCE: 278

Leu Ala Arg His Asp Ala Arg
1   5

<210> SEQ ID NO 279
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_F05 DE loop

<400> SEQUENCE: 279

Pro Asp Arg Met
1

<210> SEQ ID NO 280
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_F05 FG loop

<400> SEQUENCE: 280

Leu Glu Gln Ala His Tyr Tyr Arg Leu Tyr
1   5   10

<210> SEQ ID NO 281
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_F05 w/ N leader

<400> SEQUENCE: 281

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

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Thr Ser Leu Leu Ile Ser Trp Leu Ala Arg His Asp Ala Arg Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

Val Pro Asp Arg Met Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50                  55                  60

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Gln Ala His Tyr Tyr Arg Leu
65                  70                  75                  80

Tyr Ile Ser Ile Asn Tyr Arg Thr
                85


<210> SEQ ID NO 282
<211> LENGTH: 94
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_F05 w/ N leader + his tag

<400> SEQUENCE: 282

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Leu Ala Arg His Asp Ala Arg Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

Val Pro Asp Arg Met Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50                  55                  60

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Gln Ala His Tyr Tyr Arg Leu
65                  70                  75                  80

Tyr Ile Ser Ile Asn Tyr Arg Thr His His His His His His
                85                  90


<210> SEQ ID NO 283
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_F05 w/ N leader and C tail

<400> SEQUENCE: 283

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Leu Ala Arg His Asp Ala Arg Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

Val Pro Asp Arg Met Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50                  55                  60

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Gln Ala His Tyr Tyr Arg Leu
65                  70                  75                  80

Tyr Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95


<210> SEQ ID NO 284
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
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-continued

<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_F05 w/ N leader and C
tail + his tag

<400> SEQUENCE: 284

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Leu Ala Arg His Asp Ala Arg Tyr Arg
20 25 30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
35 40 45

Val Pro Asp Arg Met Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
50 55 60

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Gln Ala His Tyr Tyr Arg Leu
65 70 75 80

Tyr Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His
85 90 95

His His His His His
100

<210> SEQ ID NO 285
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_F05 w/ N leader and
modified C-terminus including PC

<400> SEQUENCE: 285

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Leu Ala Arg His Asp Ala Arg Tyr Arg
20 25 30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
35 40 45

Val Pro Asp Arg Met Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
50 55 60

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Gln Ala His Tyr Tyr Arg Leu
65 70 75 80

Tyr Ile Ser Ile Asn Tyr Arg Thr Pro Cys
85 90

<210> SEQ ID NO 286
<211> LENGTH: 96
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_F05 w/ N leader and
modified C-terminus including PC + his tag

<400> SEQUENCE: 286

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Leu Ala Arg His Asp Ala Arg Tyr Arg
20 25 30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
35 40 45

-continued

Val Pro Asp Arg Met Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50   55   60

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Gln Ala His Tyr Tyr Arg Leu
65   70   75   80

Tyr Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His His His His
                85   90   95

<210> SEQ ID NO 287
<211> LENGTH: 102
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_F05 full length

<400> SEQUENCE: 287

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1   5   10   15

Pro Thr Ser Leu Leu Ile Ser Trp Leu Ala Arg His Asp Ala Arg Tyr
            20   25   30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35   40   45

Thr Val Pro Asp Arg Met Ala Thr Ile Ser Gly Leu Lys Pro Gly Val
    50   55   60

Asp Tyr Thr Ile Thr Val Tyr Ala Leu Glu Gln Ala His Tyr Tyr Arg
65   70   75   80

Leu Tyr Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85   90   95

His His His His His His
            100

<210> SEQ ID NO 288
<211> LENGTH: 82
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_G07 core

<400> SEQUENCE: 288

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp His Ser
1   5   10   15

Pro Thr Ser Gly Ile Thr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly
            20   25   30

Asn Ser Pro Val Gln Glu Phe Thr Val Pro Tyr Asp Pro Ser Ala Thr
        35   40   45

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

Pro Tyr Gly Ser Gln Tyr Tyr Pro Gly Tyr His Ile Ser Ile Asn Tyr
65   70   75   80

Arg Thr

<210> SEQ ID NO 289
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_G07 BC loop

<400> SEQUENCE: 289

-continued

```
His Ser Pro Thr Ser Gly Ile Thr
1               5


<210> SEQ ID NO 290
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_G07 DE loop

<400> SEQUENCE: 290

Pro Tyr Asp Pro Ser
1               5


<210> SEQ ID NO 291
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_G07 FG loop

<400> SEQUENCE: 291

Pro Tyr Gly Ser Gln Tyr Tyr Pro Gly Tyr His
1               5                   10


<210> SEQ ID NO 292
<211> LENGTH: 91
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_G07 w/ N leader

<400> SEQUENCE: 292

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp His Ser Pro Thr Ser Gly Ile Thr Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Pro Tyr Gly Ser Gln Tyr Tyr
65                  70                  75                  80

Pro Gly Tyr His Ile Ser Ile Asn Tyr Arg Thr
                85                  90


<210> SEQ ID NO 293
<211> LENGTH: 97
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_G07 w/ N leader + his tag

<400> SEQUENCE: 293

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp His Ser Pro Thr Ser Gly Ile Thr Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45
```

-continued

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Pro Tyr Gly Ser Gln Tyr Tyr
65                  70                  75                  80

Pro Gly Tyr His Ile Ser Ile Asn Tyr Arg Thr His His His His His
                85                  90                  95

His


<210> SEQ ID NO 294
<211> LENGTH: 98
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_G07 w/ N leader and C tail

<400> SEQUENCE: 294

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp His Ser Pro Thr Ser Gly Ile Thr Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Pro Tyr Gly Ser Gln Tyr Tyr
65                  70                  75                  80

Pro Gly Tyr His Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro
                85                  90                  95

Ser Gln


<210> SEQ ID NO 295
<211> LENGTH: 104
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_G07 w/ N leader and C
      tail + his tag

<400> SEQUENCE: 295

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp His Ser Pro Thr Ser Gly Ile Thr Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Pro Tyr Gly Ser Gln Tyr Tyr
65                  70                  75                  80

Pro Gly Tyr His Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro
                85                  90                  95

Ser Gln His His His His His His
            100


<210> SEQ ID NO 296
```

-continued

<211> LENGTH: 93
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_G07 w/ N leader and modified C-terminus including PC

<400> SEQUENCE: 296

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp His Ser Pro Thr Ser Gly Ile Thr Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Pro Tyr Gly Ser Gln Tyr Tyr
65                  70                  75                  80

Pro Gly Tyr His Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90
```

<210> SEQ ID NO 297
<211> LENGTH: 99
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_G07 w/ N leader and modified C-terminus including PC + his tag

<400> SEQUENCE: 297

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp His Ser Pro Thr Ser Gly Ile Thr Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Pro Tyr Gly Ser Gln Tyr Tyr
65                  70                  75                  80

Pro Gly Tyr His Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His
                85                  90                  95

His His His
```

<210> SEQ ID NO 298
<211> LENGTH: 105
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_G07 full length

<400> SEQUENCE: 298

```
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp His Ser Pro Thr Ser Gly Ile Thr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45
```

-continued

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

Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Pro Tyr Gly Ser Gln Tyr
65                  70                  75                  80

Tyr Pro Gly Tyr His Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys
                85                  90                  95

Pro Ser Gln His His His His His His
            100                 105
```

<210> SEQ ID NO 299
<211> LENGTH: 79
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_H03 core

<400> SEQUENCE: 299

```
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Val Tyr
1               5                   10                  15

His Tyr Asp Ala Gln Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn
            20                  25                  30

Ser Pro Val Gln Glu Phe Thr Val Pro Asp Ser Ser Ala Thr Ile Ser
        35                  40                  45

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

Gln Ala His Ile Asp Arg Thr Thr Ile Ser Ile Asn Tyr Arg Thr
65                  70                  75
```

<210> SEQ ID NO 300
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_H03 BC loop

<400> SEQUENCE: 300

```
Val Tyr His Tyr Asp Ala Gln
1               5
```

<210> SEQ ID NO 301
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_H03 DE loop

<400> SEQUENCE: 301

```
Pro Asp Ser Ser
1
```

<210> SEQ ID NO 302
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_H03 FG loop

<400> SEQUENCE: 302

```
Leu Glu Gln Ala His Ile Asp Arg Thr Thr
1               5                   10
```

-continued

<210> SEQ ID NO 303
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_H03 w/ N leader

<400> SEQUENCE: 303

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

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

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Gln Ala His Ile Asp Arg Thr
65                  70                  75                  80

Thr Ile Ser Ile Asn Tyr Arg Thr
                85
```

<210> SEQ ID NO 304
<211> LENGTH: 94
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_H03 w/ N leader + his tag

<400> SEQUENCE: 304

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

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

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Gln Ala His Ile Asp Arg Thr
65                  70                  75                  80

Thr Ile Ser Ile Asn Tyr Arg Thr His His His His His His
                85                  90
```

<210> SEQ ID NO 305
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_H03 w/ N leader and C tail

<400> SEQUENCE: 305

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

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

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45
```

-continued

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Gln Ala His Ile Asp Arg Thr
65   70   75   80

Thr Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85   90   95

<210> SEQ ID NO 306
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_H03 w/ N leader and C
      tail + his tag

<400> SEQUENCE: 306

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

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

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35   40   45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Gln Ala His Ile Asp Arg Thr
65   70   75   80

Thr Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His
                85   90   95

His His His His His
            100

<210> SEQ ID NO 307
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_H03 w/ N leader and
      modified C-terminus including PC

<400> SEQUENCE: 307

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

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

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35   40   45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Gln Ala His Ile Asp Arg Thr
65   70   75   80

Thr Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85   90

<210> SEQ ID NO 308
<211> LENGTH: 96
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

-continued

<223> OTHER INFORMATION: Synthetic: ATI_1421_H03 w/ N leader and
      modified C-terminus including PC + his tag

<400> SEQUENCE: 308

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

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

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Gln Ala His Ile Asp Arg Thr
65                  70                  75                  80

Thr Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His His His His
                85                  90                  95
```

<210> SEQ ID NO 309
<211> LENGTH: 102
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_H03 full length

<400> SEQUENCE: 309

```
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp Val Tyr His Tyr Asp Ala Gln Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Leu Glu Gln Ala His Ile Asp Arg
65                  70                  75                  80

Thr Thr Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95

His His His His His His
            100
```

<210> SEQ ID NO 310
<211> LENGTH: 79
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_H05 core

<400> SEQUENCE: 310

```
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Thr Ser
1               5                   10                  15

Val Leu Leu Lys Asp Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn
            20                  25                  30

Ser Pro Val Gln Glu Phe Thr Val Pro Asp Gln His Ala Thr Ile Ser
        35                  40                  45

Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Leu Gln
    50                  55                  60
```

-continued

Asn Ala His His Glu Arg Leu Tyr Ile Ser Ile Asn Tyr Arg Thr
65 70 75

<210> SEQ ID NO 311
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_H05 BC loop

<400> SEQUENCE: 311

Thr Ser Val Leu Leu Lys Asp
1 5

<210> SEQ ID NO 312
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_H05 DE loop

<400> SEQUENCE: 312

Pro Asp Gln His
1

<210> SEQ ID NO 313
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_H05 FG loop

<400> SEQUENCE: 313

Leu Gln Asn Ala His His Glu Arg Leu Tyr
1 5 10

<210> SEQ ID NO 314
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_H05 w/ N leader

<400> SEQUENCE: 314

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Thr Ser Val Leu Leu Lys Asp Tyr Arg
20 25 30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
35 40 45

Val Pro Asp Gln His Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
50 55 60

Tyr Thr Ile Thr Val Tyr Ala Leu Gln Asn Ala His His Glu Arg Leu
65 70 75 80

Tyr Ile Ser Ile Asn Tyr Arg Thr
85

<210> SEQ ID NO 315
<211> LENGTH: 94
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

-continued

<223> OTHER INFORMATION: Synthetic: ATI_1421_H05 w/ N leader + his tag

<400> SEQUENCE: 315

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Thr Ser Val Leu Leu Lys Asp Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

Val Pro Asp Gln His Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50                  55                  60

Tyr Thr Ile Thr Val Tyr Ala Leu Gln Asn Ala His His Glu Arg Leu
65                  70                  75                  80

Tyr Ile Ser Ile Asn Tyr Arg Thr His His His His His His
                85                  90
```

<210> SEQ ID NO 316
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_H05 w/ N leader and C tail

<400> SEQUENCE: 316

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Thr Ser Val Leu Leu Lys Asp Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

Val Pro Asp Gln His Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50                  55                  60

Tyr Thr Ile Thr Val Tyr Ala Leu Gln Asn Ala His His Glu Arg Leu
65                  70                  75                  80

Tyr Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95
```

<210> SEQ ID NO 317
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_H05 w/ N leader and C
      tail + his tag

<400> SEQUENCE: 317

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Thr Ser Val Leu Leu Lys Asp Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

Val Pro Asp Gln His Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50                  55                  60

Tyr Thr Ile Thr Val Tyr Ala Leu Gln Asn Ala His His Glu Arg Leu
65                  70                  75                  80
```

-continued

```
Tyr Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His
                85                  90                  95

His His His His His
            100


<210> SEQ ID NO 318
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_H05 w/ N leader and
      modified C-terminus including PC

<400> SEQUENCE: 318

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Thr Ser Val Leu Leu Lys Asp Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

Val Pro Asp Gln His Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50                  55                  60

Tyr Thr Ile Thr Val Tyr Ala Leu Gln Asn Ala His His Glu Arg Leu
65                  70                  75                  80

Tyr Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90


<210> SEQ ID NO 319
<211> LENGTH: 96
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_H05 w/ N leader and
      modified C-terminus including PC + his tag

<400> SEQUENCE: 319

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Thr Ser Val Leu Leu Lys Asp Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

Val Pro Asp Gln His Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50                  55                  60

Tyr Thr Ile Thr Val Tyr Ala Leu Gln Asn Ala His His Glu Arg Leu
65                  70                  75                  80

Tyr Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His His His His
                85                  90                  95


<210> SEQ ID NO 320
<211> LENGTH: 102
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1421_H05 full length

<400> SEQUENCE: 320

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15
```

-continued

```
Pro Thr Ser Leu Leu Ile Ser Trp Thr Ser Val Leu Leu Lys Asp Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

Thr Val Pro Asp Gln His Ala Thr Ile Ser Gly Leu Lys Pro Gly Val
    50                  55                  60

Asp Tyr Thr Ile Thr Val Tyr Ala Leu Gln Asn Ala His His Glu Arg
65                  70                  75                  80

Leu Tyr Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95

His His His His His His
            100
```

```
<210> SEQ ID NO 321
<211> LENGTH: 79
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_E06 core

<400> SEQUENCE: 321

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Leu Pro
1               5                   10                  15

Ser Tyr Tyr Ile Thr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn
            20                  25                  30

Ser Pro Val Gln Glu Phe Thr Val Ser Lys Asp Leu Ala Thr Ile Ser
        35                  40                  45

Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Phe Asn
    50                  55                  60

Gly Ser Ser Tyr Tyr Thr Phe Gly Ile Ser Ile Asn Tyr Arg Thr
65                  70                  75
```

```
<210> SEQ ID NO 322
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_E06 BC loop

<400> SEQUENCE: 322

Leu Pro Ser Tyr Tyr Ile Thr
1               5
```

```
<210> SEQ ID NO 323
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_E06 DE loop

<400> SEQUENCE: 323

Ser Lys Asp Leu
1
```

```
<210> SEQ ID NO 324
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
```

-continued

<223> OTHER INFORMATION: Synthetic: ATI_1422_E06 FG loop

<400> SEQUENCE: 324

```
Phe Asn Gly Ser Ser Tyr Tyr Thr Phe Gly
1               5                   10
```

<210> SEQ ID NO 325
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_E06 w/ N leader

<400> SEQUENCE: 325

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Leu Pro Ser Tyr Tyr Ile Thr Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Phe Asn Gly Ser Ser Tyr Tyr Thr Phe
65                  70                  75                  80

Gly Ile Ser Ile Asn Tyr Arg Thr
                85
```

<210> SEQ ID NO 326
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_E06 w/ N leader + his tag

<400> SEQUENCE: 326

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Leu Pro Ser Tyr Tyr Ile Thr Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Phe Asn Gly Ser Ser Tyr Tyr Thr Phe
65                  70                  75                  80

Gly Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His
                85                  90                  95

His His His His His
            100
```

<210> SEQ ID NO 327
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_E06 w/ N leader and C tail

<400> SEQUENCE: 327

-continued

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Leu Pro Ser Tyr Tyr Ile Thr Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Phe Asn Gly Ser Ser Tyr Tyr Thr Phe
65                  70                  75                  80

Gly Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His
                85                  90                  95

His His His His His
            100
```

<210> SEQ ID NO 328
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_E06 w/ N leader and C tail + his tag

<400> SEQUENCE: 328

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Leu Pro Ser Tyr Tyr Ile Thr Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Phe Asn Gly Ser Ser Tyr Tyr Thr Phe
65                  70                  75                  80

Gly Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90
```

<210> SEQ ID NO 329
<211> LENGTH: 96
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_E06 w/ N leader and modified C-terminus including PC

<400> SEQUENCE: 329

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Leu Pro Ser Tyr Tyr Ile Thr Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Phe Asn Gly Ser Ser Tyr Tyr Thr Phe
65                  70                  75                  80
```

-continued

```
Gly Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His His His His
                85                  90                  95


<210> SEQ ID NO 330
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_E06 w/ N leader and
      modified C-terminus including PC + his tag

<400> SEQUENCE: 330

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Leu Pro Ser Tyr Tyr Ile Thr Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Phe Asn Gly Ser Ser Tyr Tyr Thr Phe
65                  70                  75                  80

Gly Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His
                85                  90                  95

His His His His His
            100


<210> SEQ ID NO 331
<211> LENGTH: 89
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_E06 full length

<400> SEQUENCE: 331

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp Leu Pro Ser Tyr Tyr Ile Thr Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Phe Asn Gly Ser Ser Tyr Tyr Thr
65                  70                  75                  80

Phe Gly Ile Ser Ile Asn Tyr Arg Thr
                85


<210> SEQ ID NO 332
<211> LENGTH: 78
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_F04 core

<400> SEQUENCE: 332

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Ser Ile
1               5                   10                  15
```

-continued

```
Pro Ser Tyr Phe Ile Ser Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly
            20                  25                  30

Asn Ser Pro Val Gln Glu Phe Thr Val Tyr Lys Asn Tyr Ala Thr Ile
        35                  40                  45

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

Glu Gly Ile Met Phe Tyr Asn Ile Ser Ile Asn Tyr Arg Thr
65                  70                  75


<210> SEQ ID NO 333
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_F04 BC loop

<400> SEQUENCE: 333

Ser Ile Pro Ser Tyr Phe Ile Ser
1               5


<210> SEQ ID NO 334
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_F04 DE loop

<400> SEQUENCE: 334

Tyr Lys Asn Tyr
1


<210> SEQ ID NO 335
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_F04 FG loop

<400> SEQUENCE: 335

Ser Glu Gly Ile Met Phe Tyr Asn
1               5


<210> SEQ ID NO 336
<211> LENGTH: 87
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_F04w/ N leader

<400> SEQUENCE: 336

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ser Ile Pro Ser Tyr Phe Ile Ser Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Ser Glu Gly Ile Met Phe Tyr Asn
65                  70                  75                  80
```

-continued

```
Ile Ser Ile Asn Tyr Arg Thr
                85


<210> SEQ ID NO 337
<211> LENGTH: 93
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_F04w/ N leader + his tag

<400> SEQUENCE: 337

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ser Ile Pro Ser Tyr Phe Ile Ser Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Ser Glu Gly Ile Met Phe Tyr Asn
65                  70                  75                  80

Ile Ser Ile Asn Tyr Arg Thr His His His His His His
                85                  90


<210> SEQ ID NO 338
<211> LENGTH: 94
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_F04 w/ N leader and C tail

<400> SEQUENCE: 338

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ser Ile Pro Ser Tyr Phe Ile Ser Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Ser Glu Gly Ile Met Phe Tyr Asn
65                  70                  75                  80

Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90


<210> SEQ ID NO 339
<211> LENGTH: 100
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_F04 w/ N leader and C
      tail + his tag

<400> SEQUENCE: 339

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ser Ile Pro Ser Tyr Phe Ile Ser Tyr
            20                  25                  30
```

-continued

```
Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Ser Glu Gly Ile Met Phe Tyr Asn
65                  70                  75                  80

Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His His
                85                  90                  95

His His His His
            100


<210> SEQ ID NO 340
<211> LENGTH: 89
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_F04 w/ N leader and
      modified C-terminus including PC

<400> SEQUENCE: 340

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ser Ile Pro Ser Tyr Phe Ile Ser Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Ser Glu Gly Ile Met Phe Tyr Asn
65                  70                  75                  80

Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85


<210> SEQ ID NO 341
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_F04 w/ N leader and
      modified C-terminus including PC + his tag

<400> SEQUENCE: 341

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ser Ile Pro Ser Tyr Phe Ile Ser Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Ser Glu Gly Ile Met Phe Tyr Asn
65                  70                  75                  80

Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His His His His
                85                  90                  95


<210> SEQ ID NO 342
<211> LENGTH: 101
```

-continued

```
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_F04 full length

<400> SEQUENCE: 342

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp Ser Ile Pro Ser Tyr Phe Ile Ser
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Ser Glu Gly Ile Met Phe Tyr
65                  70                  75                  80

Asn Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His
                85                  90                  95

His His His His His
            100


<210> SEQ ID NO 343
<211> LENGTH: 77
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_F05 core

<400> SEQUENCE: 343

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Pro Tyr
1               5                   10                  15

Pro Arg Gly Pro Tyr Val Phe Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
            20                  25                  30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Tyr Pro Gly Gln Ala Thr
        35                  40                  45

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

Tyr Thr Ser Gly Tyr Val Ile Ser Ile Asn Tyr Arg Thr
65                  70                  75


<210> SEQ ID NO 344
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_F05 BC loop

<400> SEQUENCE: 344

Pro Tyr Pro Arg Gly Pro Tyr Val Phe
1               5


<210> SEQ ID NO 345
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_F05 DE loop

<400> SEQUENCE: 345
```

-continued

Tyr Pro Gly Gln
1

<210> SEQ ID NO 346
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_F05 FG loop

<400> SEQUENCE: 346

Tyr Thr Ser Gly Tyr Val
1   5

<210> SEQ ID NO 347
<211> LENGTH: 86
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_F05 w/ N leader

<400> SEQUENCE: 347

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Pro Tyr Pro Arg Gly Pro Tyr Val Phe
            20   25   30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35   40   45

Phe Thr Val Tyr Pro Gly Gln Ala Thr Ile Ser Gly Leu Lys Pro Gly
    50   55   60

Val Asp Tyr Thr Ile Thr Val Tyr Ala Tyr Thr Ser Gly Tyr Val Ile
65   70   75   80

Ser Ile Asn Tyr Arg Thr
                85

<210> SEQ ID NO 348
<211> LENGTH: 99
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_F05 w/ N leader + his tag

<400> SEQUENCE: 348

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Pro Tyr Pro Arg Gly Pro Tyr Val Phe
            20   25   30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35   40   45

Phe Thr Val Tyr Pro Gly Gln Ala Thr Ile Ser Gly Leu Lys Pro Gly
    50   55   60

Val Asp Tyr Thr Ile Thr Val Tyr Ala Tyr Thr Ser Gly Tyr Val Ile
65   70   75   80

Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His
                85   90   95

His His His

<210> SEQ ID NO 349

-continued

<211> LENGTH: 93
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_F05 w/ N leader and C tail

<400> SEQUENCE: 349

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Pro Tyr Pro Arg Gly Pro Tyr Val Phe
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Tyr Pro Gly Gln Ala Thr Ile Ser Gly Leu Lys Pro Gly
    50                  55                  60

Val Asp Tyr Thr Ile Thr Val Tyr Ala Tyr Thr Ser Gly Tyr Val Ile
65                  70                  75                  80

Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90
```

<210> SEQ ID NO 350
<211> LENGTH: 99
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_F05 w/ N leader and C tail + his tag

<400> SEQUENCE: 350

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Pro Tyr Pro Arg Gly Pro Tyr Val Phe
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Tyr Pro Gly Gln Ala Thr Ile Ser Gly Leu Lys Pro Gly
    50                  55                  60

Val Asp Tyr Thr Ile Thr Val Tyr Ala Tyr Thr Ser Gly Tyr Val Ile
65                  70                  75                  80

Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His
                85                  90                  95

His His His
```

<210> SEQ ID NO 351
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_F05 w/ N leader and modified C-terminus including PC

<400> SEQUENCE: 351

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Pro Tyr Pro Arg Gly Pro Tyr Val Phe
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45
```

-continued

```
Phe Thr Val Tyr Pro Gly Gln Ala Thr Ile Ser Gly Leu Lys Pro Gly
    50                  55                  60

Val Asp Tyr Thr Ile Thr Val Tyr Ala Tyr Thr Ser Gly Tyr Val Ile
65                  70                  75                  80

Ser Ile Asn Tyr Arg Thr Pro Cys
                85


&lt;210&gt; SEQ ID NO 352
&lt;211&gt; LENGTH: 94
&lt;212&gt; TYPE: PRT
&lt;213&gt; ORGANISM: Artificial Sequence
&lt;220&gt; FEATURE:
&lt;223&gt; OTHER INFORMATION: Synthetic: ATI_1422_F05 w/ N leader and
      modified C-terminus including PC + his tag

&lt;400&gt; SEQUENCE: 352

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Pro Tyr Pro Arg Gly Pro Tyr Val Phe
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Tyr Pro Gly Gln Ala Thr Ile Ser Gly Leu Lys Pro Gly
    50                  55                  60

Val Asp Tyr Thr Ile Thr Val Tyr Ala Tyr Thr Ser Gly Tyr Val Ile
65                  70                  75                  80

Ser Ile Asn Tyr Arg Thr Pro Cys His His His His His His
                85                  90


&lt;210&gt; SEQ ID NO 353
&lt;211&gt; LENGTH: 100
&lt;212&gt; TYPE: PRT
&lt;213&gt; ORGANISM: Artificial Sequence
&lt;220&gt; FEATURE:
&lt;223&gt; OTHER INFORMATION: Synthetic: ATI_1422_F05 full length

&lt;400&gt; SEQUENCE: 353

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp Pro Tyr Pro Arg Gly Pro Tyr Val
            20                  25                  30

Phe Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
        35                  40                  45

Glu Phe Thr Val Tyr Pro Gly Gln Ala Thr Ile Ser Gly Leu Lys Pro
    50                  55                  60

Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Tyr Thr Ser Gly Tyr Val
65                  70                  75                  80

Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His His
                85                  90                  95

His His His His
            100


&lt;210&gt; SEQ ID NO 354
&lt;211&gt; LENGTH: 80
&lt;212&gt; TYPE: PRT
&lt;213&gt; ORGANISM: Artificial Sequence
&lt;220&gt; FEATURE:
```

-continued

<223> OTHER INFORMATION: Synthetic: ATI_1422_H04 core

<400> SEQUENCE: 354

```
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Tyr Leu
1               5                   10                  15

Pro Ser Tyr Tyr Val Gln Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly
            20                  25                  30

Asn Ser Pro Val Gln Glu Phe Thr Val Lys Ser Tyr Asn Ala Thr Ile
        35                  40                  45

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

Met Gly Val Tyr Tyr Leu Ser Tyr Ser Ile Ser Ile Asn Tyr Arg Thr
65                  70                  75                  80
```

<210> SEQ ID NO 355
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_H04 BC loop

<400> SEQUENCE: 355

```
Tyr Leu Pro Ser Tyr Tyr Val Gln
1               5
```

<210> SEQ ID NO 356
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_H04 DE loop

<400> SEQUENCE: 356

```
Lys Ser Tyr Asn
1
```

<210> SEQ ID NO 357
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_H04 FG loop

<400> SEQUENCE: 357

```
Arg Met Gly Val Tyr Tyr Leu Ser Tyr Ser
1               5                   10
```

<210> SEQ ID NO 358
<211> LENGTH: 89
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_H04 w/ N leader

<400> SEQUENCE: 358

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Tyr Leu Pro Ser Tyr Tyr Val Gln Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45
```

-continued

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

Asp Tyr Thr Ile Thr Val Tyr Ala Arg Met Gly Val Tyr Tyr Leu Ser
65                  70                  75                  80

Tyr Ser Ile Ser Ile Asn Tyr Arg Thr
                85


<210> SEQ ID NO 359
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_H04 w/ N leader + his tag

<400> SEQUENCE: 359

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Tyr Leu Pro Ser Tyr Tyr Val Gln Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Arg Met Gly Val Tyr Tyr Leu Ser
65                  70                  75                  80

Tyr Ser Ile Ser Ile Asn Tyr Arg Thr His His His His His His
                85                  90                  95


<210> SEQ ID NO 360
<211> LENGTH: 96
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_H04 w/ N leader and C tail

<400> SEQUENCE: 360

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Tyr Leu Pro Ser Tyr Tyr Val Gln Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Arg Met Gly Val Tyr Tyr Leu Ser
65                  70                  75                  80

Tyr Ser Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95


<210> SEQ ID NO 361
<211> LENGTH: 102
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_H04 w/ N leader and C
      tail + his tag

<400> SEQUENCE: 361
```

-continued

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Tyr Leu Pro Ser Tyr Tyr Val Gln Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Arg Met Gly Val Tyr Tyr Leu Ser
65                  70                  75                  80

Tyr Ser Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95

His His His His His His
            100
```

<210> SEQ ID NO 362
<211> LENGTH: 91
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_H04 w/ N leader and modified C-terminus including PC

<400> SEQUENCE: 362

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Tyr Leu Pro Ser Tyr Tyr Val Gln Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Arg Met Gly Val Tyr Tyr Leu Ser
65                  70                  75                  80

Tyr Ser Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90
```

<210> SEQ ID NO 363
<211> LENGTH: 97
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_H04 w/ N leader and modified C-terminus including PC + his tag

<400> SEQUENCE: 363

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Tyr Leu Pro Ser Tyr Tyr Val Gln Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Arg Met Gly Val Tyr Tyr Leu Ser
65                  70                  75                  80
```

-continued

```
Tyr Ser Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His His His
                85                  90                  95

His


<210> SEQ ID NO 364
<211> LENGTH: 103
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_H04  full length

<400> SEQUENCE: 364

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp Tyr Leu Pro Ser Tyr Tyr Val Gln
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Arg Met Gly Val Tyr Tyr Leu
65                  70                  75                  80

Ser Tyr Ser Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser
                85                  90                  95

Gln His His His His His His
            100


<210> SEQ ID NO 365
<211> LENGTH: 78
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_H05 core

<400> SEQUENCE: 365

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

Gln Leu Ser Pro Ser Phe Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly
            20                  25                  30

Asn Ser Pro Val Gln Glu Phe Thr Val Val Ala Gly Met Ala Thr Ile
        35                  40                  45

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

Ser Asp Val Tyr Phe Tyr Ser Ile Ser Ile Asn Tyr Arg Thr
65                  70                  75


<210> SEQ ID NO 366
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_H05 BC loop

<400> SEQUENCE: 366

Gln Gly Gln Leu Ser Pro Ser Phe
1               5
```

-continued

<210> SEQ ID NO 367
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_H05 DE loop

<400> SEQUENCE: 367

```
Val Ala Gly Met
1
```

<210> SEQ ID NO 368
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_H05 FG loop

<400> SEQUENCE: 368

```
Thr Ser Asp Val Tyr Phe Tyr Ser
1               5
```

<210> SEQ ID NO 369
<211> LENGTH: 87
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_H05 w/ N leader

<400> SEQUENCE: 369

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Gln Gly Gln Leu Ser Pro Ser Phe Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

Thr Val Val Ala Gly Met Ala Thr Ile Ser Gly Leu Lys Pro Gly Val
    50                  55                  60

Asp Tyr Thr Ile Thr Val Tyr Ala Thr Ser Asp Val Tyr Phe Tyr Ser
65                  70                  75                  80

Ile Ser Ile Asn Tyr Arg Thr
                85
```

<210> SEQ ID NO 370
<211> LENGTH: 93
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_H05 w/ N leader + his tag

<400> SEQUENCE: 370

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Gln Gly Gln Leu Ser Pro Ser Phe Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

Thr Val Val Ala Gly Met Ala Thr Ile Ser Gly Leu Lys Pro Gly Val
    50                  55                  60

Asp Tyr Thr Ile Thr Val Tyr Ala Thr Ser Asp Val Tyr Phe Tyr Ser
```

-continued

```
65                  70                  75                  80

Ile Ser Ile Asn Tyr Arg Thr His His His His His His
                85                  90


<210> SEQ ID NO 371
<211> LENGTH: 94
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_H05 w/ N leader and C tail

<400> SEQUENCE: 371

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Gln Gly Gln Leu Ser Pro Ser Phe Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

Thr Val Val Ala Gly Met Ala Thr Ile Ser Gly Leu Lys Pro Gly Val
    50                  55                  60

Asp Tyr Thr Ile Thr Val Tyr Ala Thr Ser Asp Val Tyr Phe Tyr Ser
65                  70                  75                  80

Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90


<210> SEQ ID NO 372
<211> LENGTH: 100
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_H05 w/ N leader and C
      tail + his tag

<400> SEQUENCE: 372

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Gln Gly Gln Leu Ser Pro Ser Phe Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

Thr Val Val Ala Gly Met Ala Thr Ile Ser Gly Leu Lys Pro Gly Val
    50                  55                  60

Asp Tyr Thr Ile Thr Val Tyr Ala Thr Ser Asp Val Tyr Phe Tyr Ser
65                  70                  75                  80

Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His His
                85                  90                  95

His His His His
            100


<210> SEQ ID NO 373
<211> LENGTH: 89
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_H05 w/ N leader and
      modified C-terminus including PC

<400> SEQUENCE: 373
```

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```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Gln Gly Gln Leu Ser Pro Ser Phe Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

Thr Val Val Ala Gly Met Ala Thr Ile Ser Gly Leu Lys Pro Gly Val
    50                  55                  60

Asp Tyr Thr Ile Thr Val Tyr Ala Thr Ser Asp Val Tyr Phe Tyr Ser
65                  70                  75                  80

Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85


<210> SEQ ID NO 374
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_H05 w/ N leader and
      modified C-terminus including PC + his tag

<400> SEQUENCE: 374

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Gln Gly Gln Leu Ser Pro Ser Phe Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

Thr Val Val Ala Gly Met Ala Thr Ile Ser Gly Leu Lys Pro Gly Val
    50                  55                  60

Asp Tyr Thr Ile Thr Val Tyr Ala Thr Ser Asp Val Tyr Phe Tyr Ser
65                  70                  75                  80

Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His His His His
                85                  90                  95


<210> SEQ ID NO 375
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic:  full length

<400> SEQUENCE: 375

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp Gln Gly Gln Leu Ser Pro Ser Phe
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Val Ala Gly Met Ala Thr Ile Ser Gly Leu Lys Pro Gly
    50                  55                  60

Val Asp Tyr Thr Ile Thr Val Tyr Ala Thr Ser Asp Val Tyr Phe Tyr
65                  70                  75                  80

Ser Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His
                85                  90                  95

His His His His His
```

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100

<210> SEQ ID NO 376
<211> LENGTH: 82
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_G05 core

<400> SEQUENCE: 376

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Ile Ala
1   5   10   15

Pro Tyr Tyr Ser Val Ile Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly
            20   25   30

Asn Ser Pro Val Gln Glu Phe Thr Val Thr Gly Ser Gly Tyr Ala Thr
        35   40   45

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

Thr Tyr Cys Ala Ser Val Ala Ser Tyr Ala Phe Ile Ser Ile Asn Tyr
65   70   75   80

Arg Thr

<210> SEQ ID NO 377
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_G05 BC loop

<400> SEQUENCE: 377

Ile Ala Pro Tyr Tyr Ser Val Ile
1   5

<210> SEQ ID NO 378
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_G05 DE loop

<400> SEQUENCE: 378

Thr Gly Ser Gly Tyr
1   5

<210> SEQ ID NO 379
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_G05 FG loop

<400> SEQUENCE: 379

Thr Tyr Cys Ala Ser Val Ala Ser Tyr Ala Phe
1   5   10

<210> SEQ ID NO 380
<211> LENGTH: 91
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_G05 w/ N leader

-continued

<400> SEQUENCE: 380

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Tyr Tyr Ser Val Ile Tyr
            20   25   30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35   40   45

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Thr Tyr Cys Ala Ser Val Ala
65   70   75   80

Ser Tyr Ala Phe Ile Ser Ile Asn Tyr Arg Thr
                85   90

<210> SEQ ID NO 381
<211> LENGTH: 97
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_G05 w/ N leader + his tag

<400> SEQUENCE: 381

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Tyr Tyr Ser Val Ile Tyr
            20   25   30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35   40   45

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Thr Tyr Cys Ala Ser Val Ala
65   70   75   80

Ser Tyr Ala Phe Ile Ser Ile Asn Tyr Arg Thr His His His His His
                85   90   95

His

<210> SEQ ID NO 382
<211> LENGTH: 98
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_G05 w/ N leader and C tail

<400> SEQUENCE: 382

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Tyr Tyr Ser Val Ile Tyr
            20   25   30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35   40   45

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Thr Tyr Cys Ala Ser Val Ala
65   70   75   80

Ser Tyr Ala Phe Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro

-continued

```
                85                  90                  95

Ser Gln


<210> SEQ ID NO 383
<211> LENGTH: 104
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_G05 w/ N leader and C
      tail + his tag

<400> SEQUENCE: 383

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Tyr Tyr Ser Val Ile Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Thr Tyr Cys Ala Ser Val Ala
65                  70                  75                  80

Ser Tyr Ala Phe Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro
                85                  90                  95

Ser Gln His His His His His His
            100


<210> SEQ ID NO 384
<211> LENGTH: 93
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_G05 w/ N leader and
      modified C-terminus including PC

<400> SEQUENCE: 384

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Tyr Tyr Ser Val Ile Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Thr Tyr Cys Ala Ser Val Ala
65                  70                  75                  80

Ser Tyr Ala Phe Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90


<210> SEQ ID NO 385
<211> LENGTH: 99
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_G05 w/ N leader and
      modified C-terminus including PC + his tag

<400> SEQUENCE: 385
```

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```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Tyr Tyr Ser Val Ile Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Thr Tyr Cys Ala Ser Val Ala
65                  70                  75                  80

Ser Tyr Ala Phe Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His
                85                  90                  95

His His His


<210> SEQ ID NO 386
<211> LENGTH: 105
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1422_G05 full length

<400> SEQUENCE: 386

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Tyr Tyr Ser Val Ile
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

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

Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Thr Tyr Cys Ala Ser Val
65                  70                  75                  80

Ala Ser Tyr Ala Phe Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys
                85                  90                  95

Pro Ser Gln His His His His His His
            100                 105


<210> SEQ ID NO 387
<211> LENGTH: 82
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1760_C02 core

<400> SEQUENCE: 387

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Ile Ala
1               5                   10                  15

Pro Tyr Tyr Ser Val Ile Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly
            20                  25                  30

Asn Ser Pro Val Gln Glu Phe Thr Val Pro Gly Ser Ala Tyr Ala Thr
        35                  40                  45

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

Ser Ser Gly Ala Ser Ile Ala Ala Tyr Ala Phe Ile Ser Ile Asn Tyr
65                  70                  75                  80
```

Arg Thr

<210> SEQ ID NO 388
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1760_C02 BC loop

<400> SEQUENCE: 388

Ile Ala Pro Tyr Tyr Ser Val Ile
1   5

<210> SEQ ID NO 389
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1760_C02 DE loop

<400> SEQUENCE: 389

Pro Gly Ser Ala Tyr
1   5

<210> SEQ ID NO 390
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1760_C02 FG loop

<400> SEQUENCE: 390

Ser Ser Gly Ala Ser Ile Ala Ala Tyr Ala Phe
1   5   10

<210> SEQ ID NO 391
<211> LENGTH: 91
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1760_C02 w/ N leader

<400> SEQUENCE: 391

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Tyr Tyr Ser Val Ile Tyr
            20   25   30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35   40   45

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Ser Ser Gly Ala Ser Ile Ala
65   70   75   80

Ala Tyr Ala Phe Ile Ser Ile Asn Tyr Arg Thr
                85   90

<210> SEQ ID NO 392
<211> LENGTH: 97
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1760_C02 w/ N leader + his tag

-continued

<400> SEQUENCE: 392

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Tyr Tyr Ser Val Ile Tyr
            20   25   30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35   40   45

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Ser Ser Gly Ala Ser Ile Ala
65   70   75   80

Ala Tyr Ala Phe Ile Ser Ile Asn Tyr Arg Thr His His His His His
                85   90   95

His

<210> SEQ ID NO 393
<211> LENGTH: 98
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1760_C02 w/ N leader and C tail

<400> SEQUENCE: 393

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Tyr Tyr Ser Val Ile Tyr
            20   25   30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35   40   45

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Ser Ser Gly Ala Ser Ile Ala
65   70   75   80

Ala Tyr Ala Phe Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro
                85   90   95

Ser Gln

<210> SEQ ID NO 394
<211> LENGTH: 104
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1760_C02 w/ N leader and C
      tail + his tag

<400> SEQUENCE: 394

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Tyr Tyr Ser Val Ile Tyr
            20   25   30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35   40   45

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

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Val Asp Tyr Thr Ile Thr Val Tyr Ala Ser Ser Gly Ala Ser Ile Ala
65 70 75 80

Ala Tyr Ala Phe Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro
85 90 95

Ser Gln His His His His His His
100

<210> SEQ ID NO 395
<211> LENGTH: 93
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1760_C02 w/ N leader and modified C-terminus including PC

<400> SEQUENCE: 395

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Tyr Tyr Ser Val Ile Tyr
20 25 30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
35 40 45

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Ser Ser Gly Ala Ser Ile Ala
65 70 75 80

Ala Tyr Ala Phe Ile Ser Ile Asn Tyr Arg Thr Pro Cys
85 90

<210> SEQ ID NO 396
<211> LENGTH: 99
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1760_C02 w/ N leader and modified C-terminus including PC + his tag

<400> SEQUENCE: 396

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Tyr Tyr Ser Val Ile Tyr
20 25 30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
35 40 45

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Ser Ser Gly Ala Ser Ile Ala
65 70 75 80

Ala Tyr Ala Phe Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His
85 90 95

His His His

<210> SEQ ID NO 397
<211> LENGTH: 105
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1760_C02 full length

<400> SEQUENCE: 397

```
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Tyr Tyr Ser Val Ile
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

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

Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Ser Ser Gly Ala Ser Ile
65                  70                  75                  80

Ala Ala Tyr Ala Phe Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys
                85                  90                  95

Pro Ser Gln His His His His His His
            100                 105
```

<210> SEQ ID NO 398
<211> LENGTH: 82
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1760_E01 core

<400> SEQUENCE: 398

```
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Ile Ala
1               5                   10                  15

Pro Tyr Tyr Ser Val Lys Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly
            20                  25                  30

Asn Ser Pro Val Gln Glu Phe Thr Val Ala Gly Ala Asp Tyr Ala Thr
        35                  40                  45

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

Thr Tyr Gly Ala Ser Ile Ala Ser Tyr Ala Phe Ile Ser Ile Asn Tyr
65                  70                  75                  80

Arg Thr
```

<210> SEQ ID NO 399
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1760_E01 BC loop

<400> SEQUENCE: 399

```
Ile Ala Pro Tyr Tyr Ser Val Lys
1               5
```

<210> SEQ ID NO 400
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1760_E01 DE loop

<400> SEQUENCE: 400

```
Ala Gly Ala Asp Tyr
1               5
```

-continued

<210> SEQ ID NO 401
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1760_E01 FG loop

<400> SEQUENCE: 401

```
Thr Tyr Gly Ala Ser Ile Ala Ser Tyr Ala Phe
1               5                   10
```

<210> SEQ ID NO 402
<211> LENGTH: 91
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1760_E01 w/ N leader

<400> SEQUENCE: 402

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Tyr Tyr Ser Val Lys Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Thr Tyr Gly Ala Ser Ile Ala
65                  70                  75                  80

Ser Tyr Ala Phe Ile Ser Ile Asn Tyr Arg Thr
                85                  90
```

<210> SEQ ID NO 403
<211> LENGTH: 97
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1760_E01 w/ N leader + his tag

<400> SEQUENCE: 403

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Tyr Tyr Ser Val Lys Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Thr Tyr Gly Ala Ser Ile Ala
65                  70                  75                  80

Ser Tyr Ala Phe Ile Ser Ile Asn Tyr Arg Thr His His His His His
                85                  90                  95

His
```

<210> SEQ ID NO 404
<211> LENGTH: 98
<212> TYPE: PRT

-continued

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1760_E01 w/ N leader and C tail

<400> SEQUENCE: 404

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Tyr Tyr Ser Val Lys Tyr
            20   25   30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35   40   45

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Thr Tyr Gly Ala Ser Ile Ala
65   70   75   80

Ser Tyr Ala Phe Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro
                85   90   95

Ser Gln

<210> SEQ ID NO 405
<211> LENGTH: 104
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1760_E01 w/ N leader and C
      tail + his tag

<400> SEQUENCE: 405

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Tyr Tyr Ser Val Lys Tyr
            20   25   30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35   40   45

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Thr Tyr Gly Ala Ser Ile Ala
65   70   75   80

Ser Tyr Ala Phe Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro
                85   90   95

Ser Gln His His His His His His
            100

<210> SEQ ID NO 406
<211> LENGTH: 93
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1760_E01 w/ N leader and
      modified C-terminus including PC

<400> SEQUENCE: 406

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Tyr Tyr Ser Val Lys Tyr
            20   25   30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe

-continued

```
        35                  40                  45

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Thr Tyr Gly Ala Ser Ile Ala
65                  70                  75                  80

Ser Tyr Ala Phe Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90


&lt;210&gt; SEQ ID NO 407
&lt;211&gt; LENGTH: 99
&lt;212&gt; TYPE: PRT
&lt;213&gt; ORGANISM: Artificial Sequence
&lt;220&gt; FEATURE:
&lt;223&gt; OTHER INFORMATION: Synthetic: ATI_1760_E01 w/ N leader and
      modified C-terminus including PC + his tag

&lt;400&gt; SEQUENCE: 407

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Tyr Tyr Ser Val Lys Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Thr Tyr Gly Ala Ser Ile Ala
65                  70                  75                  80

Ser Tyr Ala Phe Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His
                85                  90                  95

His His His


&lt;210&gt; SEQ ID NO 408
&lt;211&gt; LENGTH: 105
&lt;212&gt; TYPE: PRT
&lt;213&gt; ORGANISM: Artificial Sequence
&lt;220&gt; FEATURE:
&lt;223&gt; OTHER INFORMATION: Synthetic: ATI_1760_E01 full length

&lt;400&gt; SEQUENCE: 408

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Tyr Tyr Ser Val Lys
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

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

Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Thr Tyr Gly Ala Ser Ile
65                  70                  75                  80

Ala Ser Tyr Ala Phe Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys
                85                  90                  95

Pro Ser Gln His His His His His His
            100                 105


&lt;210&gt; SEQ ID NO 409
&lt;211&gt; LENGTH: 82
```

-continued

<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1760_F01 core

<400> SEQUENCE: 409

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Ile Ala
1   5   10   15

Pro Tyr Tyr Ala Val Met Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly
            20   25   30

Asn Ser Pro Val Gln Glu Phe Thr Val Pro Gly Gly Gly Tyr Ala Thr
        35   40   45

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

Thr Gly Gly Ala Ser Ile Ala Ala Tyr Ala Phe Ile Ser Ile Asn Tyr
65   70   75   80

Arg Thr

<210> SEQ ID NO 410
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1760_F01 BC loop

<400> SEQUENCE: 410

Ile Ala Pro Tyr Tyr Ala Val Met
1   5

<210> SEQ ID NO 411
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1760_F01 DE loop

<400> SEQUENCE: 411

Pro Gly Gly Gly Tyr
1   5

<210> SEQ ID NO 412
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1760_F01 FG loop

<400> SEQUENCE: 412

Thr Gly Gly Ala Ser Ile Ala Ala Tyr Ala Phe
1   5   10

<210> SEQ ID NO 413
<211> LENGTH: 91
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1760_F01 w/ N leader

<400> SEQUENCE: 413

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

-continued

```
Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Tyr Tyr Ala Val Met Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Thr Gly Gly Ala Ser Ile Ala
65                  70                  75                  80

Ala Tyr Ala Phe Ile Ser Ile Asn Tyr Arg Thr
                85                  90


<210> SEQ ID NO 414
<211> LENGTH: 97
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1760_F01 w/ N leader + his tag

<400> SEQUENCE: 414

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Tyr Tyr Ala Val Met Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Thr Gly Gly Ala Ser Ile Ala
65                  70                  75                  80

Ala Tyr Ala Phe Ile Ser Ile Asn Tyr Arg Thr His His His His His
                85                  90                  95

His


<210> SEQ ID NO 415
<211> LENGTH: 98
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1760_F01 w/ N leader and C tail

<400> SEQUENCE: 415

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Tyr Tyr Ala Val Met Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Thr Gly Gly Ala Ser Ile Ala
65                  70                  75                  80

Ala Tyr Ala Phe Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro
                85                  90                  95

Ser Gln
```

-continued

```
<210> SEQ ID NO 416
<211> LENGTH: 104
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1760_F01 w/ N leader and C
      tail + his tag

<400> SEQUENCE: 416

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Tyr Tyr Ala Val Met Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Thr Gly Gly Ala Ser Ile Ala
65                  70                  75                  80

Ala Tyr Ala Phe Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro
                85                  90                  95

Ser Gln His His His His His His
            100


<210> SEQ ID NO 417
<211> LENGTH: 93
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1760_F01 w/ N leader and
      modified C-terminus including PC

<400> SEQUENCE: 417

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Tyr Tyr Ala Val Met Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Thr Gly Gly Ala Ser Ile Ala
65                  70                  75                  80

Ala Tyr Ala Phe Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90


<210> SEQ ID NO 418
<211> LENGTH: 99
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1760_F01 w/ N leader and
      modified C-terminus including PC + his tag

<400> SEQUENCE: 418

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Tyr Tyr Ala Val Met Tyr
            20                  25                  30
```

-continued

```
Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Thr Gly Gly Ala Ser Ile Ala
65                  70                  75                  80

Ala Tyr Ala Phe Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His
                85                  90                  95

His His His


<210> SEQ ID NO 419
<211> LENGTH: 105
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1760_F01 full length

<400> SEQUENCE: 419

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp Ile Ala Pro Tyr Tyr Ala Val Met
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

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

Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Thr Gly Gly Ala Ser Ile
65                  70                  75                  80

Ala Ala Tyr Ala Phe Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys
                85                  90                  95

Pro Ser Gln His His His His His His
            100                 105


<210> SEQ ID NO 420
<211> LENGTH: 79
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1494_D03 core

<400> SEQUENCE: 420

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Ser Tyr
1               5                   10                  15

Pro Ser Tyr His Leu Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn
            20                  25                  30

Ser Pro Val Gln Glu Phe Thr Val His Ile Asp Tyr Ala Thr Ile Ser
        35                  40                  45

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

Pro Pro Tyr Asp Ile Tyr Tyr Glu Ile Ser Ile Asn Tyr Arg Thr
65                  70                  75


<210> SEQ ID NO 421
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
```

-continued

<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1494_D03 BC loop

<400> SEQUENCE: 421

Ser Tyr Pro Ser Tyr His Leu
1   5

<210> SEQ ID NO 422
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1494_D03 DE loop

<400> SEQUENCE: 422

His Ile Asp Tyr
1

<210> SEQ ID NO 423
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1494_D03 FG loop

<400> SEQUENCE: 423

Gln Ser Pro Pro Tyr Asp Ile Tyr Tyr Glu
1   5   10

<210> SEQ ID NO 424
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1494_D03 w/ N leader

<400> SEQUENCE: 424

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Ser Tyr Pro Ser Tyr His Leu Tyr Arg
            20   25   30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35   40   45

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

Tyr Thr Ile Thr Val Tyr Ala Gln Ser Pro Pro Tyr Asp Ile Tyr Tyr
65   70   75   80

Glu Ile Ser Ile Asn Tyr Arg Thr
                85

<210> SEQ ID NO 425
<211> LENGTH: 94
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1494_D03 w/ N leader + his tag

<400> SEQUENCE: 425

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Ser Tyr Pro Ser Tyr His Leu Tyr Arg

-continued

```
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Gln Ser Pro Pro Tyr Asp Ile Tyr Tyr
65                  70                  75                  80

Glu Ile Ser Ile Asn Tyr Arg Thr His His His His His His
                85                  90


<210> SEQ ID NO 426
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1494_D03 w/ N leader and C tail

<400> SEQUENCE: 426

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ser Tyr Pro Ser Tyr His Leu Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Gln Ser Pro Pro Tyr Asp Ile Tyr Tyr
65                  70                  75                  80

Glu Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95


<210> SEQ ID NO 427
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1494_D03 w/ N leader and C
      tail + his tag

<400> SEQUENCE: 427

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ser Tyr Pro Ser Tyr His Leu Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Gln Ser Pro Pro Tyr Asp Ile Tyr Tyr
65                  70                  75                  80

Glu Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His
                85                  90                  95

His His His His His
            100


<210> SEQ ID NO 428
```

-continued

<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1494_D03 w/ N leader and modified C-terminus including PC

<400> SEQUENCE: 428

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ser Tyr Pro Ser Tyr His Leu Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Gln Ser Pro Pro Tyr Asp Ile Tyr Tyr
65                  70                  75                  80

Glu Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90
```

<210> SEQ ID NO 429
<211> LENGTH: 96
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1494_D03 w/ N leader and modified C-terminus including PC + his tag

<400> SEQUENCE: 429

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ser Tyr Pro Ser Tyr His Leu Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Gln Ser Pro Pro Tyr Asp Ile Tyr Tyr
65                  70                  75                  80

Glu Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His His His His
                85                  90                  95
```

<210> SEQ ID NO 430
<211> LENGTH: 102
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1494_D03 full length

<400> SEQUENCE: 430

```
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp Ser Tyr Pro Ser Tyr His Leu Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

Thr Val His Ile Asp Tyr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val
```

-continued

```
    50                  55                  60

Asp Tyr Thr Ile Thr Val Tyr Ala Gln Ser Pro Pro Tyr Asp Ile Tyr
65                  70                  75                  80

Tyr Glu Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95

His His His His His His
            100


<210> SEQ ID NO 431
<211> LENGTH: 79
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1494_D04 core

<400> SEQUENCE: 431

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

Ser Ser Ser Asn Ser Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn
            20                  25                  30

Ser Pro Val Gln Glu Phe Thr Val Pro Asp Gln Leu Ala Thr Ile Ser
        35                  40                  45

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

Asn Ala His Tyr Met Arg Val Gly Ile Ser Ile Asn Tyr Arg Thr
65                  70                  75


<210> SEQ ID NO 432
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1494_D04 BC loop

<400> SEQUENCE: 432

Met Glu Ser Ser Ser Asn Ser
1               5


<210> SEQ ID NO 433
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1494_D04 DE loop

<400> SEQUENCE: 433

Pro Asp Gln Leu
1


<210> SEQ ID NO 434
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1494_D04 FG loop

<400> SEQUENCE: 434

Leu Ala Asn Ala His Tyr Met Arg Val Gly
1               5                   10
```

-continued

<210> SEQ ID NO 435
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1494_D04 w/ N leader

<400> SEQUENCE: 435

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Met Glu Ser Ser Ser Asn Ser Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Ala Asn Ala His Tyr Met Arg Val
65                  70                  75                  80

Gly Ile Ser Ile Asn Tyr Arg Thr
                85
```

<210> SEQ ID NO 436
<211> LENGTH: 94
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1494_D04 w/ N leader + his tag

<400> SEQUENCE: 436

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Met Glu Ser Ser Ser Asn Ser Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Ala Asn Ala His Tyr Met Arg Val
65                  70                  75                  80

Gly Ile Ser Ile Asn Tyr Arg Thr His His His His His His
                85                  90
```

<210> SEQ ID NO 437
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1494_D04 w/ N leader and C tail

<400> SEQUENCE: 437

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Met Glu Ser Ser Ser Asn Ser Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

Val Pro Asp Gln Leu Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50                  55                  60
```

-continued

Tyr Thr Ile Thr Val Tyr Ala Leu Ala Asn Ala His Tyr Met Arg Val
65 70 75 80

Gly Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
85 90 95

<210> SEQ ID NO 438
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1494_D04 w/ N leader and C tail + his tag

<400> SEQUENCE: 438

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Met Glu Ser Ser Ser Asn Ser Tyr Arg
20 25 30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
35 40 45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Ala Asn Ala His Tyr Met Arg Val
65 70 75 80

Gly Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His
85 90 95

His His His His His
100

<210> SEQ ID NO 439
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1494_D04 w/ N leader and modified C-terminus including PC

<400> SEQUENCE: 439

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Met Glu Ser Ser Ser Asn Ser Tyr Arg
20 25 30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
35 40 45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Ala Asn Ala His Tyr Met Arg Val
65 70 75 80

Gly Ile Ser Ile Asn Tyr Arg Thr Pro Cys
85 90

<210> SEQ ID NO 440
<211> LENGTH: 96
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1494_D04 w/ N leader and modified C-terminus including PC + his tag

-continued

<400> SEQUENCE: 440

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Met Glu Ser Ser Ser Asn Ser Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Ala Asn Ala His Tyr Met Arg Val
65                  70                  75                  80

Gly Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His His His His
                85                  90                  95
```

<210> SEQ ID NO 441
<211> LENGTH: 102
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1494_D04 full length

<400> SEQUENCE: 441

```
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp Met Glu Ser Ser Ser Asn Ser Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Leu Ala Asn Ala His Tyr Met Arg
65                  70                  75                  80

Val Gly Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95

His His His His His His
            100
```

<210> SEQ ID NO 442
<211> LENGTH: 79
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_A08 core
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 442

```
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Ile Ser
1               5                   10                  15

Val Gln Thr Tyr Xaa Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn
            20                  25                  30

Ser Pro Val Gln Glu Phe Thr Val Pro Asp Gln Ser Ala Thr Ile Ser
        35                  40                  45

Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Leu Glu
```

-continued

```
    50                  55                  60

Lys Ala His Tyr Tyr Arg Gln Asn Ile Ser Ile Asn Tyr Arg Thr
65                  70                  75


<210> SEQ ID NO 443
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_A08 BC loop
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (7)..(7)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 443

Ile Ser Val Gln Thr Tyr Xaa
1               5


<210> SEQ ID NO 444
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_A08 DE loop

<400> SEQUENCE: 444

Pro Asp Gln Ser
1


<210> SEQ ID NO 445
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_A08 FG loop

<400> SEQUENCE: 445

Leu Glu Lys Ala His Tyr Tyr Arg Gln Asn
1               5                   10


<210> SEQ ID NO 446
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_A08 w/ N leader
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (30)..(30)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 446

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ile Ser Val Gln Thr Tyr Xaa Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Lys Ala His Tyr Tyr Arg Gln
65                  70                  75                  80
```

-continued

```
Asn Ile Ser Ile Asn Tyr Arg Thr
                85


<210> SEQ ID NO 447
<211> LENGTH: 94
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_A08 w/ N leader + his tag
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (30)..(30)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 447

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ile Ser Val Gln Thr Tyr Xaa Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Lys Ala His Tyr Tyr Arg Gln
65                  70                  75                  80

Asn Ile Ser Ile Asn Tyr Arg Thr His His His His His His
                85                  90


<210> SEQ ID NO 448
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_A08 w/ N leader and C tail
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (30)..(30)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 448

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ile Ser Val Gln Thr Tyr Xaa Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Lys Ala His Tyr Tyr Arg Gln
65                  70                  75                  80

Asn Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95


<210> SEQ ID NO 449
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_A08 w/ N leader and C
      tail + his tag
```

-continued

```
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (30)..(30)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 449

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ile Ser Val Gln Thr Tyr Xaa Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Lys Ala His Tyr Tyr Arg Gln
65                  70                  75                  80

Asn Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His
                85                  90                  95

His His His His His
            100


<210> SEQ ID NO 450
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_A08 w/ N leader and
      modified C-terminus including PC
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (30)..(30)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 450

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ile Ser Val Gln Thr Tyr Xaa Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Lys Ala His Tyr Tyr Arg Gln
65                  70                  75                  80

Asn Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90


<210> SEQ ID NO 451
<211> LENGTH: 96
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_A08 w/ N leader and
      modified C-terminus including PC + his tag
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (30)..(30)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 451
```

-continued

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Ile Ser Val Gln Thr Tyr Xaa Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Lys Ala His Tyr Tyr Arg Gln
65                  70                  75                  80

Asn Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His His His His
                85                  90                  95


<210> SEQ ID NO 452
<211> LENGTH: 102
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_A08 full length
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (31)..(31)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 452

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp Ile Ser Val Gln Thr Tyr Xaa Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Leu Glu Lys Ala His Tyr Tyr Arg
65                  70                  75                  80

Gln Asn Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95

His His His His His His
            100


<210> SEQ ID NO 453
<211> LENGTH: 79
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_B10 core
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 453

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Val Tyr
1               5                   10                  15

His Tyr Asp Xaa Gln Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn
            20                  25                  30

Ser Pro Val Gln Glu Phe Thr Val Pro Asp Gln Lys Ala Thr Ile Ser
        35                  40                  45
```

-continued

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

Glu Ala His His Lys Arg Asp Ser Ile Ser Ile Asn Tyr Arg Thr
65                  70                  75
```

<210> SEQ ID NO 454
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_B10 BC loop
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 454

```
Val Tyr His Tyr Asp Xaa Gln
1               5
```

<210> SEQ ID NO 455
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_B10 DE loop

<400> SEQUENCE: 455

```
Pro Asp Gln Lys
1
```

<210> SEQ ID NO 456
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_B10 FG loop

<400> SEQUENCE: 456

```
Leu Ser Glu Ala His His Lys Arg Asp Ser
1               5                   10
```

<210> SEQ ID NO 457
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_B10 w/ N leader
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (29)..(29)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 457

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Val Tyr His Tyr Asp Xaa Gln Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Ser Glu Ala His His Lys Arg Asp
```

-continued

```
65                  70                  75                  80

Ser Ile Ser Ile Asn Tyr Arg Thr
                85


<210> SEQ ID NO 458
<211> LENGTH: 94
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_B10 w/ N leader + his tag
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (29)..(29)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 458

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Val Tyr His Tyr Asp Xaa Gln Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Ser Glu Ala His His Lys Arg Asp
65                  70                  75                  80

Ser Ile Ser Ile Asn Tyr Arg Thr His His His His His His
                85                  90


<210> SEQ ID NO 459
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_B10 w/ N leader and C tail
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (29)..(29)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 459

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Val Tyr His Tyr Asp Xaa Gln Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Ser Glu Ala His His Lys Arg Asp
65                  70                  75                  80

Ser Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95


<210> SEQ ID NO 460
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_B10 w/ N leader and C
```

-continued

```
      tail + his tag
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (29)..(29)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 460

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Val Tyr His Tyr Asp Xaa Gln Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Ser Glu Ala His His Lys Arg Asp
65                  70                  75                  80

Ser Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His
                85                  90                  95

His His His His His
            100


<210> SEQ ID NO 461
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_B10 w/ N leader and
      modified C-terminus including PC
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (29)..(29)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 461

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Val Tyr His Tyr Asp Xaa Gln Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Ser Glu Ala His His Lys Arg Asp
65                  70                  75                  80

Ser Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90


<210> SEQ ID NO 462
<211> LENGTH: 96
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_B10 w/ N leader and
      modified C-terminus including PC + his tag
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (29)..(29)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 462
```

-continued

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Val Tyr His Tyr Asp Xaa Gln Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Ser Glu Ala His His Lys Arg Asp
65                  70                  75                  80

Ser Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His His His His
                85                  90                  95


<210> SEQ ID NO 463
<211> LENGTH: 102
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_B10  full length
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (30)..(30)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 463

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp Val Tyr His Tyr Asp Xaa Gln Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Leu Ser Glu Ala His His Lys Arg
65                  70                  75                  80

Asp Ser Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95

His His His His His His
            100


<210> SEQ ID NO 464
<211> LENGTH: 79
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_C07 core

<400> SEQUENCE: 464

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Arg Met
1               5                   10                  15

His Thr Asp Pro Asp Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn
            20                  25                  30

Ser Pro Val Gln Glu Phe Thr Val Pro Asp Gln Glu Ala Thr Ile Ser
        35                  40                  45

Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Ile Gln
    50                  55                  60
```

-continued

Thr Ala His Tyr Tyr Arg Ile Asn Ile Ser Ile Asn Tyr Arg Thr
65 70 75

<210> SEQ ID NO 465
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_C07 BC loop

<400> SEQUENCE: 465

Arg Met His Thr Asp Pro Asp
1 5

<210> SEQ ID NO 466
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_C07 DE loop

<400> SEQUENCE: 466

Pro Asp Gln Glu
1

<210> SEQ ID NO 467
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_C07 FG loop

<400> SEQUENCE: 467

Ile Gln Thr Ala His Tyr Tyr Arg Ile Asn
1 5 10

<210> SEQ ID NO 468
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_C07 w/ N leader

<400> SEQUENCE: 468

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Arg Met His Thr Asp Pro Asp Tyr Arg
20 25 30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
35 40 45

Val Pro Asp Gln Glu Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
50 55 60

Tyr Thr Ile Thr Val Tyr Ala Ile Gln Thr Ala His Tyr Tyr Arg Ile
65 70 75 80

Asn Ile Ser Ile Asn Tyr Arg Thr
85

<210> SEQ ID NO 469
<211> LENGTH: 94
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

-continued

<223> OTHER INFORMATION: Synthetic: ATI_1523_C07 w/ N leader + his tag

<400> SEQUENCE: 469

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Arg Met His Thr Asp Pro Asp Tyr Arg
            20   25   30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35   40   45

Val Pro Asp Gln Glu Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50   55   60

Tyr Thr Ile Thr Val Tyr Ala Ile Gln Thr Ala His Tyr Tyr Arg Ile
65   70   75   80

Asn Ile Ser Ile Asn Tyr Arg Thr His His His His His His
                85   90

<210> SEQ ID NO 470
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_C07 w/ N leader and C tail

<400> SEQUENCE: 470

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Arg Met His Thr Asp Pro Asp Tyr Arg
            20   25   30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35   40   45

Val Pro Asp Gln Glu Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50   55   60

Tyr Thr Ile Thr Val Tyr Ala Ile Gln Thr Ala His Tyr Tyr Arg Ile
65   70   75   80

Asn Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85   90   95

<210> SEQ ID NO 471
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_C07 w/ N leader and C
      tail + his tag

<400> SEQUENCE: 471

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Arg Met His Thr Asp Pro Asp Tyr Arg
            20   25   30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35   40   45

Val Pro Asp Gln Glu Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50   55   60

Tyr Thr Ile Thr Val Tyr Ala Ile Gln Thr Ala His Tyr Tyr Arg Ile
65   70   75   80

-continued

```
Asn Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His
                85                  90                  95

His His His His His
            100


<210> SEQ ID NO 472
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_C07 w/ N leader and
      modified C-terminus including PC

<400> SEQUENCE: 472

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Arg Met His Thr Asp Pro Asp Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

Val Pro Asp Gln Glu Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50                  55                  60

Tyr Thr Ile Thr Val Tyr Ala Ile Gln Thr Ala His Tyr Tyr Arg Ile
65                  70                  75                  80

Asn Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90


<210> SEQ ID NO 473
<211> LENGTH: 96
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_C07 w/ N leader and
      modified C-terminus including PC + his tag

<400> SEQUENCE: 473

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Arg Met His Thr Asp Pro Asp Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

Val Pro Asp Gln Glu Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50                  55                  60

Tyr Thr Ile Thr Val Tyr Ala Ile Gln Thr Ala His Tyr Tyr Arg Ile
65                  70                  75                  80

Asn Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His His His His
                85                  90                  95


<210> SEQ ID NO 474
<211> LENGTH: 102
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_C07 full length

<400> SEQUENCE: 474

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15
```

-continued

Pro Thr Ser Leu Leu Ile Ser Trp Arg Met His Thr Asp Pro Asp Tyr
            20   25   30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35   40   45

Thr Val Pro Asp Gln Glu Ala Thr Ile Ser Gly Leu Lys Pro Gly Val
    50   55   60

Asp Tyr Thr Ile Thr Val Tyr Ala Ile Gln Thr Ala His Tyr Tyr Arg
65   70   75   80

Ile Asn Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85   90   95

His His His His His His
            100

<210> SEQ ID NO 475
<211> LENGTH: 79
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_D07 core

<400> SEQUENCE: 475

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Glu Asn
1   5   10   15

Leu Ala Ser Tyr Gln Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn
            20   25   30

Ser Pro Val Gln Glu Phe Thr Val Pro Asp Val Gln Ala Thr Ile Ser
        35   40   45

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

Tyr Ile His Met Lys Gln Arg Val Ile Ser Ile Asn Tyr Arg Thr
65   70   75

<210> SEQ ID NO 476
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_D07 BC loop

<400> SEQUENCE: 476

Glu Asn Leu Ala Ser Tyr Gln
1   5

<210> SEQ ID NO 477
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_D07 DE loop

<400> SEQUENCE: 477

Pro Asp Val Gln
1

<210> SEQ ID NO 478
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

-continued

<223> OTHER INFORMATION: Synthetic: ATI_1523_D07 FG loop

<400> SEQUENCE: 478

Leu Pro Tyr Ile His Met Lys Gln Arg Val
1   5   10

<210> SEQ ID NO 479
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_D07 w/ N leader

<400> SEQUENCE: 479

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Glu Asn Leu Ala Ser Tyr Gln Tyr Arg
            20   25   30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35   40   45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Pro Tyr Ile His Met Lys Gln Arg
65   70   75   80

Val Ile Ser Ile Asn Tyr Arg Thr
                85

<210> SEQ ID NO 480
<211> LENGTH: 94
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_D07 w/ N leader + his tag

<400> SEQUENCE: 480

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Glu Asn Leu Ala Ser Tyr Gln Tyr Arg
            20   25   30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35   40   45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Pro Tyr Ile His Met Lys Gln Arg
65   70   75   80

Val Ile Ser Ile Asn Tyr Arg Thr His His His His His His
                85   90

<210> SEQ ID NO 481
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_D07 w/ N leader and C tail

<400> SEQUENCE: 481

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

-continued

```
Thr Ser Leu Leu Ile Ser Trp Glu Asn Leu Ala Ser Tyr Gln Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Pro Tyr Ile His Met Lys Gln Arg
65                  70                  75                  80

Val Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95


<210> SEQ ID NO 482
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_D07 w/ N leader and C
      tail + his tag

<400> SEQUENCE: 482

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Glu Asn Leu Ala Ser Tyr Gln Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Pro Tyr Ile His Met Lys Gln Arg
65                  70                  75                  80

Val Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His
                85                  90                  95

His His His His His
            100


<210> SEQ ID NO 483
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_D07 w/ N leader and
      modified C-terminus including PC

<400> SEQUENCE: 483

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Glu Asn Leu Ala Ser Tyr Gln Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Pro Tyr Ile His Met Lys Gln Arg
65                  70                  75                  80

Val Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90
```

-continued

<210> SEQ ID NO 484
<211> LENGTH: 96
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_D07 w/ N leader and modified C-terminus including PC + his tag

<400> SEQUENCE: 484

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Glu Asn Leu Ala Ser Tyr Gln Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Pro Tyr Ile His Met Lys Gln Arg
65                  70                  75                  80

Val Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His His His His
                85                  90                  95
```

<210> SEQ ID NO 485
<211> LENGTH: 102
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_D07 full length

<400> SEQUENCE: 485

```
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp Glu Asn Leu Ala Ser Tyr Gln Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Leu Pro Tyr Ile His Met Lys Gln
65                  70                  75                  80

Arg Val Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95

His His His His His His
            100
```

<210> SEQ ID NO 486
<211> LENGTH: 79
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_D08 core

<400> SEQUENCE: 486

```
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Met Arg
1               5                   10                  15

Tyr Tyr Asp Ala Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn
            20                  25                  30
```

-continued

```
Ser Pro Val Gln Glu Phe Thr Val Pro Asp Gln Ser Ala Thr Ile Ser
        35                  40                  45

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

Lys Ala His Tyr Tyr Arg Gln Asn Ile Ser Ile Asn Tyr Arg Thr
65                  70                  75


<210> SEQ ID NO 487
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_D08 BC loop

<400> SEQUENCE: 487

Met Arg Tyr Tyr Asp Ala Tyr
1               5


<210> SEQ ID NO 488
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_D08 DE loop

<400> SEQUENCE: 488

Pro Asp Gln Ser
1


<210> SEQ ID NO 489
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_D08 FG loop

<400> SEQUENCE: 489

Leu Glu Lys Ala His Tyr Tyr Arg Gln Asn
1               5                   10


<210> SEQ ID NO 490
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_D08 w/ N leader

<400> SEQUENCE: 490

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Met Arg Tyr Tyr Asp Ala Tyr Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Lys Ala His Tyr Tyr Arg Gln
65                  70                  75                  80

Asn Ile Ser Ile Asn Tyr Arg Thr
                85
```

-continued

<210> SEQ ID NO 491
<211> LENGTH: 94
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_D08 w/ N leader + his tag

<400> SEQUENCE: 491

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Met Arg Tyr Tyr Asp Ala Tyr Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Lys Ala His Tyr Tyr Arg Gln
65                  70                  75                  80

Asn Ile Ser Ile Asn Tyr Arg Thr His His His His His His
                85                  90
```

<210> SEQ ID NO 492
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_D08 w/ N leader and C tail

<400> SEQUENCE: 492

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Met Arg Tyr Tyr Asp Ala Tyr Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Lys Ala His Tyr Tyr Arg Gln
65                  70                  75                  80

Asn Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95
```

<210> SEQ ID NO 493
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_D08 w/ N leader and C
      tail + his tag

<400> SEQUENCE: 493

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Met Arg Tyr Tyr Asp Ala Tyr Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45
```

-continued

```
Val Pro Asp Gln Ser Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50                  55                  60

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Lys Ala His Tyr Tyr Arg Gln
65                  70                  75                  80

Asn Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His
                85                  90                  95

His His His His His
            100
```

<210> SEQ ID NO 494
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_D08 w/ N leader and modified C-terminus including PC

<400> SEQUENCE: 494

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Met Arg Tyr Tyr Asp Ala Tyr Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Lys Ala His Tyr Tyr Arg Gln
65                  70                  75                  80

Asn Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90
```

<210> SEQ ID NO 495
<211> LENGTH: 96
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_D08 w/ N leader and modified C-terminus including PC + his tag

<400> SEQUENCE: 495

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Met Arg Tyr Tyr Asp Ala Tyr Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Lys Ala His Tyr Tyr Arg Gln
65                  70                  75                  80

Asn Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His His His His
                85                  90                  95
```

<210> SEQ ID NO 496
<211> LENGTH: 102
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

-continued

<223> OTHER INFORMATION: Synthetic: ATI_1523_D08 full length

<400> SEQUENCE: 496

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1   5   10   15

Pro Thr Ser Leu Leu Ile Ser Trp Met Arg Tyr Tyr Asp Ala Tyr Tyr
            20   25   30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35   40   45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Leu Glu Lys Ala His Tyr Tyr Arg
65   70   75   80

Gln Asn Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85   90   95

His His His His His His
            100

<210> SEQ ID NO 497
<211> LENGTH: 79
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_E08 core

<400> SEQUENCE: 497

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp His His
1   5   10   15

Tyr Gln His Tyr Glu Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn
            20   25   30

Ser Pro Val Gln Glu Phe Thr Val Pro Asp Met Gly Ala Thr Ile Ser
        35   40   45

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

Glu Ala His Ser Asp Arg Ser Ser Ile Ser Ile Asn Tyr Arg Thr
65   70   75

<210> SEQ ID NO 498
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_E08 BC loop

<400> SEQUENCE: 498

His His Tyr Gln His Tyr Glu
1   5

<210> SEQ ID NO 499
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_E08 DE loop

<400> SEQUENCE: 499

Pro Asp Met Gly
1

-continued

<210> SEQ ID NO 500
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_E08 FG loop

<400> SEQUENCE: 500

```
Leu Glu Glu Ala His Ser Asp Arg Ser Ser
1               5                   10
```

<210> SEQ ID NO 501
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_E08 w/ N leader

<400> SEQUENCE: 501

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp His His Tyr Gln His Tyr Glu Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Glu Ala His Ser Asp Arg Ser
65                  70                  75                  80

Ser Ile Ser Ile Asn Tyr Arg Thr
                85
```

<210> SEQ ID NO 502
<211> LENGTH: 94
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_E08 w/ N leader + his tag

<400> SEQUENCE: 502

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp His His Tyr Gln His Tyr Glu Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Glu Ala His Ser Asp Arg Ser
65                  70                  75                  80

Ser Ile Ser Ile Asn Tyr Arg Thr His His His His His His
                85                  90
```

<210> SEQ ID NO 503
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_E08 w/ N leader and C tail

-continued

<400> SEQUENCE: 503

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp His His Tyr Gln His Tyr Glu Tyr Arg
20 25 30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
35 40 45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Glu Ala His Ser Asp Arg Ser
65 70 75 80

Ser Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
85 90 95

<210> SEQ ID NO 504
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_E08 w/ N leader and C tail + his tag

<400> SEQUENCE: 504

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp His His Tyr Gln His Tyr Glu Tyr Arg
20 25 30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
35 40 45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Glu Ala His Ser Asp Arg Ser
65 70 75 80

Ser Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His
85 90 95

His His His His His
100

<210> SEQ ID NO 505
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_E08 w/ N leader and modified C-terminus including PC

<400> SEQUENCE: 505

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp His His Tyr Gln His Tyr Glu Tyr Arg
20 25 30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
35 40 45

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

-continued

```
Tyr Thr Ile Thr Val Tyr Ala Leu Glu Glu Ala His Ser Asp Arg Ser
65                  70                  75                  80

Ser Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90


<210> SEQ ID NO 506
<211> LENGTH: 96
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_E08 w/ N leader and
      modified C-terminus including PC + his tag

<400> SEQUENCE: 506

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp His His Tyr Gln His Tyr Glu Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Glu Glu Ala His Ser Asp Arg Ser
65                  70                  75                  80

Ser Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His His His His
                85                  90                  95


<210> SEQ ID NO 507
<211> LENGTH: 102
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_E08 full length

<400> SEQUENCE: 507

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp His His Tyr Gln His Tyr Glu Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Leu Glu Glu Ala His Ser Asp Arg
65                  70                  75                  80

Ser Ser Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95

His His His His His His
            100


<210> SEQ ID NO 508
<211> LENGTH: 76
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_F01 core

<400> SEQUENCE: 508
```

-continued

```
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Tyr Lys
1               5                   10                  15

Pro Ser Thr Ile Val Thr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly
            20                  25                  30

Asn Ser Pro Val Gln Glu Phe Thr Val Tyr Gly Tyr Asn Ala Thr Ile
        35                  40                  45

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

His Gly Val Arg Phe Ile Ser Ile Asn Tyr Arg Thr
65                  70                  75


<210> SEQ ID NO 509
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_F01 BC loop

<400> SEQUENCE: 509

Tyr Lys Pro Ser Thr Ile Val Thr
1               5


<210> SEQ ID NO 510
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_F01 DE loop

<400> SEQUENCE: 510

Tyr Gly Tyr Asn
1


<210> SEQ ID NO 511
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_F01 FG loop

<400> SEQUENCE: 511

Val His Gly Val Arg Phe
1               5


<210> SEQ ID NO 512
<211> LENGTH: 85
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_F01 w/ N leader

<400> SEQUENCE: 512

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Tyr Lys Pro Ser Thr Ile Val Thr Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

-continued

```
Asp Tyr Thr Ile Thr Val Tyr Ala Val His Gly Val Arg Phe Ile Ser
65                  70                  75                  80

Ile Asn Tyr Arg Thr
                85
```

<210> SEQ ID NO 513
<211> LENGTH: 91
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_F01 w/ N leader + his tag

<400> SEQUENCE: 513

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Tyr Lys Pro Ser Thr Ile Val Thr Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Val His Gly Val Arg Phe Ile Ser
65                  70                  75                  80

Ile Asn Tyr Arg Thr His His His His His His
                85                  90
```

<210> SEQ ID NO 514
<211> LENGTH: 92
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_F01 w/ N leader and C tail

<400> SEQUENCE: 514

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Tyr Lys Pro Ser Thr Ile Val Thr Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Val His Gly Val Arg Phe Ile Ser
65                  70                  75                  80

Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90
```

<210> SEQ ID NO 515
<211> LENGTH: 98
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_F01 w/ N leader and C
      tail + his tag

<400> SEQUENCE: 515

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15
```

-continued

```
Thr Ser Leu Leu Ile Ser Trp Tyr Lys Pro Ser Thr Ile Val Thr Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Val His Gly Val Arg Phe Ile Ser
65                  70                  75                  80

Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His
                85                  90                  95

His His


<210> SEQ ID NO 516
<211> LENGTH: 87
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_F01 w/ N leader and
      modified C-terminus including PC

<400> SEQUENCE: 516

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Tyr Lys Pro Ser Thr Ile Val Thr Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Val His Gly Val Arg Phe Ile Ser
65                  70                  75                  80

Ile Asn Tyr Arg Thr Pro Cys
                85


<210> SEQ ID NO 517
<211> LENGTH: 93
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_F01 w/ N leader and
      modified C-terminus including PC + his tag

<400> SEQUENCE: 517

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Tyr Lys Pro Ser Thr Ile Val Thr Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Val His Gly Val Arg Phe Ile Ser
65                  70                  75                  80

Ile Asn Tyr Arg Thr Pro Cys His His His His His His
                85                  90
```

-continued

<210> SEQ ID NO 518
<211> LENGTH: 99
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_F01 full length

<400> SEQUENCE: 518

```
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp Tyr Lys Pro Ser Thr Ile Val Thr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

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

Val Asp Tyr Thr Ile Thr Val Tyr Ala Val His Gly Val Arg Phe Ile
65                  70                  75                  80

Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His
                85                  90                  95

His His His
```

<210> SEQ ID NO 519
<211> LENGTH: 78
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_F04 core

<400> SEQUENCE: 519

```
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Gly Gly
1               5                   10                  15

Ser Leu Ser Pro Thr Phe Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly
            20                  25                  30

Asn Ser Pro Val Gln Glu Phe Thr Val Thr Tyr Gln Gly Ala Thr Ile
        35                  40                  45

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

Glu Gly Ile Val Tyr Tyr Gln Ile Ser Ile Asn Tyr Arg Thr
65                  70                  75
```

<210> SEQ ID NO 520
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_F04 BC loop

<400> SEQUENCE: 520

```
Gly Gly Ser Leu Ser Pro Thr Phe
1               5
```

<210> SEQ ID NO 521
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_F04 DE loop

<400> SEQUENCE: 521

-continued

Thr Tyr Gln Gly
1

<210> SEQ ID NO 522
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_F04 FG loop

<400> SEQUENCE: 522

Thr Glu Gly Ile Val Tyr Tyr Gln
1   5

<210> SEQ ID NO 523
<211> LENGTH: 87
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_F04 w/ N leader

<400> SEQUENCE: 523

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Gly Gly Ser Leu Ser Pro Thr Phe Tyr
            20   25   30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35   40   45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Thr Glu Gly Ile Val Tyr Tyr Gln
65   70   75   80

Ile Ser Ile Asn Tyr Arg Thr
                85

<210> SEQ ID NO 524
<211> LENGTH: 93
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_F04 w/ N leader + his tag

<400> SEQUENCE: 524

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Gly Gly Ser Leu Ser Pro Thr Phe Tyr
            20   25   30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35   40   45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Thr Glu Gly Ile Val Tyr Tyr Gln
65   70   75   80

Ile Ser Ile Asn Tyr Arg Thr His His His His His His
                85   90

<210> SEQ ID NO 525
<211> LENGTH: 94

-continued

```
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_F04 w/ N leader and C tail

<400> SEQUENCE: 525

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Gly Gly Ser Leu Ser Pro Thr Phe Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Thr Glu Gly Ile Val Tyr Tyr Gln
65                  70                  75                  80

Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90


<210> SEQ ID NO 526
<211> LENGTH: 100
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_F04 w/ N leader and C
      tail + his tag

<400> SEQUENCE: 526

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Gly Gly Ser Leu Ser Pro Thr Phe Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Thr Glu Gly Ile Val Tyr Tyr Gln
65                  70                  75                  80

Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His His
                85                  90                  95

His His His His
            100


<210> SEQ ID NO 527
<211> LENGTH: 89
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_F04 w/ N leader and
      modified C-terminus including PC

<400> SEQUENCE: 527

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Gly Gly Ser Leu Ser Pro Thr Phe Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45
```

-continued

```
Thr Val Thr Tyr Gln Gly Ala Thr Ile Ser Gly Leu Lys Pro Gly Val
    50                  55                  60

Asp Tyr Thr Ile Thr Val Tyr Ala Thr Glu Gly Ile Val Tyr Tyr Gln
65                  70                  75                  80

Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85
```

<210> SEQ ID NO 528
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_F04 w/ N leader and modified C-terminus including PC + his tag

<400> SEQUENCE: 528

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Gly Gly Ser Leu Ser Pro Thr Phe Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Thr Glu Gly Ile Val Tyr Tyr Gln
65                  70                  75                  80

Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His His His His
                85                  90                  95
```

<210> SEQ ID NO 529
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_F04 full length

<400> SEQUENCE: 529

```
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp Gly Gly Ser Leu Ser Pro Thr Phe
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Thr Tyr Gln Gly Ala Thr Ile Ser Gly Leu Lys Pro Gly
    50                  55                  60

Val Asp Tyr Thr Ile Thr Val Tyr Ala Thr Glu Gly Ile Val Tyr Tyr
65                  70                  75                  80

Gln Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His
                85                  90                  95

His His His His His
            100
```

<210> SEQ ID NO 530
<211> LENGTH: 79
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

-continued

<223> OTHER INFORMATION: Synthetic: ATI_1523_F08 core

<400> SEQUENCE: 530

```
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Val Tyr
1               5                   10                  15

His Tyr Asp Ala Gln Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn
            20                  25                  30

Ser Pro Val Gln Glu Phe Thr Val Pro Asp Gln Lys Ala Thr Ile Ser
        35                  40                  45

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

Arg Ala His Met Asp Arg Ser His Ile Ser Ile Asn Tyr Arg Thr
65                  70                  75
```

<210> SEQ ID NO 531
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_F08 BC loop

<400> SEQUENCE: 531

```
Val Tyr His Tyr Asp Ala Gln
1               5
```

<210> SEQ ID NO 532
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_F08 DE loop

<400> SEQUENCE: 532

```
Pro Asp Gln Lys
1
```

<210> SEQ ID NO 533
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_F08 FG loop

<400> SEQUENCE: 533

```
Leu Pro Arg Ala His Met Asp Arg Ser His
1               5                   10
```

<210> SEQ ID NO 534
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_F08 w/ N leader

<400> SEQUENCE: 534

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

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

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45
```

-continued

```
Val Pro Asp Gln Lys Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50                  55                  60

Tyr Thr Ile Thr Val Tyr Ala Leu Pro Arg Ala His Met Asp Arg Ser
65                  70                  75                  80

His Ile Ser Ile Asn Tyr Arg Thr
                85


<210> SEQ ID NO 535
<211> LENGTH: 94
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_F08 w/ N leader + his tag

<400> SEQUENCE: 535

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

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

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Pro Arg Ala His Met Asp Arg Ser
65                  70                  75                  80

His Ile Ser Ile Asn Tyr Arg Thr His His His His His His
                85                  90


<210> SEQ ID NO 536
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_F08 w/ N leader and C tail

<400> SEQUENCE: 536

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

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

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Pro Arg Ala His Met Asp Arg Ser
65                  70                  75                  80

His Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95


<210> SEQ ID NO 537
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_F08 w/ N leader and C
      tail + his tag

<400> SEQUENCE: 537
```

-continued

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

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

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Pro Arg Ala His Met Asp Arg Ser
65                  70                  75                  80

His Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His
                85                  90                  95

His His His His His
            100


<210> SEQ ID NO 538
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_F08 w/ N leader and
      modified C-terminus including PC

<400> SEQUENCE: 538

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

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

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Pro Arg Ala His Met Asp Arg Ser
65                  70                  75                  80

His Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90


<210> SEQ ID NO 539
<211> LENGTH: 96
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_F08 w/ N leader and
      modified C-terminus including PC + his tag

<400> SEQUENCE: 539

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

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

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Pro Arg Ala His Met Asp Arg Ser
65                  70                  75                  80
```

-continued

```
His Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His His His His
                85                  90                  95
```

<210> SEQ ID NO 540
<211> LENGTH: 102
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_F08 full length

<400> SEQUENCE: 540

```
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp Val Tyr His Tyr Asp Ala Gln Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Leu Pro Arg Ala His Met Asp Arg
65                  70                  75                  80

Ser His Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95

His His His His His His
            100
```

<210> SEQ ID NO 541
<211> LENGTH: 79
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_G06 core

<400> SEQUENCE: 541

```
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Arg Ile
1               5                   10                  15

Lys Ser Tyr His Lys Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn
            20                  25                  30

Ser Pro Val Gln Glu Phe Thr Val Arg Ser Tyr Ala Ala Thr Ile Ser
        35                  40                  45

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

Glu Glu Thr His Leu Ala Tyr Ala Ile Ser Ile Asn Tyr Arg Thr
65                  70                  75
```

<210> SEQ ID NO 542
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_G06 BC loop

<400> SEQUENCE: 542

```
Arg Ile Lys Ser Tyr His Lys
1               5
```

<210> SEQ ID NO 543
<211> LENGTH: 4

-continued

<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_G06 DE loop

<400> SEQUENCE: 543

Arg Ser Tyr Ala
1

<210> SEQ ID NO 544
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_G06 FG loop

<400> SEQUENCE: 544

Ile Met Glu Glu Thr His Leu Ala Tyr Ala
1   5   10

<210> SEQ ID NO 545
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_G06 w/ N leader

<400> SEQUENCE: 545

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Arg Ile Lys Ser Tyr His Lys Tyr Arg
            20   25   30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35   40   45

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

Tyr Thr Ile Thr Val Tyr Ala Ile Met Glu Glu Thr His Leu Ala Tyr
65   70   75   80

Ala Ile Ser Ile Asn Tyr Arg Thr
                85

<210> SEQ ID NO 546
<211> LENGTH: 94
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_G06 w/ N leader + his tag

<400> SEQUENCE: 546

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Arg Ile Lys Ser Tyr His Lys Tyr Arg
            20   25   30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35   40   45

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

Tyr Thr Ile Thr Val Tyr Ala Ile Met Glu Glu Thr His Leu Ala Tyr
65   70   75   80

-continued

```
Ala Ile Ser Ile Asn Tyr Arg Thr His His His His His His
                85                  90


<210> SEQ ID NO 547
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_G06 w/ N leader and C tail

<400> SEQUENCE: 547

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Arg Ile Lys Ser Tyr His Lys Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Ile Met Glu Glu Thr His Leu Ala Tyr
65                  70                  75                  80

Ala Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95


<210> SEQ ID NO 548
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_G06 w/ N leader and C
      tail + his tag

<400> SEQUENCE: 548

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Arg Ile Lys Ser Tyr His Lys Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Ile Met Glu Glu Thr His Leu Ala Tyr
65                  70                  75                  80

Ala Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His
                85                  90                  95

His His His His His
            100


<210> SEQ ID NO 549
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_G06 w/ N leader and
      modified C-terminus including PC

<400> SEQUENCE: 549

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15
```

-continued

```
Thr Ser Leu Leu Ile Ser Trp Arg Ile Lys Ser Tyr His Lys Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Ile Met Glu Glu Thr His Leu Ala Tyr
65                  70                  75                  80

Ala Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90
```

<210> SEQ ID NO 550
<211> LENGTH: 96
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_G06 w/ N leader and modified C-terminus including PC + his tag

<400> SEQUENCE: 550

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Arg Ile Lys Ser Tyr His Lys Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Ile Met Glu Glu Thr His Leu Ala Tyr
65                  70                  75                  80

Ala Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His His His His
                85                  90                  95
```

<210> SEQ ID NO 551
<211> LENGTH: 102
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_G06 full length

<400> SEQUENCE: 551

```
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp Arg Ile Lys Ser Tyr His Lys Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

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

Asp Tyr Thr Ile Thr Val Tyr Ala Ile Met Glu Glu Thr His Leu Ala
65                  70                  75                  80

Tyr Ala Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95

His His His His His His
            100
```

-continued

<210> SEQ ID NO 552
<211> LENGTH: 79
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_G07 core

<400> SEQUENCE: 552

```
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Val Tyr
1               5                   10                  15

Pro Gln Ala Asp Asp Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn
            20                  25                  30

Ser Pro Val Gln Glu Phe Thr Val Pro Asp Gln Asn Ala Thr Ile Ser
        35                  40                  45

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

Glu Ala His Leu Val Arg Ile Tyr Ile Ser Ile Asn Tyr Arg Thr
65                  70                  75
```

<210> SEQ ID NO 553
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_G07 BC loop

<400> SEQUENCE: 553

```
Val Tyr Pro Gln Ala Asp Asp
1               5
```

<210> SEQ ID NO 554
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_G07 DE loop

<400> SEQUENCE: 554

```
Pro Asp Gln Asn
1
```

<210> SEQ ID NO 555
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_G07 FG loop

<400> SEQUENCE: 555

```
Leu Ala Glu Ala His Leu Val Arg Ile Tyr
1               5                   10
```

<210> SEQ ID NO 556
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_G07 w/ N leader

<400> SEQUENCE: 556

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15
```

-continued

```
Thr Ser Leu Leu Ile Ser Trp Val Tyr Pro Gln Ala Asp Asp Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

Val Pro Asp Gln Asn Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50                  55                  60

Tyr Thr Ile Thr Val Tyr Ala Leu Ala Glu Ala His Leu Val Arg Ile
65                  70                  75                  80

Tyr Ile Ser Ile Asn Tyr Arg Thr
                85


<210> SEQ ID NO 557
<211> LENGTH: 94
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_G07 w/ N leader + his tag

<400> SEQUENCE: 557

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

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

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

Val Pro Asp Gln Asn Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50                  55                  60

Tyr Thr Ile Thr Val Tyr Ala Leu Ala Glu Ala His Leu Val Arg Ile
65                  70                  75                  80

Tyr Ile Ser Ile Asn Tyr Arg Thr His His His His His His
                85                  90


<210> SEQ ID NO 558
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_G07 w/ N leader and C tail

<400> SEQUENCE: 558

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

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

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

Val Pro Asp Gln Asn Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50                  55                  60

Tyr Thr Ile Thr Val Tyr Ala Leu Ala Glu Ala His Leu Val Arg Ile
65                  70                  75                  80

Tyr Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95


<210> SEQ ID NO 559
<211> LENGTH: 101
<212> TYPE: PRT
```

-continued

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_G07 w/ N leader and C tail + his tag

<400> SEQUENCE: 559

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

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

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

Val Pro Asp Gln Asn Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50                  55                  60

Tyr Thr Ile Thr Val Tyr Ala Leu Ala Glu Ala His Leu Val Arg Ile
65                  70                  75                  80

Tyr Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His
                85                  90                  95

His His His His His
            100
```

<210> SEQ ID NO 560
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_G07 w/ N leader and modified C-terminus including PC

<400> SEQUENCE: 560

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

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

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

Val Pro Asp Gln Asn Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50                  55                  60

Tyr Thr Ile Thr Val Tyr Ala Leu Ala Glu Ala His Leu Val Arg Ile
65                  70                  75                  80

Tyr Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90
```

<210> SEQ ID NO 561
<211> LENGTH: 96
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_G07 w/ N leader and modified C-terminus including PC + his tag

<400> SEQUENCE: 561

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

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

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45
```

-continued

```
Val Pro Asp Gln Asn Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50                  55                  60

Tyr Thr Ile Thr Val Tyr Ala Leu Ala Glu Ala His Leu Val Arg Ile
65                  70                  75                  80

Tyr Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His His His His
                85                  90                  95


<210> SEQ ID NO 562
<211> LENGTH: 102
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_G07 full length

<400> SEQUENCE: 562

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1               5                   10                  15

Pro Thr Ser Leu Leu Ile Ser Trp Val Tyr Pro Gln Ala Asp Asp Tyr
            20                  25                  30

Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
        35                  40                  45

Thr Val Pro Asp Gln Asn Ala Thr Ile Ser Gly Leu Lys Pro Gly Val
    50                  55                  60

Asp Tyr Thr Ile Thr Val Tyr Ala Leu Ala Glu Ala His Leu Val Arg
65                  70                  75                  80

Ile Tyr Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85                  90                  95

His His His His His His
            100


<210> SEQ ID NO 563
<211> LENGTH: 79
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_H07 core
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 563

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Val Tyr
1               5                   10                  15

His Tyr Asp Ala Xaa Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn
            20                  25                  30

Ser Pro Val Gln Glu Phe Thr Val Pro Asp Gln Lys Ala Thr Ile Ser
        35                  40                  45

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

Glu Ala His His Lys Arg Asp Ser Ile Ser Ile Asn Tyr Arg Thr
65                  70                  75


<210> SEQ ID NO 564
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
```

-continued

<223> OTHER INFORMATION: Synthetic: ATI_1523_H07 BC loop
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (7)..(7)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 564

Val Tyr His Tyr Asp Ala Xaa
1   5

<210> SEQ ID NO 565
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_H07 DE loop

<400> SEQUENCE: 565

Pro Asp Gln Lys
1

<210> SEQ ID NO 566
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_H07 FG loop

<400> SEQUENCE: 566

Leu Ser Glu Ala His His Lys Arg Asp Ser
1   5   10

<210> SEQ ID NO 567
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_H07 w/ N leader
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (30)..(30)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 567

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Val Tyr His Tyr Asp Ala Xaa Tyr Arg
            20   25   30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35   40   45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Ser Glu Ala His His Lys Arg Asp
65   70   75   80

Ser Ile Ser Ile Asn Tyr Arg Thr
                85

<210> SEQ ID NO 568
<211> LENGTH: 94
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_H07 w/ N leader + his tag

-continued

<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (30)..(30)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 568

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Val Tyr His Tyr Asp Ala Xaa Tyr Arg
            20   25   30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35   40   45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Ser Glu Ala His His Lys Arg Asp
65   70   75   80

Ser Ile Ser Ile Asn Tyr Arg Thr His His His His His His
                85   90

<210> SEQ ID NO 569
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_H07 w/ N leader and C tail
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (30)..(30)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 569

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Val Tyr His Tyr Asp Ala Xaa Tyr Arg
            20   25   30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35   40   45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Ser Glu Ala His His Lys Arg Asp
65   70   75   80

Ser Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
                85   90   95

<210> SEQ ID NO 570
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_H07 w/ N leader and C
      tail + his tag
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (30)..(30)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 570

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1   5   10   15

Thr Ser Leu Leu Ile Ser Trp Val Tyr His Tyr Asp Ala Xaa Tyr Arg

-continued

```
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Ser Glu Ala His His Lys Arg Asp
65                  70                  75                  80

Ser Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His
                85                  90                  95

His His His His His
            100


<210> SEQ ID NO 571
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_H07 w/ N leader and
      modified C-terminus including PC
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (30)..(30)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 571

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Val Tyr His Tyr Asp Ala Xaa Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Ser Glu Ala His His Lys Arg Asp
65                  70                  75                  80

Ser Ile Ser Ile Asn Tyr Arg Thr Pro Cys
                85                  90


<210> SEQ ID NO 572
<211> LENGTH: 96
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_H07 w/ N leader and
      modified C-terminus including PC + his tag
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (30)..(30)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 572

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Val Tyr His Tyr Asp Ala Xaa Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

Val Pro Asp Gln Lys Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
    50                  55                  60
```

-continued

```
Tyr Thr Ile Thr Val Tyr Ala Leu Ser Glu Ala His His Lys Arg Asp
65                  70                  75                  80

Ser Ile Ser Ile Asn Tyr Arg Thr Pro Cys His His His His His His
                85                  90                  95


<210> SEQ ID NO 573
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: ATI_1523_H07 full length
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (30)..(30)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 573

Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Val Tyr His Tyr Asp Ala Xaa Tyr Arg
            20                  25                  30

Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr
        35                  40                  45

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

Tyr Thr Ile Thr Val Tyr Ala Leu Ser Glu Ala His His Lys Arg Asp
65                  70                  75                  80

Ser Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His
                85                  90                  95

His His His His His
            100


<210> SEQ ID NO 574
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: N-terminal leader

<400> SEQUENCE: 574

Met Gly Val Ser Asp Val Pro Arg Asp Leu
1               5                   10


<210> SEQ ID NO 575
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: N-terminal leader

<400> SEQUENCE: 575

Gly Val Ser Asp Val Pro Arg Asp Leu
1               5


<210> SEQ ID NO 576
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: N-terminal leader
<220> FEATURE:
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<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(2)
<223> OTHER INFORMATION: Xaa may or may not be present; if one is
      present, Xaa is Met or Gly; if two are present, Xaa is Met-Gly

<400> SEQUENCE: 576

Xaa Xaa Ser Asp Val Pro Arg Asp Leu
1               5


<210> SEQ ID NO 577
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: N-terminal leader
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(2)
<223> OTHER INFORMATION: Xaa may or may not be present; if one is
      present, Xaa is Met or Gly; if two are present, Xaa is Met-Gly

<400> SEQUENCE: 577

Xaa Xaa Asp Val Pro Arg Asp Leu
1               5


<210> SEQ ID NO 578
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: N-terminal leader
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(2)
<223> OTHER INFORMATION: Xaa may or may not be present; if one is
      present, Xaa is Met or Gly; if two are present, Xaa is Met-Gly

<400> SEQUENCE: 578

Xaa Xaa Val Pro Arg Asp Leu
1               5


<210> SEQ ID NO 579
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: N-terminal leader
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(2)
<223> OTHER INFORMATION: Xaa may or may not be present; if one is
      present, Xaa is Met or Gly; if two are present, Xaa is Met-Gly

<400> SEQUENCE: 579

Xaa Xaa Pro Arg Asp Leu
1               5


<210> SEQ ID NO 580
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: N-terminal leader
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(2)
<223> OTHER INFORMATION: Xaa may or may not be present; if one is
      present, Xaa is Met or Gly; if two are present, Xaa is Met-Gly
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<400> SEQUENCE: 580

Xaa Xaa Arg Asp Leu
1   5

<210> SEQ ID NO 581
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: N-terminal leader
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(2)
<223> OTHER INFORMATION: Xaa may or may not be present; if one is present, Xaa is Met or Gly; if two are present, Xaa is Met-Gly

<400> SEQUENCE: 581

Xaa Xaa Asp Leu
1

<210> SEQ ID NO 582
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: N-terminal leader

<400> SEQUENCE: 582

Met Ala Ser Thr Ser Gly
1   5

<210> SEQ ID NO 583
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: N-terminal leader

<400> SEQUENCE: 583

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1   5   10   15

Gly Ser Thr Gly
            20

<210> SEQ ID NO 584
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 584

Glu Ile Glu Lys
1

<210> SEQ ID NO 585
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 585

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Glu Gly Ser Gly Cys
1 5

<210> SEQ ID NO 586
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 586

Glu Ile Glu Lys Pro Cys Gln
1 5

<210> SEQ ID NO 587
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 587

Glu Ile Glu Lys Pro Ser Gln
1 5

<210> SEQ ID NO 588
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 588

Glu Ile Glu Lys Pro
1 5

<210> SEQ ID NO 589
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 589

Glu Ile Glu Lys Pro Ser
1 5

<210> SEQ ID NO 590
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 590

Glu Ile Glu Lys Pro Cys
1 5

<210> SEQ ID NO 591
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

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<400> SEQUENCE: 591

Glu Ile Asp Lys
1

<210> SEQ ID NO 592
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 592

Glu Ile Asp Lys Pro Cys Gln
1   5

<210> SEQ ID NO 593
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 593

Glu Ile Asp Lys Pro Ser Gln
1   5

<210> SEQ ID NO 594
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 594

Glu Ile Glu Pro Lys Ser Ser
1   5

<210> SEQ ID NO 595
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 595

Glu Ile Asp Lys Pro Cys
1   5

<210> SEQ ID NO 596
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 596

Glu Ile Asp Lys Pro
1   5

<210> SEQ ID NO 597
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 597

Glu Ile Asp Lys Pro Ser
1   5

<210> SEQ ID NO 598
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 598

Glu Ile Asp Lys Pro Ser Gln Leu Glu
1   5

<210> SEQ ID NO 599
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 599

Glu Ile Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
1   5   10

<210> SEQ ID NO 600
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 600

Glu Gly Ser Gly Ser
1   5

<210> SEQ ID NO 601
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 601

Glu Ile Asp Lys Pro Cys Gln Leu Glu
1   5

<210> SEQ ID NO 602
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 602

Glu Ile Asp Lys Pro Ser Gln His His His His His His
1   5   10

<210> SEQ ID NO 603
<211> LENGTH: 10
<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 603

Gly Ser Gly Cys His His His His His His
1   5   10

<210> SEQ ID NO 604
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 604

Glu Gly Ser Gly Cys His His His His His His
1   5   10

<210> SEQ ID NO 605
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 605

Pro Ile Asp Lys
1

<210> SEQ ID NO 606
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 606

Pro Ile Glu Lys
1

<210> SEQ ID NO 607
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 607

Pro Ile Asp Lys Pro
1   5

<210> SEQ ID NO 608
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 608

Pro Ile Glu Lys Pro
1   5

<210> SEQ ID NO 609

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<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 609

Pro Ile Asp Lys Pro Ser
1   5

<210> SEQ ID NO 610
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 610

Pro Ile Glu Lys Pro Ser
1   5

<210> SEQ ID NO 611
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 611

Pro Ile Asp Lys Pro Cys
1   5

<210> SEQ ID NO 612
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 612

Pro Ile Glu Lys Pro Cys
1   5

<210> SEQ ID NO 613
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 613

Pro Ile Asp Lys Pro Ser Gln
1   5

<210> SEQ ID NO 614
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 614

Pro Ile Glu Lys Pro Ser Gln
1   5

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<210> SEQ ID NO 615
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 615

Pro Ile Asp Lys Pro Cys Gln
1   5

<210> SEQ ID NO 616
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 616

Pro Ile Glu Lys Pro Cys Gln
1   5

<210> SEQ ID NO 617
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 617

Pro His His His His His His
1   5

<210> SEQ ID NO 618
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-terminal tail

<400> SEQUENCE: 618

Pro Cys His His His His His His
1   5

<210> SEQ ID NO 619
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: 6X-His tag

<400> SEQUENCE: 619

His His His His His His
1   5

<210> SEQ ID NO 620
<211> LENGTH: 227
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Human IgG1 Fc domain

<400> SEQUENCE: 620

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly

-continued

```
1               5                   10                  15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220

Pro Gly Lys
225
```

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<210> SEQ ID NO 621
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Core hinge region of Fc

<400> SEQUENCE: 621

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1               5                   10                  15
```

```
<210> SEQ ID NO 622
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Exemplary hinge sequence

<400> SEQUENCE: 622

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1               5                   10                  15

Pro Glu Leu Leu Gly Gly Pro Ser
            20
```

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<210> SEQ ID NO 623
<211> LENGTH: 24
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-continued

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

<400> SEQUENCE: 623

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1   5   10   15

Pro Glu Leu Leu Gly Gly Ser Ser
            20

<210> SEQ ID NO 624
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Exemplary hinge sequence

<400> SEQUENCE: 624

Glu Pro Lys Ser Ser Gly Ser Thr His Thr Cys Pro Pro Cys Pro Ala
1   5   10   15

Pro Glu Leu Leu Gly Gly Ser Ser
            20

<210> SEQ ID NO 625
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Exemplary hinge sequence

<400> SEQUENCE: 625

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1   5   10   15

Gly Pro Ser

<210> SEQ ID NO 626
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Exemplary hinge sequence

<400> SEQUENCE: 626

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1   5   10   15

Gly Ser Ser

<210> SEQ ID NO 627
<211> LENGTH: 208
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Fc with CH2 and CH3 regions of IgG1
      for Adnectin-hinge-Fc construct

<400> SEQUENCE: 627

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
1   5   10   15

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            20   25   30

-continued

```
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        35                  40                  45

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    50                  55                  60

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
65                  70                  75                  80

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
                85                  90                  95

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            100                 105                 110

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
        115                 120                 125

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    130                 135                 140

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
145                 150                 155                 160

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                165                 170                 175

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            180                 185                 190

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        195                 200                 205


<210> SEQ ID NO 628
<211> LENGTH: 206
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Fc with CH2 and CH3 regions of IgG1
      for Fc-hinge-Adnectin construct

<400> SEQUENCE: 628

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
1               5                   10                  15

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            20                  25                  30

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        35                  40                  45

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    50                  55                  60

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
65                  70                  75                  80

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
                85                  90                  95

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            100                 105                 110

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
        115                 120                 125

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    130                 135                 140

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
145                 150                 155                 160

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                165                 170                 175
```

-continued

```
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            180                 185                 190

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        195                 200                 205


<210> SEQ ID NO 629
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 1

<400> SEQUENCE: 629

Gly Ala Gly Gly Gly Gly Ser Gly
1               5


<210> SEQ ID NO 630
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 2

<400> SEQUENCE: 630

Glu Pro Lys Ser Ser Asp
1               5


<210> SEQ ID NO 631
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 3

<400> SEQUENCE: 631

Pro Val Gly Val Val
1               5


<210> SEQ ID NO 632
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 4

<400> SEQUENCE: 632

Glu Ser Pro Lys Ala Gln Ala Ser Ser Val Pro Thr Ala Gln Pro Gln
1               5                   10                  15

Ala Glu Gly Leu Ala
            20


<210> SEQ ID NO 633
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 5

<400> SEQUENCE: 633

Glu Leu Gln Leu Glu Glu Ser Ala Ala Glu Ala Gln Asp Gly Glu Leu
1               5                   10                  15

Asp
```

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<210> SEQ ID NO 634
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 6

<400> SEQUENCE: 634

Gly Gln Pro Asp Glu Pro Gly Gly Ser
1   5

<210> SEQ ID NO 635
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 7

<400> SEQUENCE: 635

Gly Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
1   5   10

<210> SEQ ID NO 636
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 8

<400> SEQUENCE: 636

Glu Leu Gln Leu Glu Glu Ser Ala Ala Glu Ala Gln Glu Gly Glu Leu
1   5   10   15

Glu

<210> SEQ ID NO 637
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 9

<400> SEQUENCE: 637

Gly Ser Gly Ser Gly
1   5

<210> SEQ ID NO 638
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 10

<400> SEQUENCE: 638

Gly Ser Gly Cys
1

<210> SEQ ID NO 639
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 11

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<400> SEQUENCE: 639

Ala Gly Gly Gly Gly Ser Gly
1 5

<210> SEQ ID NO 640
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 12

<400> SEQUENCE: 640

Gly Ser Gly Ser
1

<210> SEQ ID NO 641
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 13

<400> SEQUENCE: 641

Gln Pro Asp Glu Pro Gly Gly Ser
1 5

<210> SEQ ID NO 642
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 14

<400> SEQUENCE: 642

Gly Ser Gly Ser Gly Ser
1 5

<210> SEQ ID NO 643
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 15

<400> SEQUENCE: 643

Thr Val Ala Ala Pro Ser
1 5

<210> SEQ ID NO 644
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 16

<400> SEQUENCE: 644

Lys Ala Gly Gly Gly Gly Ser Gly
1 5

<210> SEQ ID NO 645
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic: Linker 17

<400> SEQUENCE: 645

Lys Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
1   5   10

<210> SEQ ID NO 646
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 18

<400> SEQUENCE: 646

Lys Gln Pro Asp Glu Pro Gly Gly Ser
1   5

<210> SEQ ID NO 647
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 19

<400> SEQUENCE: 647

Lys Glu Leu Gln Leu Glu Glu Ser Ala Ala Glu Ala Gln Asp Gly Glu
1   5   10   15

Leu Asp

<210> SEQ ID NO 648
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 20

<400> SEQUENCE: 648

Lys Thr Val Ala Ala Pro Ser
1   5

<210> SEQ ID NO 649
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 21

<400> SEQUENCE: 649

Lys Ala Gly Gly Gly Gly Ser Gly Gly
1   5

<210> SEQ ID NO 650
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 22

<400> SEQUENCE: 650

Lys Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
1   5   10

<210> SEQ ID NO 651

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<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 23

<400> SEQUENCE: 651

Lys Gln Pro Asp Glu Pro Gly Gly Ser Gly
1 5 10

<210> SEQ ID NO 652
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 24

<400> SEQUENCE: 652

Lys Glu Leu Gln Leu Glu Glu Ser Ala Ala Glu Ala Gln Asp Gly Glu
1 5 10 15

Leu Asp Gly

<210> SEQ ID NO 653
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 25

<400> SEQUENCE: 653

Lys Thr Val Ala Ala Pro Ser Gly
1 5

<210> SEQ ID NO 654
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 26

<400> SEQUENCE: 654

Ala Gly Gly Gly Gly Ser Gly Gly
1 5

<210> SEQ ID NO 655
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 27

<400> SEQUENCE: 655

Ala Gly Gly Gly Gly Ser Gly
1 5

<210> SEQ ID NO 656
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 28

<400> SEQUENCE: 656

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly

-continued

1 5 10

<210> SEQ ID NO 657
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 29

<400> SEQUENCE: 657

Gln Pro Asp Glu Pro Gly Gly Ser Gly
1 5

<210> SEQ ID NO 658
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 30

<400> SEQUENCE: 658

Thr Val Ala Ala Pro Ser Gly
1 5

<210> SEQ ID NO 659
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 31

<400> SEQUENCE: 659

Pro Ser Thr Ser Thr Ser Thr
1 5

<210> SEQ ID NO 660
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 32

<400> SEQUENCE: 660

Glu Ile Asp Lys Pro Ser Gln
1 5

<210> SEQ ID NO 661
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 33

<400> SEQUENCE: 661

Gly Ser Gly Ser Gly Ser Gly Ser
1 5

<210> SEQ ID NO 662
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 34

<400> SEQUENCE: 662

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Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
1 5 10

<210> SEQ ID NO 663
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 35

<400> SEQUENCE: 663

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
1 5 10

<210> SEQ ID NO 664
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 36

<400> SEQUENCE: 664

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
1 5 10

<210> SEQ ID NO 665
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 37

<400> SEQUENCE: 665

Gly Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
1 5 10

<210> SEQ ID NO 666
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 38

<400> SEQUENCE: 666

Gly Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
1 5 10 15

<210> SEQ ID NO 667
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 39

<400> SEQUENCE: 667

Gly Ser Glu Gly Ser Glu Gly Ser Glu Gly Ser Glu Gly Ser Glu
1 5 10 15

<210> SEQ ID NO 668
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 40

-continued

<400> SEQUENCE: 668

Gly Gly Ser Glu Gly Gly Ser Glu
1   5

<210> SEQ ID NO 669
<211> LENGTH: 35
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 41

<400> SEQUENCE: 669

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1   5   10   15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
            20   25   30

Gly Gly Ser
        35

<210> SEQ ID NO 670
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 42

<400> SEQUENCE: 670

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1   5   10   15

Gly Gly Gly Ser Gly Gly Gly Gly Ser
            20   25

<210> SEQ ID NO 671
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 43

<400> SEQUENCE: 671

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1   5   10   15

<210> SEQ ID NO 672
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 44

<400> SEQUENCE: 672

Gly Pro Gly Pro Gly Pro Gly
1   5

<210> SEQ ID NO 673
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 45

<400> SEQUENCE: 673

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Gly Pro Gly Pro Gly Pro Gly Pro Gly Pro Gly
1   5   10

<210> SEQ ID NO 674
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 46

<400> SEQUENCE: 674

Pro Ala Pro Ala Pro Ala
1   5

<210> SEQ ID NO 675
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 47

<400> SEQUENCE: 675

Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala
1   5   10

<210> SEQ ID NO 676
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 48

<400> SEQUENCE: 676

Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala
1   5   10   15

Pro Ala

<210> SEQ ID NO 677
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 49

<400> SEQUENCE: 677

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
1   5   10   15

Gly Ser Gly Ser
            20

<210> SEQ ID NO 678
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker 50

<400> SEQUENCE: 678

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1   5   10   15

Gly Gly Gly Ser
            20

1. A method of visualizing PD-L1 protein in a subject, comprising:
(a) administering to the subject a PD-L1 imaging agent at a dose of about 3-10 mCi (100-333 MBq); and
(b) conducting a PET scan of the subject about 30-120 minutes after step (a).

2-4. (canceled)

5. The method of claim **1**, wherein the subject has at least one tumor.

6. (canceled)

7. The method of claim **1**, for determining whether a subject is likely to respond to a treatment with an immuno-oncology agent.

8-9. (canceled)

10. The method of claim **1**, wherein the subject is being treated with a therapeutic agent.

11-14. (canceled)

15. The method of claim **1**, wherein the PD-L1 imaging agent is a protein binding specifically to human PD-L1, wherein the protein is linked to a detectable agent.

16. The method of claim **15**, wherein the PD-L1 imaging agent is an anti-PD-L1 adnectin.

17. The method of claim **15**, wherein the detectable agent is a radioactive PET tracer.

18-23. (canceled)

24. The method of claim **16**, wherein the anti-human PD-L1 adnectin comprises a fibronectin type III tenth domain (^{10}Fn3), wherein (a) the ^{10}Fn3 domain comprises AB, BC, CD, DE, EF, and FG loops, (b) the ^{10}Fn3 has at least one loop selected from loop BC, DE, and FG with an altered amino acid sequence relative to the sequence of the corresponding loop of the human ^{10}Fn3 domain (SEQ ID NO: 1), and (c) the polypeptide specifically binds to human PD-L1.

25-26. (canceled)

27. The method of claim **24**, wherein the BC, DE, and FG loops comprise the amino acid sequences of:
(a) SEQ ID NOs: 6, 7, and 8, respectively;
(b) SEQ ID NOs: 21, 22, and 23, respectively;
(c) SEQ ID NOs: 36, 37, and 38, respectively;
(d) SEQ ID NOs: 51, 52, and 53, respectively;
(e) SEQ ID NOs: 66, 67, and 68, respectively;
(f) SEQ ID NOs: 81, 82, and 83, respectively;
(g) SEQ ID NOs: 97, 98, and 99, respectively;
(h) SEQ ID NOs: 113, 114, and 115, respectively;
(i) SEQ ID NOs: 124, 125 and 126, respectively;
(i) SEQ ID NOs: 135, 136 and 137, respectively;
(k) SEQ ID NOs: 146, 147 and 148, respectively;
(l) SEQ ID NOs: 157, 158 and 159, respectively;
(m) SEQ ID NOs: 168, 169 and 170, respectively;
(n) SEQ ID NOs: 179, 180 and 181, respectively;
(o) SEQ ID NOs: 190, 191 and 192, respectively;
(p) SEQ ID NOs: 201, 202 and 203, respectively;
(q) SEQ ID NOs: 212, 213 and 214, respectively;
(r) SEQ ID NOs: 223, 224 and 225, respectively;
(s) SEQ ID NOs: 234, 235, and 236, respectively;
(t) SEQ ID NOs: 245, 246 and 247, respectively;
(u) SEQ ID NOs: 256, 257 and 258, respectively;
(v) SEQ ID NOs: 267, 268 and 269, respectively;
(w) SEQ ID NOs: 278, 279 and 280, respectively;
(x) SEQ ID NOs: 289, 290 and 291, respectively;
(y) SEQ ID NOs: 300, 301 and 302, respectively;
(z) SEQ ID NOs: 311, 312 and 313, respectively;
(aa) SEQ ID NOs: 322, 323 and 324, respectively;
(bb) SEQ ID NOs: 333, 334 and 335, respectively;
(cc) SEQ ID NOs: 344, 345 and 346, respectively;
(dd) SEQ ID NOs: 355, 356 and 357, respectively;
(ee) SEQ ID NOs: 366, 367 and 368, respectively;
(ff) SEQ ID NOs: 377, 378 and 379, respectively;
(g) SEQ ID NOs: 388, 389 and 390 respectively;
(hh) SEQ ID NOs: 399, 400 and 401, respectively;
(ii) SEQ ID NOs: 410, 411 and 412, respectively;
(ii) SEQ ID NOs: 421, 422 and 423, respectively;
(kk) SEQ ID NOs: 432, 433 and 434 respectively;
(ll) SEQ ID NOs: 443, 444 and 445, respectively;
(mm) SEQ ID NOs: 454, 455 and 456, respectively;
(nn) SEQ ID NOs: 465, 466 and 467, respectively;
(oo) SEQ ID NOs: 476, 477 and 478, respectively;
(pp) SEQ ID NOs: 487, 488 and 489, respectively;
(qq) SEQ ID NOs: 498, 499 and 500, respectively;
(rr) SEQ ID NOs: 509, 510 and 511, respectively;
(ss) SEQ ID NOs: 520, 521 and 522, respectively;
(tt) SEQ ID NOs: 531, 530 and 531, respectively;
(uu) SEQ ID NOs: 542, 543 and 544, respectively;
(vv) SEQ ID NOs: 553, 554 and 555, respectively; or
(ww) SEQ ID NOs: 564, 565 and 566, respectively.

28. The method claim **24**, wherein the polypeptide comprises an amino acid sequence at least 80%, 85%, 90%, 95%, 98%, 99% or 100% identical to SEQ ID NO: 5, 20, 35, 50, 65, 80, 96, 112, 123, 134, 145, 156, 167, 178, 189, 200, 211, 222, 233, 244, 255, 266, 277, 288, 299, 310, 321, 332, 343, 354, 365, 376, 387, 398, 409, 420, 431, 442, 453, 464, 475, 486, 497, 508, 519, 530, 541, 552 and 563.

29-30. (canceled)

31. The method of claim **24**, wherein the polypeptide comprises an amino acid sequence at least 80%, 85%, 90%, 95%, 98%, 99% or 100% identical to the non-BC, DE, and FG loop regions of SEQ ID NO: 5, 20, 35, 50, 65, 80, 96, 112, 123, 134, 145, 156, 167, 178, 189, 200, 211, 222, 233, 244, 255, 266, 277, 288, 299, 310, 321, 332, 343, 354, 365, 376, 387, 398, 409, 420, 431, 442, 453, 464, 475, 486, 497, 508, 519, 530, 541, 552 and 563.

32. (canceled)

33. The method of claim **24**, wherein the polypeptide comprises an amino acid sequence at least 80%, 85%, 90%, 95%, 98%, 99% or 100% identical to the non-BC, DE, and FG loop regions of an amino acid sequence selected from the group consisting of: SEQ ID NOs: 9-15, 24-30, 39-45, 54-60, 69-75, 84-91, 100-116-122, 127-133, 138-144, 150-155, 160-166, 171-177, 182-188, 193-199, 204-210, 215-221, 227-232, 237-243, 248-254, 259-265, 271-276, 291-287, 292-298, 303-309, 314-320, 325-331, 337-342, 347-353, 358-364, 369-375, 380-386, 391-397, 402-408, 413-419, 424-430, 435-441, 446-452, 457-463, 468-474, 479-485, 490-496, 501-507, 512-518, 523-529, 534-540, 545-551, and 556-562.

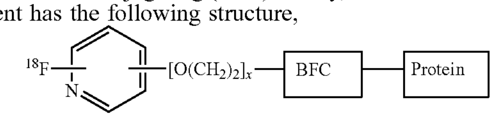
34. The method of claim **24**, wherein the polypeptide comprises an N-terminal leader selected from the group consisting of SEQ ID NOs: 112-121, and/or a C-terminal tail selected from the group consisting of SEQ ID NOs: 122-156.

35. The method of claim **24**, wherein the polypeptide comprises one or more pharmacokinetic (PK) moieties selected from the group consisting of polyethylene glycol and sialic acid.

36. (canceled)

37. The method of claim **35**, wherein the PK moiety and the polypeptide are linked via a linker with an amino acid sequence selected from the group consisting of SEQ ID NOs: 167-216.

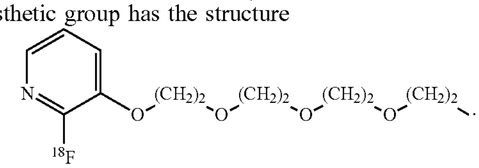
38. The method of claim **1**, wherein the imaging agent comprises the an ^{18}F-radiolabeled prosthetic group and a bifunctional conjugating (BFC) moiety, wherein the imaging agent has the following structure,



wherein the ^{18}F is ortho to the N atom, x is an integer from 1 to 8, or pharmaceutically acceptable salt thereof.

39-50. (canceled)

51. The method of claim **38**, wherein the ^{18}F-radiolabeled prosthetic group has the structure



52-55. (canceled)

56. The method of claim **38**, wherein the BFC is a cyclooctyne comprising a reactive group that forms a covalent bond with an amine, carboxyl, carbonyl or thiol functional group on the protein.

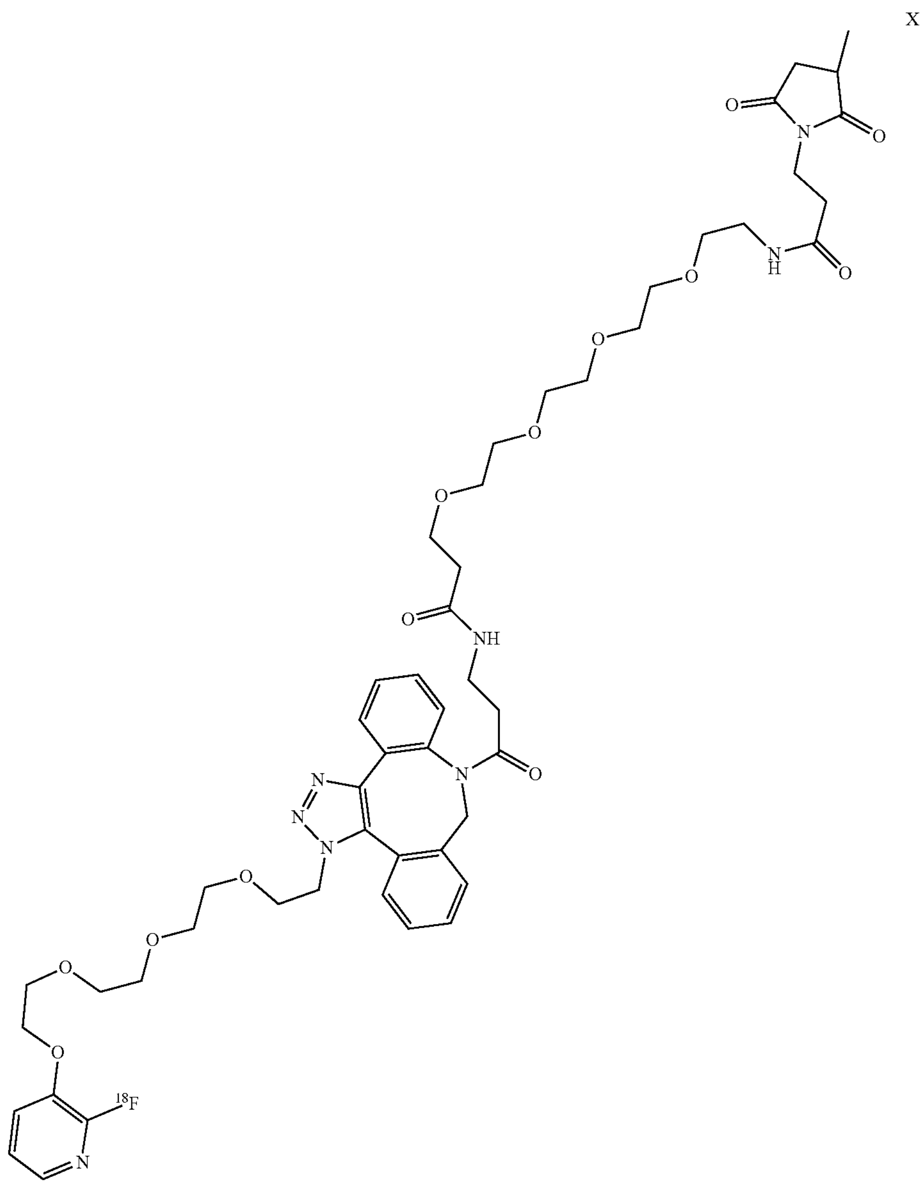
57. The method of claim **56**, wherein the cyclooctyne is selected from the group consisting of dibenzocyclooctyne (DIBO), biarylazacyclooctynone (BARAC), dimethoxyazacyclooctyne (DIMAC) and dibenzocyclooctyne (DBCO).

58. (canceled)

59. The method of claim **38**, wherein the BFC further comprises a polyethylene glycol $(PEG)_y$ spacer arm, wherein y is an integer from 1 to 8.

60-63. (canceled)

64. The method of claim **38**, wherein the imaging agent has the structure:



wherein X is a polypeptide comprising an anti-human PD-L1 adnectin comprising a fibronectin type III tenth domain (^{10}Fn3), wherein the BC, DE, and FG loops of the ^{10}Fn3 domain comprise the amino acid sequences of:

(a) SEQ ID NOs: 6, 7, and 8, respectively;
(b) SEQ ID NOs: 21, 22, and 23, respectively;
(c) SEQ ID NOs: 36, 37, and 38, respectively;
(d) SEQ ID NOs: 51, 52, and 53, respectively;
(e) SEQ ID NOs: 66, 67, and 68, respectively;
(f) SEQ ID NOs: 81, 82, and 83, respectively;
(g) SEQ ID NOs: 97, 98, and 99, respectively;
(h) SEQ ID NOs: 113, 114, and 115, respectively;
(i) SEQ ID NOs: 124, 125 and 126, respectively;
(j) SEQ ID NOs: 135, 136 and 137, respectively;
(k) SEQ ID NOs: 146, 147 and 148, respectively;
(l) SEQ ID NOs: 157, 158 and 159, respectively;
(m) SEQ ID NOs: 168, 169 and 170, respectively;
(n) SEQ ID NOs: 179, 180 and 181, respectively;
(o) SEQ ID NOs: 190, 191 and 192, respectively;
(p) SEQ ID NOs: 201, 202 and 203, respectively;
(q) SEQ ID NOs: 212, 213 and 214, respectively;
(r) SEQ ID NOs: 223, 224 and 225, respectively;
(s) SEQ ID NOs: 234, 235, and 236, respectively;
(t) SEQ ID NOs: 245, 246 and 247, respectively;
(u) SEQ ID NOs: 256, 257 and 258, respectively;
(v) SEQ ID NOs: 267, 268 and 269, respectively;
(w) SEQ ID NOs: 278, 279 and 280, respectively;
(x) SEQ ID NOs: 289, 290 and 291, respectively;
(y) SEQ ID NOs: 300, 301 and 302, respectively;
(z) SEQ ID NOs: 311, 312 and 313, respectively;
(aa) SEQ ID NOs: 322, 323 and 324, respectively;
(bb) SEQ ID NOs: 333, 334 and 335, respectively;
(cc) SEQ ID NOs: 344, 345 and 346, respectively;
(dd) SEQ ID NOs: 355, 356 and 357, respectively;
(ee) SEQ ID NOs: 366, 367 and 368, respectively;
(ff) SEQ ID NOs: 377, 378 and 379, respectively;
(g) SEQ ID NOs: 388, 389 and 390 respectively;
(hh) SEQ ID NOs: 399, 400 and 401, respectively;
(ii) SEQ ID NOs: 410, 411 and 412, respectively;
(jj) SEQ ID NOs: 421, 422 and 423, respectively;
(kk) SEQ ID NOs: 432, 433 and 434 respectively;
(ll) SEQ ID NOs: 443, 444 and 445, respectively;
(mm) SEQ ID NOs: 454, 455 and 456, respectively;
(nn) SEQ ID NOs: 465, 466 and 467, respectively;
(oo) SEQ ID NOs: 476, 477 and 478, respectively;
(pp) SEQ ID NOs: 487, 488 and 489, respectively;
(qq) SEQ ID NOs: 498, 499 and 500, respectively;
(rr) SEQ ID NOs: 509, 510 and 511, respectively;
(ss) SEQ ID NOs: 520, 521 and 522, respectively;
(tt) SEQ ID NOs: 531, 530 and 531, respectively;
(uu) SEQ ID NOs: 542, 543 and 544, respectively;
(vv) SEQ ID NOs: 553, 554 and 555, respectively; or
(ww) SEQ ID NOs: 564, 565 and 566, respectively.

65-66. (canceled)

67. The method of claim **64**, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: SEQ ID NOs: 9-15, 24-30, 39-45, 54-60, 69-75, 84-91, 100-107, 116-122, 127-133, 138-144, 150-155, 160-166, 171-177, 182-188, 193-199, 204-210, 215-221, 227-232, 237-243, 248-254, 259-265, 271-276, 291-287, 292-298, 303-309, 314-320, 325-331, 337-342, 347-353, 358-364, 369-375, 380-386, 391-397, 402-408, 413-419, 424-430, 435-441, 446-452, 457-463, 468-474, 479-485, 490-496, 501-507, 512-518, 523-529, 534-540, 545-551, and 556-562.

68. The method of claim **64**, wherein the BFC is conjugated to the polypeptide at a cysteine residue near the C-terminus of the polypeptide.

* * * * *