

SEQUENCE LISTING

<110> BIOND BIOLOGICS LTD.

<120> SMALL SHEDDING BLOCKING AGENTS

<130> BDB-P-008-PCT

<150> 62/954802

<151> 2019-12-30

<150> 62/942,240

<151> 2019-12-02

<150> 62/818351

<151> 2019-03-14

<160> 49

<170> PATENTIN VERSION 3.5

<210> 1

<211> 220

<212> PRT

<213> HOMO SAPIENS

<400> 1

MET LEU ARG LEU LEU LEU ALA LEU ASN LEU PHE PRO SER ILE GLN VAL

1 5 10 15

THR GLY ASN LYS ILE LEU VAL LYS GLN SER PRO MET LEU VAL ALA TYR

20 25 30

ASP ASN ALA VAL ASN LEU SER CYS LYS TYR SER TYR ASN LEU PHE SER

35 40 45

ARG GLU PHE ARG ALA SER LEU HIS LYS GLY LEU ASP SER ALA VAL GLU

50 55 60

VAL CYS VAL VAL TYR GLY ASN TYR SER GLN GLN LEU GLN VAL TYR SER

65 70 75 80

LYS THR GLY PHE ASN CYS ASP GLY LYS LEU GLY ASN GLU SER VAL THR

85 90 95

PHE TYR LEU GLN ASN LEU TYR VAL ASN GLN THR ASP ILE TYR PHE CYS

100 105 110

LYS ILE GLU VAL MET TYR PRO PRO PRO TYR LEU ASP ASN GLU LYS SER

115 120 125

ASN GLY THR ILE ILE HIS VAL LYS GLY LYS HIS LEU CYS PRO SER PRO

130 135 140

LEU PHE PRO GLY PRO SER LYS PRO PHE TRP VAL LEU VAL VAL VAL GLY

145 150 155 160

GLY VAL LEU ALA CYS TYR SER LEU LEU VAL THR VAL ALA PHE ILE ILE

165 170 175

PHE TRP VAL ARG SER LYS ARG SER ARG LEU LEU HIS SER ASP TYR MET

180 185 190

ASN MET THR PRO ARG ARG PRO GLY PRO THR ARG LYS HIS TYR GLN PRO

195 200 205

TYR ALA PRO PRO ARG ASP PHE ALA ALA TYR ARG SER

210 215 220

<210> 2

<211> 202

<212> PRT

<213> HOMO SAPIENS

<400> 2

ASN LYS ILE LEU VAL LYS GLN SER PRO MET LEU VAL ALA TYR ASP ASN

1 5 10 15

ALA VAL ASN LEU SER CYS LYS TYR SER TYR ASN LEU PHE SER ARG GLU

20 25 30

PHE ARG ALA SER LEU HIS LYS GLY LEU ASP SER ALA VAL GLU VAL CYS

35 40 45

VAL VAL TYR GLY ASN TYR SER GLN GLN LEU GLN VAL TYR SER LYS THR

50 55 60

GLY PHE ASN CYS ASP GLY LYS LEU GLY ASN GLU SER VAL THR PHE TYR

65 70 75 80

LEU GLN ASN LEU TYR VAL ASN GLN THR ASP ILE TYR PHE CYS LYS ILE

85	90	95	
GLU VAL MET TYR PRO PRO PRO TYR LEU ASP ASN GLU LYS SER ASN GLY			
100	105	110	
THR ILE ILE HIS VAL LYS GLY LYS HIS LEU CYS PRO SER PRO LEU PHE			
115	120	125	
PRO GLY PRO SER LYS PRO PHE TRP VAL LEU VAL VAL VAL GLY GLY VAL			
130	135	140	
LEU ALA CYS TYR SER LEU LEU VAL THR VAL ALA PHE ILE ILE PHE TRP			
145	150	155	160
VAL ARG SER LYS ARG SER ARG LEU LEU HIS SER ASP TYR MET ASN MET			
165	170	175	
THR PRO ARG ARG PRO GLY PRO THR ARG LYS HIS TYR GLN PRO TYR ALA			
180	185	190	
PRO PRO ARG ASP PHE ALA ALA TYR ARG SER			

195

200

<210> 3

<211> 663

<212> DNA

<213> HOMO SAPIENS

<400> 3

ATGCTCAGGC TGCTCTTGGC TCTCAACTTA TTCCCTTCAA TTCAAGTAAC
AGGAAACAAG 60

ATTTTGGTGA AGCAGTCGCC CATGCTTGTA GCGTACGACA ATGCGGTCAA
CCTTAGCTGC 120

AAGTATTCCT ACAATCTCTT CTCAAGGGAG TTCCGGGCAT CCCTTCACAA
AGGACTGGAT 180

AGTGCTGTGG AAGTCTGTGT TGTATATGGG AATTACTCCC AGCAGCTTCA
GGTTTACTCA 240

AAAACGGGGT TCAACTGTGA TGGGAAATTG GGCAATGAAT CAGTGACATT
CTACCTCCAG 300

AATTTGTATG TTAACCAAAC AGATATTTAC TTCTGCAAAA TTGAAGTTAT
GTATCCTCCT 360

CCTTACCTAG ACAATGAGAA GAGCAATGGA ACCATTATCC ATGTGAAAGG
GAAACACCTT 420

TGTCCAAGTC CCCTATTTCC CGGACCTTCT AAGCCCTTTT GGGTGCTGGT
GGTGGTTGGT 480

GGAGTCCTGG CTTGCTATAG CTTGCTAGTA ACAGTGGCCT TTATTATTTT
CTGGGTGAGG 540

AGTAAGAGGA GCAGGCTCCT GCACAGTGAC TACATGAACA TGA CTCCCCG
CCGCCCCGGG 600

CCCACCCGCA AGCATTACCA GCCCTATGCC CCACCACGCG ACTTCGCAGC
CTATCGCTCC 660

TGA 663

<210> 4

<211> 27

<212> PRT

<213> HOMO SAPIENS

<400> 4

PHE TRP VAL LEU VAL VAL VAL GLY GLY VAL LEU ALA CYS TYR SER LEU

1 5 10 15

LEU VAL THR VAL ALA PHE ILE ILE PHE TRP VAL

20 25

<210> 5

<211> 139

<212> PRT

<213> HOMO SAPIENS

<400> 5

MET LEU ARG LEU LEU LEU ALA LEU ASN LEU PHE PRO SER ILE GLN VAL

1 5 10 15

THR GLY ASN LYS ILE LEU VAL LYS GLN SER PRO MET LEU VAL ALA TYR

20 25 30

ASP ASN ALA VAL ASN LEU SER CYS LYS TYR SER TYR ASN LEU PHE SER

35 40 45

ARG GLU PHE ARG ALA SER LEU HIS LYS GLY LEU ASP SER ALA VAL GLU

50 55 60

VAL CYS VAL VAL TYR GLY ASN TYR SER GLN GLN LEU GLN VAL TYR SER

65 70 75 80

LYS THR GLY PHE ASN CYS ASP GLY LYS LEU GLY ASN GLU SER VAL THR

85 90 95
PHE TYR LEU GLN ASN LEU TYR VAL ASN GLN THR ASP ILE TYR PHE CYS
100 105 110

LYS ILE GLU VAL MET TYR PRO PRO PRO TYR LEU ASP ASN GLU LYS SER
115 120 125

ASN GLY THR ILE ILE HIS VAL LYS GLY GLU GLU
130 135

<210> 6

<211> 121

<212> PRT

<213> HOMO SAPIENS

<400> 6

ASN LYS ILE LEU VAL LYS GLN SER PRO MET LEU VAL ALA TYR ASP ASN
1 5 10 15

ALA VAL ASN LEU SER CYS LYS TYR SER TYR ASN LEU PHE SER ARG GLU
20 25 30

PHE ARG ALA SER LEU HIS LYS GLY LEU ASP SER ALA VAL GLU VAL CYS

35 40 45

VAL VAL TYR GLY ASN TYR SER GLN GLN LEU GLN VAL TYR SER LYS THR

50 55 60

GLY PHE ASN CYS ASP GLY LYS LEU GLY ASN GLU SER VAL THR PHE TYR

65 70 75 80

LEU GLN ASN LEU TYR VAL ASN GLN THR ASP ILE TYR PHE CYS LYS ILE

85 90 95

GLU VAL MET TYR PRO PRO PRO TYR LEU ASP ASN GLU LYS SER ASN GLY

100 105 110

THR ILE ILE HIS VAL LYS GLY GLU GLU

115 120

<210> 7

<211> 538

<212> DNA

<213> HOMO SAPIENS

<400> 7

ATGCTCAGGC TGCTCTTGGC TCTCAACTTA TTCCCTTCAA TTCAAGTAAC
AGGAAACAAG 60

ATTTTGGTGA AGCAGTCGCC CATGCTTGTA GCGTACGACA ATGCGGTCAA
CCTTAGCTGC 120

AAGTATTCCT ACAATCTCTT CTCAAGGGAG TTCCGGGCAT CCCTTCACAA
AGGACTGGAT 180

AGTGCTGTGG AAGTCTGTGT TGTATATGGG AATTACTCCC AGCAGCTTCA
GGTTTACTCA 240

AAAACGGGGT TCAACTGTGA TGGGAAATTG GGCAATGAAT CAGTGACATT
CTACCTCCAG 300

AATTTGTATG TTAACCAAAC AGATATTTAC TTCTGCAAAA TTGAAGTTAT
GTATCCTCCT 360

CCTTACCTAG ACAATGAGAA GAGCAATGGA ACCATTATCC ATGTGAAAGG
TGAGGAGTAA 420

GAGGAGCAGG CTCCTGCACA GTGACTACAT GAACATGACT CCCC GCCGCC
CCGGGCCCAC 480

CCGCAAGCAT TACCAGCCCT ATGCCCCACC ACGCGACTTC GCAGCCTATC
GCTCCTGA 538

<210> 8

<211> 110

<212> PRT

<213> HOMO SAPIENS

<400> 8

MET LEU VAL ALA TYR ASP ASN ALA VAL ASN LEU SER CYS LYS TYR SER

1 5 10 15

TYR ASN LEU PHE SER ARG GLU PHE ARG ALA SER LEU HIS LYS GLY LEU

20 25 30

ASP SER ALA VAL GLU VAL CYS VAL VAL TYR GLY ASN TYR SER GLN GLN

35 40 45

LEU GLN VAL TYR SER LYS THR GLY PHE ASN CYS ASP GLY LYS LEU GLY

50 55 60

ASN GLU SER VAL THR PHE TYR LEU GLN ASN LEU TYR VAL ASN GLN THR

65 70 75 80

ASP ILE TYR PHE CYS LYS ILE GLU VAL MET TYR PRO PRO PRO TYR LEU

85

90

95

ASP ASN GLU LYS SER ASN GLY THR ILE ILE HIS VAL LYS GLY

100

105

110

<210> 9

<211> 16

<212> PRT

<213> HOMO SAPIENS

<400> 9

GLY LYS HIS LEU CYS PRO SER PRO LEU PHE PRO GLY PRO SER LYS PRO

1

5

10

15

<210> 10

<211> 19

<212> PRT

<213> HOMO SAPIENS

<400> 10

HIS VAL LYS GLY LYS HIS LEU CYS PRO SER PRO LEU PHE PRO GLY PRO

1

5

10

15

SER LYS PRO

<210> 11

<211> 7

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<223> SYNTHETIC

<400> 11

GLY TYR THR LEU THR ASN TYR

1 5

<210> 12

<211> 6

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<223> SYNTHETIC

<400> 12

ASN THR TYR THR GLY LYS

1 5

<210> 13

<211> 9

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<223> SYNTHETIC

<400> 13

GLY ASP ALA ASN GLN GLN PHE ALA TYR

1 5

<210> 14

<211> 11

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<223> SYNTHETIC

<400> 14

LYS ALA SER GLN ASP ILE ASN SER TYR LEU SER

1 5 10

<210> 15

<211> 7

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<223> SYNTHETIC

<400> 15

ARG ALA ASN ARG LEU VAL ASP

1 5

<210> 16

<211> 9

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<223> SYNTHETIC

<400> 16

LEU GLN TYR ASP GLU PHE PRO PRO THR

1 5

<210> 17

<211> 10

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<223> SYNTHETIC

<400> 17

GLY PHE THR PHE SER SER TYR TYR MET SER

1 5 10

<210> 18

<211> 17

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<223> SYNTHETIC

<400> 18

THR ILE SER ASP GLY GLY ASP ASN THR TYR TYR ALA GLY THR VAL THR

1 5 10 15

GLY

<210> 19

<211> 9

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<223> SYNTHETIC

<400> 19

ILE HIS TRP PRO TYR TYR PHE ASP SER

1 5

<210> 20

<211> 10

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<223> SYNTHETIC

<400> 20

ARG ALA SER SER SER VAL SER TYR MET ASN

1 5 10

<210> 21

<211> 7

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<223> SYNTHETIC

<400> 21

ALA THR SER ASP LEU ALA SER

1 5

<210> 22

<211> 9

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<223> SYNTHETIC

<400> 22

GLN GLN TRP SER SER HIS PRO PRO THR

1 5

<210> 23

<211> 118

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<223> SYNTHETIC

<400> 23

ASP VAL LYS LEU VAL GLU SER GLY GLY GLY LEU VAL LYS LEU GLY GLY

1 5 10 15

SER LEU LYS LEU SER CYS VAL ALA SER GLY PHE THR PHE SER SER TYR

20 25 30

TYR MET SER TRP VAL ARG GLN THR PRO GLU LYS ARG LEU GLU TRP VAL

35

40

45

ALA THR ILE SER ASP GLY GLY ASP ASN THR TYR TYR ALA GLY THR VAL

50

55

60

THR GLY ARG PHE THR ILE SER ARG ASP PHE ALA LYS ASN THR LEU TYR

65

70

75

80

LEU GLN MET ASN SER LEU THR SER GLU ASP THR ALA VAL TYR TYR CYS

85

90

95

ALA ARG ILE HIS TRP PRO TYR TYR PHE ASP SER TRP GLY GLN GLY THR

100

105

110

THR LEU THR VAL SER SER

115

<210> 24

<211> 354

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> SYNTHETIC

<400> 24

GACGTGAAGC TCGTGGAGTC TGGGGGAGGC TTAGTGAAGC TTGGAGGGTC
CCTGAAACTC 60

TCCTGTGTAG CCTCTGGATT CACTTTCAGT AGCTATTACA TGTCTTGGGT
TCGCCAGACT 120

CCGGAGAAGA GGCTGGAGTG GGTCGCGACC ATAAGTGATG GTGGTGATAA
CACCTACTAC 180

GCAGGCACTG TGACGGGCCG ATTCACCATC TCCAGAGACT TTGCCAAGAA
CACCTGTAC 240

CTGCAAATGA ACAGTCTGAC CTCTGAGGAC ACAGCCGTGT ATTACTGTGC
AAGAATTCAT 300

TGGCCTTACT ATTTTGACTC CTGGGGCCAA GGCACCACTC TCACAGTCTC CTCA
354

<210> 25

<211> 106

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<223> SYNTHETIC

<400> 25

GLN PHE VAL LEU SER GLN SER PRO ALA ILE LEU SER ALA SER PRO GLY
1 5 10 15

GLU MET LEU THR MET THR CYS ARG ALA SER SER SER VAL SER TYR MET
 20 25 30

ASN TRP TYR GLN GLN LYS PRO GLY SER SER PRO LYS PRO TRP ILE TYR
 35 40 45

ALA THR SER ASP LEU ALA SER GLY VAL PRO ALA ARG PHE SER GLY SER
 50 55 60

GLY SER GLY THR SER TYR SER LEU THR ILE SER ARG VAL GLU ALA GLU
65 70 75 80

ASP ALA ALA THR TYR TYR CYS GLN GLN TRP SER SER HIS PRO PRO THR
 85 90 95

PHE GLY GLY GLY THR LYS LEU GLU ILE ARG

100

105

<210> 26

<211> 318

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> SYNTHETIC

<400> 26

CAATTTGTTC TCTCCCAGTC TCCAGCAATC CTGTCTGCAT CTCCCGGGGA
GATGCTCACA 60

ATGACTTGCA GGGCCAGCTC AAGTGTAAGT TATATGAACT GGTATCAGCA
GAAGCCAGGA 120

TCTTCCCCCA AACCCTGGAT TTATGCCACA TCCGACCTGG CTTCTGGAGT
CCCTGCTCGC 180

TTCAGTGGCA GTGGGTCTGG GACCTCTTAT TCTCTCACAA TCAGCAGAGT
GGAGGCTGAA 240

GATGCTGCCA CTTATTACTG CCAGCAGTGG AGTAGTCACC CACCCACGTT
CGGAGGGGGG 300

ACCAAGCTGG AAATAAGA

318

<210> 27

<211> 15

<212> PRT

<213> HOMO SAPIENS

<400> 27

LYS GLY LYS HIS LEU CYS PRO SER PRO LEU PHE PRO GLY PRO SER

1 5 10 15

<210> 28

<211> 134

<212> PRT

<213> HOMO SAPIENS

<400> 28

ASN LYS ILE LEU VAL LYS GLN SER PRO MET LEU VAL ALA TYR ASP ASN

1 5 10 15

ALA VAL ASN LEU SER CYS LYS TYR SER TYR ASN LEU PHE SER ARG GLU

20 25 30

PHE ARG ALA SER LEU HIS LYS GLY LEU ASP SER ALA VAL GLU VAL CYS

35 40 45

VAL VAL TYR GLY ASN TYR SER GLN GLN LEU GLN VAL TYR SER LYS THR

50 55 60

GLY PHE ASN CYS ASP GLY LYS LEU GLY ASN GLU SER VAL THR PHE TYR

65 70 75 80

LEU GLN ASN LEU TYR VAL ASN GLN THR ASP ILE TYR PHE CYS LYS ILE

85 90 95

GLU VAL MET TYR PRO PRO PRO TYR LEU ASP ASN GLU LYS SER ASN GLY

100 105 110

THR ILE ILE HIS VAL LYS GLY LYS HIS LEU CYS PRO SER PRO LEU PHE

115 120 125

PRO GLY PRO SER LYS PRO

130

<210> 29

<211> 17

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<223> SYNTHETIC

<400> 29

GLY LYS HIS LEU CYS PRO SER PRO LEU PHE PRO GLY PRO SER LYS PRO

1 5 10 15

LYS

<210> 30

<211> 117

<212> PRT

<213> ARTIFICIAL

<220>

<223> SYNTHETIC

<400> 30

GLU VAL GLN LEU VAL GLU SER GLY GLY GLY LEU VAL GLN ALA GLY GLU

1 5 10 15

SER LEU ARG LEU SER CYS ALA ALA SER GLY SER ILE ALA SER ILE ASN

20 25 30

ALA MET GLY TRP TYR ARG GLN ALA PRO GLY SER GLN ARG GLU LEU VAL

35 40 45

ALA ALA ILE SER GLY GLY GLY ASP THR TYR TYR ALA ASP SER VAL LYS

50 55 60

GLY ARG PHE THR ILE SER ARG ASP ASN ALA LYS THR THR VAL TYR LEU

65 70 75 80

GLN MET ASN SER LEU ARG PRO GLU ASP THR ALA VAL TYR TYR CYS VAL

85 90 95

VAL ASP LEU TYR GLY SER ASP TYR TRP ASP TRP GLY GLN GLY THR GLN

100 105 110

VAL THR VAL SER SER

115

<210> 31

<211> 117

<212> PRT

<213> ARTIFICIAL

<220>

<223> STNTHETIC

<400> 31

GLU VAL GLN LEU VAL GLU SER GLY GLY GLY LEU VAL GLN ALA GLY GLY

1 5 10 15

SER LEU ARG LEU SER CYS ALA ALA SER GLY SER LEU PHE SER ILE ASN

20 25 30

ALA MET ALA TRP TYR ARG GLN ALA PRO GLY LYS GLN ARG GLU LEU VAL

35 40 45

ALA ALA ILE THR SER SER GLY SER THR ASN TYR ALA ASN SER VAL LYS

50 55 60

GLY ARG PHE THR VAL SER ARG ASP ASN ALA LYS ASN THR MET TYR LEU
65 70 75 80

GLN MET ASN SER LEU LYS PRO GLU ASP THR ALA VAL TYR TYR CYS VAL
 85 90 95

VAL ASP GLU TYR GLY SER ASP TYR TRP ILE TRP GLY GLN GLY THR GLN
 100 105 110

VAL THR VAL SER SER
 115

<210> 32

<211> 117

<212> PRT

<213> ARTIFICIAL

<220>

<223> SYNTHETIC

<400> 32

GLN VAL GLN LEU VAL GLU SER GLY GLY GLY LEU VAL GLN ALA GLY GLY

1 5 10 15

SER LEU ARG LEU SER CYS ALA ALA SER GLY SER ILE PHE SER ILE ASN

20 25 30

ALA MET GLY TRP TYR ARG GLN ALA PRO GLY LYS GLN ARG GLU ARG VAL

35 40 45

ALA ALA ILE THR SER GLY GLY SER THR ASN TYR ALA ASP SER VAL LYS

50 55 60

GLY ARG PHE THR ILE SER ARG ASP ASN ALA LYS ASN THR VAL TYR LEU

65 70 75 80

GLN MET ASN ASN LEU GLU PRO ARG ASP ALA GLY VAL TYR TYR CYS VAL

85 90 95

VAL ASP LEU TYR GLY GLU ASP TYR TRP ILE TRP GLY GLN GLY THR GLN

100 105 110

VAL THR VAL SER SER

115

<210> 33

<211> 5

<212> PRT

<213> ARTIFICIAL

<220>

<223> SYNTHETIC

<400> 33

ILE ASN ALA MET GLY

1 5

<210> 34

<211> 16

<212> PRT

<213> ARTIFICIAL

<220>

<223> SYNTHETIC

<400> 34

ALA ILE SER GLY GLY GLY ASP THR TYR TYR ALA ASP SER VAL LYS GLY

1 5 10 15

<210> 35

<211> 9

<212> PRT

<213> ARTIFICIAL

<220>

<223> SYNTHETIC

<400> 35

ASP LEU TYR GLY SER ASP TYR TRP ASP

1 5

<210> 36

<211> 5

<212> PRT

<213> ARTIFICIAL

<220>

<223> SYNTHETIC

<400> 36

ILE ASN ALA MET ALA

1 5

<210> 37

<211> 16

<212> PRT

<213> ARTIFICIAL

<220>

<223> SYNTHETIC

<400> 37

ALA ILE THR SER SER GLY SER THR ASN TYR ALA ASN SER VAL LYS GLY

1 5 10 15

<210> 38

<211> 9

<212> PRT

<213> ARTIFICIAL

<220>

<223> SYNTHETIC

<400> 38

ASP GLU TYR GLY SER ASP TYR TRP ILE

1 5

<210> 39

<211> 16

<212> PRT

<213> ARTIFICIAL

<220>

<223> SYNTHETIC

<400> 39

ALA ILE THR SER GLY GLY SER THR ASN TYR ALA ASP SER VAL LYS GLY

1 5 10 15

<210> 40

<211> 9

<212> PRT

<213> ARTIFICIAL

<220>

<223> SYNTHETIC

<400> 40

ASP LEU TYR GLY GLU ASP TYR TRP ILE

1 5

<210> 41

<211> 5

<212> PRT

<213> ARTIFICIAL

<220>

<223> SYNTHETIC

<220>

<221> X

<222> (5)..(5)

<223> X IS G OR A

<400> 41

ILE ASN ALA MET XAA

1 5

<210> 42

<211> 16

<212> PRT

<213> ARTIFICIAL

<220>

<223> SYNTHETIC

<220>

<221> X

<222> (3)..(3)

<223> X IS S OR T

<220>

<221> X

<222> (4)..(4)

<223> X IS G OR S

<220>

<221> X

<222> (5)..(5)

<223> X IS G OR S

<220>

<221> X

<222> (7)..(7)

<223> X IS D OR S

<220>

<221> X

<222> (9)..(9)

<223> X IS Y OR N

<220>

<221> X

<222> (12)..(12)

<223> X IS D OR N

<400> 42

ALA ILE XAA XAA XAA GLY XAA THR XAA TYR ALA XAA SER VAL LYS GLY

1 5 10 15

<210> 43

<211> 9

<212> PRT

<213> ARTIFICIAL

<220>

<223> SYNTHETIC

<220>

<221> X

<222> (2)..(2)

<223> X IS E OR L

<220>

<221> X

<222> (5)..(5)

<223> X IS E OR S

<220>

<221> X

<222> (9)..(9)

<223> X IS D OR I

<400> 43

ASP XAA TYR GLY XAA ASP TYR TRP XAA

1 5

<210> 44

<211> 9

<212> PRT

<213> ARTIFICIAL

<220>

<223> SYNTHETIC

<220>

<221> X

<222> (2)..(2)

<223> X IS E OR L

<220>

<221> X

<222> (9)..(9)

<223> X IS D OR I

<400> 44

ASP XAA TYR GLY SER ASP TYR TRP XAA

1 5

<210> 45

<211> 126

<212> PRT

<213> ARTIFICIAL

<220>

<223> SYNTHETIC

<400> 45

GLU VAL GLN LEU VAL GLU SER GLY GLY GLY LEU VAL GLN ALA GLY GLU

1 5 10 15

SER LEU ARG LEU SER CYS ALA ALA SER GLY SER ILE ALA SER ILE ASN

20 25 30

ALA MET GLY TRP TYR ARG GLN ALA PRO GLY SER GLN ARG GLU LEU VAL

35

40

45

ALA ALA ILE SER GLY GLY GLY ASP THR TYR TYR ALA ASP SER VAL LYS

50

55

60

GLY ARG PHE THR ILE SER ARG ASP ASN ALA LYS THR THR VAL TYR LEU

65

70

75

80

GLN MET ASN SER LEU ARG PRO GLU ASP THR ALA VAL TYR TYR CYS VAL

85

90

95

VAL ASP LEU TYR GLY SER ASP TYR TRP ASP TRP GLY GLN GLY THR GLN

100

105

110

VAL THR VAL SER SER ALA ALA ALA HIS HIS HIS HIS HIS HIS

115

120

125

<210> 46

<211> 126

<212> PRT

<213> ARTIFICIAL

<220>

<223> SYNTHETIC

<400> 46

GLU VAL GLN LEU VAL GLU SER GLY GLY GLY LEU VAL GLN ALA GLY GLY
1 5 10 15

SER LEU ARG LEU SER CYS ALA ALA SER GLY SER LEU PHE SER ILE ASN
 20 25 30

ALA MET ALA TRP TYR ARG GLN ALA PRO GLY LYS GLN ARG GLU LEU VAL
 35 40 45

ALA ALA ILE THR SER SER GLY SER THR ASN TYR ALA ASN SER VAL LYS
 50 55 60

GLY ARG PHE THR VAL SER ARG ASP ASN ALA LYS ASN THR MET TYR LEU
65 70 75 80

GLN MET ASN SER LEU LYS PRO GLU ASP THR ALA VAL TYR TYR CYS VAL

85 90 95
VAL ASP GLU TYR GLY SER ASP TYR TRP ILE TRP GLY GLN GLY THR GLN
100 105 110

VAL THR VAL SER SER ALA ALA ALA HIS HIS HIS HIS HIS HIS
115 120 125

<210> 47
<211> 126
<212> PRT
<213> ARTIFICIAL

<220>
<223> SYNTHETIC

<400> 47

GLN VAL GLN LEU VAL GLU SER GLY GLY GLY LEU VAL GLN ALA GLY GLY
1 5 10 15

SER LEU ARG LEU SER CYS ALA ALA SER GLY SER ILE PHE SER ILE ASN
20 25 30

ALA MET GLY TRP TYR ARG GLN ALA PRO GLY LYS GLN ARG GLU ARG VAL

35

40

45

ALA ALA ILE THR SER GLY GLY SER THR ASN TYR ALA ASP SER VAL LYS

50

55

60

GLY ARG PHE THR ILE SER ARG ASP ASN ALA LYS ASN THR VAL TYR LEU

65

70

75

80

GLN MET ASN ASN LEU GLU PRO ARG ASP ALA GLY VAL TYR TYR CYS VAL

85

90

95

VAL ASP LEU TYR GLY GLU ASP TYR TRP ILE TRP GLY GLN GLY THR GLN

100

105

110

VAL THR VAL SER SER ALA ALA ALA HIS HIS HIS HIS HIS HIS

115

120

125

<210> 48

<211> 145

<212> PRT

<213> HOMO SAPIENS

<400> 48

MET LEU ARG LEU LEU LEU ALA LEU ASN LEU PHE PRO SER ILE GLN VAL

1 5 10 15

THR GLY ASN LYS ILE LEU VAL LYS GLN SER PRO MET LEU VAL ALA TYR

20 25 30

ASP ASN ALA VAL ASN LEU SER CYS LYS TYR SER TYR ASN LEU PHE SER

35 40 45

ARG GLU PHE ARG ALA SER LEU HIS LYS GLY LEU ASP SER ALA VAL GLU

50 55 60

VAL CYS VAL VAL TYR GLY ASN TYR SER GLN GLN LEU GLN VAL TYR SER

65 70 75 80

LYS THR GLY PHE ASN CYS ASP GLY LYS LEU GLY ASN GLU SER VAL THR

85 90 95

PHE TYR LEU GLN ASN LEU TYR VAL ASN GLN THR ASP ILE TYR PHE CYS

100

105

110

LYS ILE GLU VAL MET TYR PRO PRO PRO TYR LEU ASP ASN GLU LYS SER

115

120

125

ASN GLY THR ILE ILE HIS VAL LYS GLY LYS HIS LEU CYS PRO SER PRO

130

135

140

LEU

145

<210> 49

<211> 127

<212> PRT

<213> HOMO SAPIENS

<400> 49

ASN LYS ILE LEU VAL LYS GLN SER PRO MET LEU VAL ALA TYR ASP ASN

1

5

10

15

ALA VAL ASN LEU SER CYS LYS TYR SER TYR ASN LEU PHE SER ARG GLU

