SEQUENCE LISTING

<110> Xigen S.A.

<120> Novel Transporter Constructs and Transporter Cargo Conjugate Molecules

<130> CX01P027WO1

<150> PCT/EP2008/011003
<151> 2008-12-22

<160> 262

<170> PatentIn version 3.5

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1 5

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1 5

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1 5

<210> 4
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<400> 4

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1 5 10

<210> 5
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<223> /replace="D-amino acid"

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<223> number of repeats is 1 or 2

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<221> REPEAT
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<223> number of repeats is 1 or 2

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<222> (16)..(16)
<223> number of repeats is 0, 1 or 2

<220>
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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa

<210> 6
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DLLLD(LLLD)a

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<220>
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<400> 6

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 7
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<220>
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<400> 7

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 8
<211> 86
<212> PRT
<213> Human immunodeficiency virus type 1

<220>
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<400> 8

Met Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser
1 5 10 15

Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe
20 25 30

His Cys Gln Val Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly
35 40 45

Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr
50 55 60

His Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Arg Gly Asp
65 70 75 80

Pro Thr Gly Pro Lys Glu
85

<210> 9
<211> 36
<212> PRT

<213> Human immunodeficiency virus type 1

<220>
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<223> Description of sequence: HIV-1 TAT sequence (aa 37-72)

<400> 9

Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly Arg Lys Lys Arg
1 5 10 15

Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr His Gln Val Ser
20 25 30

Leu Ser Lys Gln
35

<210> 10
<211> 22
<212> PRT
<213> Human immunodeficiency virus type 1

<220>
<221> misc_feature
<223> Description of sequence: HIV-1 TAT sequence (aa 37-58)

<400> 10

Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly Arg Lys Lys Arg
1 5 10 15

Arg Gln Arg Arg Arg Pro
20

<210> 11
<211> 24
<212> PRT
<213> Human immunodeficiency virus type 1

<220>
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<223> Description of sequence: HIV-1 TAT sequence (aa 38-58) including an additional N-terminal GCC

<400> 11

Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly Arg Lys Lys Arg Arg
1 5 10 15

Gln Arg Arg Arg Pro Gly Gly Cys
20

<210> 12
<211> 15
<212> PRT
<213> Human immunodeficiency virus type 1

<220>
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<223> Description of sequence: HIV-1 TAT sequence (aa 47-58) including an additional C-terminal GCC

<400> 12

Cys Gly Gly Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro
1 5 10 15

<210> 13
<211> 15
<212> PRT
<213> Human immunodeficiency virus type 1

<220>
<221> misc_feature
<223> Description of sequence: HIV-1 TAT sequence (aa 47-58) including an additional N-terminal GCC

<400> 13

Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Gly Gly Cys
1 5 10 15

<210> 14
<211> 56
<212> PRT
<213> Human immunodeficiency virus type 1

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<223> Description of sequence: HIV-1 TAT sequence (aa 1-72) including a mutated Cys to Ala residue at position 37

<400> 14

Met Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser
1 5 10 15

Gln Pro Lys Thr Ala Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly
20 25 30

Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr
35 40 45

His Gln Val Ser Leu Ser Lys Gln
50 55

<210> 15
<211> 17
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: trafficking sequence L-generic-TAT (see Table 1)

<220>

<221> VARIANT
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<223> Xaa is selected from any amino acid residue

<400> 15

Xaa Xaa Xaa Xaa Arg Lys Lys Arg Arg Gln Arg Arg Arg Xaa Xaa Xaa
1 5 10 15

Xaa

<210> 16
<211> 11
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<213> Artificial

<220>
<223> Description of sequence: trafficking sequence L-generic-TAT (s) (see Table 1)

<220>
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<223> General formula: NH2-Xnb-RKKRRQRRR-Xnb-COOH (see Table 1)

<220>
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<222> (1)..(1)
<223> Xaa is Xnb as defined in the general formula, wherein Xaa represents an amino acid residue, preferably selected from any (native) amino acid residue;

<220>
<221> REPEAT
<222> (1)..(1)
<223> Xaa is Xnb as defined in the general formula, wherein n is 0-5, 5-10, 10-15, 15-20, 20-30 or more for Xnb

<220>
<221> VARIANT
<222> (11)..(11)
<223> Xaa is Xnb as defined in the general formula, wherein Xaa represents an amino acid residue, preferably selected from any (native) amino acid residue;

<220>
<221> REPEAT
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<223> Xaa is Xnb as defined in the general formula, wherein n is 0-5, 5-10, 10-15, 15-20, 20-30 or more for Xnb

<400> 16

Xaa Arg Lys Lys Arg Arg Gln Arg Arg Arg Xaa
1 5 10

<210> 17
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: trafficking sequence L-TAT (s1a) (see Table 1)

<400> 17

Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
1 5 10

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

<220>
<223> Description of sequence: trafficking sequence L-TAT (s1b) (see Table 1)

<400> 18

Arg Lys Lys Arg Arg Gln Arg Arg Arg
1 5

<210> 19
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence L-TAT (s1c) (see Table 1)

<400> 19

Tyr Asp Arg Lys Lys Arg Arg Gln Arg Arg Arg
1 5 10

<210> 20
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence r3-L-TAT (see Table 1)

<400> 20

Arg Lys Lys Arg Arg Gln Arg Arg Arg
1 5

<210> 21
<211> 9
<212> PRT
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<220>
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<400> 21

Arg Arg Arg Gln Arg Arg Lys Lys Arg
1 5

<210> 22

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

<220>
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<400> 22

Arg Lys Lys Arg Arg Gln Arg Arg Arg
1 5

<210> 23
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<220>
<223> Description of sequence: trafficking sequence betaA-r3-L-TAT (see Table 1)

<400> 23

Arg Arg Arg Gln Arg Arg Lys Lys Arg
1 5

<210> 24
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<220>
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Arg Lys Lys Arg Arg Gln Arg Arg Arg
1 5

<210> 25
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Arg Arg Arg Gln Arg Arg Lys Lys Arg
1 5

<210> 26
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Arg Ala Lys Arg Arg Gln Arg Arg Arg
1 5

<210> 27
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Arg Lys Ala Arg Arg Gln Arg Arg Arg
1 5

<210> 28
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<220>
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Arg Lys Lys Ala Arg Gln Arg Arg Arg
1 5

<210> 29
<211> 9
<212> PRT
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<220>
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<400> 29

Arg Lys Lys Arg Arg Ala Arg Arg Arg
1 5

<210> 30
<211> 9
<212> PRT
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<220>
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Arg Lys Lys Arg Arg Gln Ala Arg Arg
1 5

<210> 31
<211> 9

<212> PRT
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<220>
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<400> 31

Arg Lys Lys Arg Arg Gln Arg Ala Arg
1 5

<210> 32
<211> 9
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Arg Asp Lys Arg Arg Gln Arg Arg Arg
1 5

<210> 33
<211> 9
<212> PRT
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<220>
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<400> 33

Arg Lys Asp Arg Arg Gln Arg Arg Arg
1 5

<210> 34
<211> 9
<212> PRT
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<220>
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Arg Lys Lys Asp Arg Gln Arg Arg Arg
1 5

<210> 35
<211> 9
<212> PRT
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<220>
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<400> 35

Arg Lys Lys Arg Arg Asp Arg Arg Arg
1 5

<210> 36
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-11) (see Table 1)

<400> 36

Arg Lys Lys Arg Arg Gln Asp Arg Arg
1 5

<210> 37
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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<400> 37

Arg Lys Lys Arg Arg Gln Arg Asp Arg
1 5

<210> 38
<211> 9
<212> PRT
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<220>
<223> Description of sequence: trafficking sequence TAT(s2-13) (see Table 1)

<400> 38

Arg Glu Lys Arg Arg Gln Arg Arg Arg
1 5

<210> 39
<211> 9
<212> PRT
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<220>
<223> Description of sequence: trafficking sequence TAT(s2-14) (see Table 1)

<400> 39

Arg Lys Glu Arg Arg Gln Arg Arg Arg
1 5

<210> 40
<211> 9
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-15) (see Table 1)

<400> 40

Arg Lys Lys Glu Arg Gln Arg Arg Arg
1 5

<210> 41
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-16) (see Table 1)

<400> 41

Arg Lys Lys Arg Arg Glu Arg Arg Arg
1 5

<210> 42
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-17) (see Table 1)

<400> 42

Arg Lys Lys Arg Arg Gln Glu Arg Arg
1 5

<210> 43
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-18) (see Table 1)

<400> 43

Arg Lys Lys Arg Arg Gln Arg Glu Arg
1 5

<210> 44
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-19) (see Table 1)

<400> 44

Arg Phe Lys Arg Arg Gln Arg Arg Arg
1 5

<210> 45
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-20) (see Table 1)

<400> 45

Arg Lys Phe Arg Arg Gln Arg Arg Arg
1 5

<210> 46
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-21) (see Table 1)

<400> 46

Arg Lys Lys Phe Arg Gln Arg Arg Arg
1 5

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

<220>
<223> Description of sequence: trafficking sequence TAT(s2-22) (see Table 1)

<400> 47

Arg Lys Lys Arg Arg Phe Arg Arg Arg
1 5

<210> 48
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-23) (see Table 1)

<400> 48

Arg Lys Lys Arg Arg Gln Phe Arg Arg
1 5

<210> 49
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-24) (see Table 1)

<400> 49

Arg Lys Lys Arg Arg Gln Arg Phe Arg
1 5

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

<220>
<223> Description of sequence: trafficking sequence TAT(s2-25) (see Table 1)

<400> 50

Arg Arg Lys Arg Arg Gln Arg Arg Arg
1 5

<210> 51
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-26) (see Table 1)

<400> 51

Arg Lys Arg Arg Arg Gln Arg Arg Arg
1 5

<210> 52
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-27) (see Table 1)

<400> 52

Arg Lys Lys Lys Arg Gln Arg Arg Arg
1 5

<210> 53
<211> 9
<212> PRT
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<400> 53

Arg Lys Lys Arg Arg Arg Arg Arg Arg

1 5

<210> 54
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-29) (see Table 1)

<400> 54

Arg Lys Lys Arg Arg Gln Lys Arg Arg
1 5

<210> 55
<211> 9
<212> PRT
<213> Artificial Sequence

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<223> Description of sequence: trafficking sequence TAT(s2-30) (see Table 1)

<400> 55

Arg Lys Lys Arg Arg Gln Arg Lys Arg
1 5

<210> 56
<211> 9
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<220>
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<400> 56

Arg His Lys Arg Arg Gln Arg Arg Arg
1 5

<210> 57
<211> 9
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<220>
<223> Description of sequence: trafficking sequence TAT(s2-32) (see Table 1)

<400> 57

Arg Lys His Arg Arg Gln Arg Arg Arg
1 5

<210> 58
<211> 9
<212> PRT
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<220>
<223> Description of sequence: trafficking sequence TAT(s2-33) (see Table 1)

<400> 58

Arg Lys Lys His Arg Gln Arg Arg Arg
1 5

<210> 59
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-34) (see Table 1)

<400> 59

Arg Lys Lys Arg Arg His Arg Arg Arg
1 5

<210> 60
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-35) (see Table 1)

<400> 60

Arg Lys Lys Arg Arg Gln His Arg Arg
1 5

<210> 61
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-36) (see Table 1)

<400> 61

Arg Lys Lys Arg Arg Gln Arg His Arg
1 5

<210> 62
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-37) (see Table 1)

<400> 62

Arg Ile Lys Arg Arg Gln Arg Arg Arg
1 5

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

<220>
<223> Description of sequence: trafficking sequence TAT(s2-38) (see Table 1)

<400> 63

Arg Lys Ile Arg Arg Gln Arg Arg Arg
1 5

<210> 64
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-39) (see Table 1)

<400> 64

Arg Lys Lys Ile Arg Gln Arg Arg Arg
1 5

<210> 65
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-40) (see Table 1)

<400> 65

Arg Lys Lys Arg Arg Ile Arg Arg Arg
1 5

<210> 66
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-41) (see Table 1)

<400> 66

Arg Lys Lys Arg Arg Gln Ile Arg Arg
1 5

<210> 67
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of sequence: trafficking sequence TAT(s2-42) (see Table 1)

<400> 67

Arg Lys Lys Arg Arg Gln Arg Ile Arg
1 5

<210> 68
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<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-43) (see Table 1)

<400> 68

Arg Leu Lys Arg Arg Gln Arg Arg Arg
1 5

<210> 69
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-44) (see Table 1)

<400> 69

Arg Lys Leu Arg Arg Gln Arg Arg Arg
1 5

<210> 70
<211> 9
<212> PRT
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<220>
<223> Description of sequence: trafficking sequence TAT(s2-45) (see Table 1)

<400> 70

Arg Lys Lys Leu Arg Gln Arg Arg Arg
1 5

<210> 71
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-46) (see Table 1)

<400> 71

Arg Lys Lys Arg Arg Leu Arg Arg Arg
1 5

<210> 72
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-47) (see Table 1)

<400> 72

Arg Lys Lys Arg Arg Gln Leu Arg Arg
1 5

<210> 73
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-48) (see Table 1)

<400> 73

Arg Lys Lys Arg Arg Gln Arg Leu Arg
1 5

<210> 74
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-49) (see Table 1)

<400> 74

Arg Met Lys Arg Arg Gln Arg Arg Arg
1 5

<210> 75
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-50) (see Table 1)

<400> 75

Arg Lys Met Arg Arg Gln Arg Arg Arg
1 5

<210> 76
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-51) (see

Table 1)

<400> 76

Arg Lys Lys Met Arg Gln Arg Arg Arg
1 5

<210> 77
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-52) (see Table 1)

<400> 77

Arg Lys Lys Arg Arg Met Arg Arg Arg
1 5

<210> 78
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-53) (see Table 1)

<400> 78

Arg Lys Lys Arg Arg Gln Met Arg Arg
1 5

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

<220>
<223> Description of sequence: trafficking sequence TAT(s2-54) (see Table 1)

<400> 79

Arg Lys Lys Arg Arg Gln Arg Met Arg
1 5

<210> 80
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-55) (see Table 1)

<400> 80

Arg Asn Lys Arg Arg Gln Arg Arg Arg
1 5

<210> 81
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-56) (see Table 1)

<400> 81

Arg Lys Asn Arg Arg Gln Arg Arg Arg
1 5

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

<220>
<223> Description of sequence: trafficking sequence TAT(s2-57) (see Table 1)

<400> 82

Arg Lys Lys Asn Arg Gln Arg Arg Arg
1 5

<210> 83
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-58) (see Table 1)

<400> 83

Arg Lys Lys Arg Arg Asn Arg Arg Arg
1 5

<210> 84
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-59) (see Table 1)

<400> 84

Arg Lys Lys Arg Arg Gln Asn Arg Arg
1 5

<210> 85
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-60) (see Table 1)

<400> 85

Arg Lys Lys Arg Arg Gln Arg Asn Arg
1 5

<210> 86
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-61) (see Table 1)

<400> 86

Arg Gln Lys Arg Arg Gln Arg Arg Arg
1 5

<210> 87
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-62) (see Table 1)

<400> 87

Arg Lys Gln Arg Arg Gln Arg Arg Arg
1 5

<210> 88
<211> 9
<212> PRT
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<220>
<223> Description of sequence: trafficking sequence TAT(s2-63) (see Table 1)

<400> 88

Arg Lys Lys Gln Arg Gln Arg Arg Arg
1 5

<210> 89
<211> 9
<212> PRT
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<220>
<223> Description of sequence: trafficking sequence TAT(s2-64) (see Table 1)

<400> 89

Arg Lys Lys Arg Arg Lys Arg Arg Arg
1 5

<210> 90

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

<220>
<223> Description of sequence: trafficking sequence TAT(s2-65) (see Table 1)

<400> 90

Arg Lys Lys Arg Arg Gln Gln Arg Arg
1 5

<210> 91
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-66) (see Table 1)

<400> 91

Arg Lys Lys Arg Arg Gln Arg Gln Arg
1 5

<210> 92
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-67) (see Table 1)

<400> 92

Arg Ser Lys Arg Arg Gln Arg Arg Arg
1 5

<210> 93
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-68) (see Table 1)

<400> 93

Arg Lys Ser Arg Arg Gln Arg Arg Arg
1 5

<210> 94
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-69) (see Table 1)

<400> 94

Arg Lys Lys Ser Arg Gln Arg Arg Arg
1 5

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

<220>
<223> Description of sequence: trafficking sequence TAT(s2-70) (see Table 1)

<400> 95

Arg Lys Lys Arg Arg Ser Arg Arg Arg
1 5

<210> 96
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-71) (see Table 1)

<400> 96

Arg Lys Lys Arg Arg Gln Ser Arg Arg
1 5

<210> 97
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-72) (see Table 1)

<400> 97

Arg Lys Lys Arg Arg Gln Arg Ser Arg
1 5

<210> 98
<211> 9
<212> PRT
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<220>
<223> Description of sequence: trafficking sequence TAT(s2-73) (see Table 1)

<400> 98

Arg Thr Lys Arg Arg Gln Arg Arg Arg
1 5

<210> 99
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-74) (see Table 1)

<400> 99

Arg Lys Thr Arg Arg Gln Arg Arg Arg
1 5

<210> 100
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-75) (see Table 1)

<400> 100

Arg Lys Lys Thr Arg Gln Arg Arg Arg
1 5

<210> 101
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-76) (see Table 1)

<400> 101

Arg Lys Lys Arg Arg Thr Arg Arg Arg
1 5

<210> 102
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-77) (see Table 1)

<400> 102

Arg Lys Lys Arg Arg Gln Thr Arg Arg
1 5

<210> 103
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-78) (see Table 1)

<400> 103

Arg Lys Lys Arg Arg Gln Arg Thr Arg
1 5

<210> 104
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-79) (see Table 1)

<400> 104

Arg Val Lys Arg Arg Gln Arg Arg Arg
1 5

<210> 105
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-80) (see Table 1)

<400> 105

Arg Lys Val Arg Arg Gln Arg Arg Arg
1 5

<210> 106
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-81) (see Table 1)

<400> 106

Arg Lys Lys Val Arg Gln Arg Arg Arg
1 5

<210> 107
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-82) (see Table 1)

<400> 107

Arg Lys Lys Arg Arg Val Arg Arg Arg
1 5

<210> 108
<211> 9
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-83) (see Table 1)

<400> 108

Arg Lys Lys Arg Arg Gln Val Arg Arg
1 5

<210> 109
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-84) (see Table 1)

<400> 109

Arg Lys Lys Arg Arg Gln Arg Val Arg
1 5

<210> 110
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-85) (see Table 1)

<400> 110

Arg Trp Lys Arg Arg Gln Arg Arg Arg
1 5

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

<220>
<223> Description of sequence: trafficking sequence TAT(s2-86) (see Table 1)

<400> 111

Arg Lys Trp Arg Arg Gln Arg Arg Arg
1 5

<210> 112
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-87) (see Table 1)

<400> 112

Arg Lys Lys Trp Arg Gln Arg Arg Arg
1 5

<210> 113
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-88) (see Table 1)

<400> 113

Arg Lys Lys Arg Arg Trp Arg Arg Arg
1 5

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

<220>
<223> Description of sequence: trafficking sequence TAT(s2-89) (see Table 1)

<400> 114

Arg Lys Lys Arg Arg Gln Trp Arg Arg
1 5

<210> 115
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-90) (see Table 1)

<400> 115

Arg Lys Lys Arg Arg Gln Arg Trp Arg
1 5

<210> 116
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-91) (see Table 1)

<400> 116

Arg Tyr Lys Arg Arg Gln Arg Arg Arg
1 5

<210> 117
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-92) (see Table 1)

<400> 117

Arg Lys Tyr Arg Arg Gln Arg Arg Arg
1 5

<210> 118
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-93) (see Table 1)

<400> 118

Arg Lys Lys Tyr Arg Gln Arg Arg Arg
1 5

<210> 119
<211> 9
<212> PRT
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<220>
<223> Description of sequence: trafficking sequence TAT(s2-94) (see Table 1)

<400> 119

Arg Lys Lys Arg Arg Tyr Arg Arg Arg
1 5

<210> 120
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-95) (see Table 1)

<400> 120

Arg Lys Lys Arg Arg Gln Tyr Arg Arg
1 5

<210> 121
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence TAT(s2-96) (see Table 1)

<400> 121

Arg Lys Lys Arg Arg Gln Arg Tyr Arg

1 5

<210> 122
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence r3R6 (see Table 1)

<220>
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<222> (1)..(1)
<223> /replace="D-enatiomeric amino acid arginine"

<220>
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<223> /replace="D-enatiomeric amino acid arginine"

<220>
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<223> /replace="D-enatiomeric amino acid arginine"

<400> 122

Arg Arg Arg Arg Arg Arg Arg Arg Arg
1 5

<210> 123
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence L-R9 (see Table 1)

<400> 123

Arg Arg Arg Arg Arg Arg Arg Arg Arg
1 5

<210> 124
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence L-R8 (see Table 1)

<400> 124

Arg Arg Arg Arg Arg Arg Arg Arg
1 5

<210> 125
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence L-R7 (see Table 1)

<400> 125

Arg Arg Arg Arg Arg Arg Arg
1 5

<210> 126
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence L-R6 (see Table 1)

<400> 126

Arg Arg Arg Arg Arg Arg
1 5

<210> 127
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence L-R5 (see Table 1)

<400> 127

Arg Arg Arg Arg Arg
1 5

<210> 128
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence PTD-4 (see Table 1)

<400> 128

Tyr Ala Arg Ala Ala Ala Arg Gln Ala Arg Ala
1 5 10

<210> 129
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence PTD-4 (variant 1) (see Table 1)

<400> 129

Trp Ala Arg Ala Ala Ala Arg Gln Ala Arg Ala
1 5 10

<210> 130
<211> 11
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence PTD-4 (variant 2) (see Table 1)

<400> 130

Trp Ala Arg Ala Gln Arg Ala Ala Ala Arg Ala
1 5 10

<210> 131
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence L-P1 (Penetratin) (see Table 1)

<400> 131

Arg Gln Val Lys Val Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys
1 5 10 15

<210> 132
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence D-P1 (Penetratin) (see Table 1)

<400> 132

Lys Lys Trp Lys Met Arg Arg Asn Gln Phe Trp Val Lys Val Gln Arg
1 5 10 15

<210> 133
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence JNK1, bestfit (see Table 1)

<400> 133

Trp Lys Arg Ala Ala Ala Arg Lys Ala Arg Ala Met Ser Leu Asn Leu
1 5 10 15

Phe

<210> 134
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence JNK1, bestfit

(variant 1) (see Table 1)

<400> 134

Trp Lys Arg Ala Ala Ala Arg Ala Ala Arg Ala Met Ser Leu Asn Leu
1 5 10 15

Phe

<210> 135
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence MDCK transcytose sequence (see Table 1)

<400> 135

Arg Tyr Arg Gly Asp Leu Gly Arg Arg
1 5

<210> 136
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: trafficking sequence YKGL (see Table 1)

<400> 136

Tyr Lys Gly Leu
1

<210> 137
<211> 2953
<212> DNA
<213> Rattus norvegicus

<220>
<221> misc_feature
<223> description of sequence: rat IB1 cDNA sequence

<400> 137
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gcccgggaat ggcggagcga gagagcggcc tgagcggggg tgccgcgtcc ccaccggccg 180

cttccccatt cctgggactg cacatcgcgt cgcctcccaa tttcaggctc acccatgata 240

tcagcctgga ggagtttgag gatgaagacc tttcggagat cactgatgag tgtggcatca 300

gcctgcagtg caaagacacc ttgtctctcc ggcccccgcg cgccgggcta ctgtctgcgg 360

gtagcagcgg tagcgcgggg agccggctgc aggcggagat gctgcagatg gacctgatcg 420

acgcggcaag tgacactccg ggcgccgagg acgacgaaga ggacgacgac gagctcgctg 480

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gccagggtca gggccagggc cccggcacag gctgcggaga cacctaccgg cccaagaggc 600

ctaccacgct caacctttc ccgcaggtgc cgcggtctca ggacacgctg aataataact 660

ctttaggcaa aaagcacagt tggcaggacc gtgtgtctcg atcatcctcc cctctgaaga 720

caggggagca gacgcctcca catgaacata tctgcctgag tgatgagctg ccgccccagg 780

gcagtcctgt tcccacccag gatcgtggca cttccaccga cagcccttgt cgccgtactg 840

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cctacgagtc agccattggt gaggaatatg aggaggcccc tcaaccccgg cctcccacct 1440

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aagccctgcc tgccagggaa ggttccctct cagctggccc cagccaactg gtcactgtct 2880

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<210> 138
<211> 714
<212> PRT
<213> Rattus norvegicus

<220>
<221> misc_feature
<223> description of sequence: amino acid sequence encoded by of rat IB1 cDNA sequence

<400> 138

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1 5 10 15

Gly Gly Ala Ala Ser Pro Pro Ala Ala Ser Pro Phe Leu Gly Leu His
20 25 30

Ile Ala Ser Pro Pro Asn Phe Arg Leu Thr His Asp Ile Ser Leu Glu
35 40 45

Glu Phe Glu Asp Glu Asp Leu Ser Glu Ile Thr Asp Glu Cys Gly Ile
50 55 60

Ser Leu Gln Cys Lys Asp Thr Leu Ser Leu Arg Pro Pro Arg Ala Gly
65 70 75 80

Leu Leu Ser Ala Gly Ser Ser Gly Ser Ala Gly Ser Arg Leu Gln Ala
85 90 95

Glu Met Leu Gln Met Asp Leu Ile Asp Ala Ala Ser Asp Thr Pro Gly
100 105 110

Ala Glu Asp Asp Glu Glu Asp Asp Asp Glu Leu Ala Ala Gln Arg Pro
115 120 125

Gly Val Gly Pro Ser Lys Ala Glu Ser Gly Gln Glu Pro Ala Ser Arg
130 135 140

Ser Gln Gly Gln Gly Gln Gly Pro Gly Thr Gly Cys Gly Asp Thr Tyr
145 150 155 160

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Arg Pro Lys Arg Pro Thr Thr Leu Asn Leu Phe Pro Gln Val Pro Arg
                165                 170                 175

Ser Gln Asp Thr Leu Asn Asn Asn Ser Leu Gly Lys Lys His Ser Trp
            180                 185                 190

Gln Asp Arg Val Ser Arg Ser Ser Ser Pro Leu Lys Thr Gly Glu Gln
        195                 200                 205

Thr Pro Pro His Glu His Ile Cys Leu Ser Asp Glu Leu Pro Pro Gln
    210                 215                 220

Gly Ser Pro Val Pro Thr Gln Asp Arg Gly Thr Ser Thr Asp Ser Pro
225                 230                 235                 240

Cys Arg Arg Thr Ala Ala Thr Gln Met Ala Pro Pro Ser Gly Pro Pro
                245                 250                 255

Ala Thr Ala Pro Gly Gly Arg Gly His Ser His Arg Asp Arg Ser Ile
            260                 265                 270

Ser Ala Asp Val Arg Leu Glu Ala Thr Glu Glu Ile Tyr Leu Thr Pro
        275                 280                 285

Val Gln Arg Pro Pro Asp Pro Ala Glu Pro Thr Ser Thr Phe Leu Pro
    290                 295                 300

Pro Thr Glu Ser Arg Met Ser Val Ser Ser Asp Pro Asp Pro Ala Ala
305                 310                 315                 320

Tyr Ser Val Thr Ala Gly Arg Pro His Pro Ser Ile Ser Glu Glu Asp
                325                 330                 335

Glu Gly Phe Asp Cys Leu Ser Ser Pro Glu Gln Ala Glu Pro Pro Gly
            340                 345                 350

Gly Gly Trp Arg Gly Ser Leu Gly Glu Pro Pro Pro Pro Pro Arg Ala
        355                 360                 365

Ser Leu Ser Ser Asp Thr Ser Ala Leu Ser Tyr Asp Ser Val Lys Tyr
    370                 375                 380

Thr Leu Val Val Asp Glu His Ala Gln Leu Glu Leu Val Ser Leu Arg
385                 390                 395                 400

Pro Cys Phe Gly Asp Tyr Ser Asp Glu Ser Asp Ser Ala Thr Val Tyr
                405                 410                 415

Asp Asn Cys Ala Ser Ala Ser Ser Pro Tyr Glu Ser Ala Ile Gly Glu
            420                 425                 430
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Glu Tyr Glu Glu Ala Pro Gln Pro Arg Pro Pro Thr Cys Leu Ser Glu
        435                 440                 445

Asp Ser Thr Pro Asp Glu Pro Asp Val His Phe Ser Lys Lys Phe Leu
    450                 455                 460

Asn Val Phe Met Ser Gly Arg Ser Arg Ser Ser Ser Ala Glu Ser Phe
465                 470                 475                 480

Gly Leu Phe Ser Cys Val Ile Asn Gly Glu Glu His Glu Gln Thr His
                485                 490                 495

Arg Ala Ile Phe Arg Phe Val Pro Arg His Glu Asp Glu Leu Glu Leu
            500                 505                 510

Glu Val Asp Asp Pro Leu Leu Val Glu Leu Gln Ala Glu Asp Tyr Trp
        515                 520                 525

Tyr Glu Ala Tyr Asn Met Arg Thr Gly Ala Arg Gly Val Phe Pro Ala
    530                 535                 540

Tyr Tyr Ala Ile Glu Val Thr Lys Glu Pro Glu His Met Ala Ala Leu
545                 550                 555                 560

Ala Lys Asn Ser Asp Trp Ile Asp Gln Phe Arg Val Lys Phe Leu Gly
                565                 570                 575

Ser Val Gln Val Pro Tyr His Lys Gly Asn Asp Val Leu Cys Ala Ala
            580                 585                 590

Met Gln Lys Ile Ala Thr Thr Arg Arg Leu Thr Val His Phe Asn Pro
        595                 600                 605

Pro Ser Ser Cys Val Leu Glu Ile Ser Val Arg Gly Val Lys Ile Gly
    610                 615                 620

Val Lys Ala Asp Glu Ala Gln Glu Ala Lys Gly Asn Lys Cys Ser His
625                 630                 635                 640

Phe Phe Gln Leu Lys Asn Ile Ser Phe Cys Gly Tyr His Pro Lys Asn
                645                 650                 655

Asn Lys Tyr Phe Gly Phe Ile Thr Lys His Pro Ala Asp His Arg Phe
            660                 665                 670

Ala Cys His Val Phe Val Ser Glu Asp Ser Thr Lys Ala Leu Ala Glu
        675                 680                 685

Ser Val Gly Arg Ala Phe Gln Gln Phe Tyr Lys Gln Phe Val Glu Tyr
    690                 695                 700
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Thr Cys Pro Thr Glu Asp Ile Tyr Leu Glu
705 710

<210> 139
<211> 711
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> description of sequence: human IB1 protein sequence

<220>
<221> misc_feature
<223> description of sequence: human IB1 protein sequence

<400> 139

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

Pro Ala Ala Ser Pro Phe Leu Gly Leu His Ile Ala Ser Pro Pro Asn
20 25 30

Phe Arg Leu Thr His Asp Ile Ser Leu Glu Glu Phe Glu Asp Glu Asp
35 40 45

Leu Ser Glu Ile Thr Asp Glu Cys Gly Ile Ser Leu Gln Cys Lys Asp
50 55 60

Thr Leu Ser Leu Arg Pro Pro Arg Ala Gly Leu Leu Ser Ala Gly Gly
65 70 75 80

Gly Gly Ala Gly Ser Arg Leu Gln Ala Glu Met Leu Gln Met Asp Leu
85 90 95

Ile Asp Ala Thr Gly Asp Thr Pro Gly Ala Glu Asp Asp Glu Glu Asp
100 105 110

Asp Asp Glu Glu Arg Ala Ala Arg Arg Pro Gly Ala Gly Pro Pro Lys
115 120 125

Ala Glu Ser Gly Gln Glu Pro Ala Ser Arg Gly Gln Gly Gln Ser Gln
130 135 140

Gly Gln Ser Gln Gly Pro Gly Ser Gly Asp Thr Tyr Arg Pro Lys Arg
145 150 155 160

Pro Thr Thr Leu Asn Leu Phe Pro Gln Val Pro Arg Ser Gln Asp Thr
165 170 175

Leu Asn Asn Asn Ser Leu Gly Lys Lys His Ser Trp Gln Asp Arg Val
180 185 190

Ser Arg Ser Ser Ser Pro Leu Lys Thr Gly Glu Gln Thr Pro Pro His
195 200 205

Glu His Ile Cys Leu Ser Asp Glu Leu Pro Pro Gln Ser Gly Pro Ala
210 215 220

Pro Thr Thr Asp Arg Gly Thr Ser Thr Asp Ser Pro Cys Arg Arg Ser
225 230 235 240

Thr Ala Thr Gln Met Ala Pro Pro Gly Gly Pro Pro Ala Ala Pro Pro
245 250 255

Gly Gly Arg Gly His Ser His Arg Asp Arg Ile His Tyr Gln Ala Asp
260 265 270

Val Arg Leu Glu Ala Thr Glu Glu Ile Tyr Leu Thr Pro Val Gln Arg
275 280 285

Pro Pro Asp Ala Ala Glu Pro Thr Ser Ala Phe Leu Pro Pro Thr Glu
290 295 300

Ser Arg Met Ser Val Ser Ser Asp Pro Asp Pro Ala Ala Tyr Pro Ser
305 310 315 320

Thr Ala Gly Arg Pro His Pro Ser Ile Ser Glu Glu Glu Glu Gly Phe
325 330 335

Asp Cys Leu Ser Ser Pro Glu Arg Ala Glu Pro Pro Gly Gly Gly Trp
340 345 350

Arg Gly Ser Leu Gly Glu Pro Pro Pro Pro Pro Arg Ala Ser Leu Ser
355 360 365

Ser Asp Thr Ser Ala Leu Ser Tyr Asp Ser Val Lys Tyr Thr Leu Val
370 375 380

Val Asp Glu His Ala Gln Leu Glu Leu Val Ser Leu Arg Pro Cys Phe
385 390 395 400

Gly Asp Tyr Ser Asp Glu Ser Asp Ser Ala Thr Val Tyr Asp Asn Cys
405 410 415

Ala Ser Val Ser Ser Pro Tyr Glu Ser Ala Ile Gly Glu Glu Tyr Glu
420 425 430

Glu Ala Pro Arg Pro Gln Pro Pro Ala Cys Leu Ser Glu Asp Ser Thr
435 440 445

Pro Asp Glu Pro Asp Val His Phe Ser Lys Lys Phe Leu Asn Val Phe
450 455 460

```
Met Ser Gly Arg Ser Arg Ser Ser Ser Ala Glu Ser Phe Gly Leu Phe
465                 470                 475                 480

Ser Cys Ile Ile Asn Gly Glu Glu Gln Glu Gln Thr His Arg Ala Ile
                485                 490                 495

Phe Arg Phe Val Pro Arg His Glu Asp Glu Leu Glu Leu Glu Val Asp
            500                 505                 510

Asp Pro Leu Leu Val Glu Leu Gln Ala Glu Asp Tyr Trp Tyr Glu Ala
        515                 520                 525

Tyr Asn Met Arg Thr Gly Ala Arg Gly Val Phe Pro Ala Tyr Tyr Ala
    530                 535                 540

Ile Glu Val Thr Lys Glu Pro Glu His Met Ala Ala Leu Ala Lys Asn
545                 550                 555                 560

Ser Asp Trp Val Asp Gln Phe Arg Val Lys Phe Leu Gly Ser Val Gln
                565                 570                 575

Val Pro Tyr His Lys Gly Asn Asp Val Leu Cys Ala Ala Met Gln Lys
            580                 585                 590

Ile Ala Thr Thr Arg Arg Leu Thr Val His Phe Asn Pro Pro Ser Ser
        595                 600                 605

Cys Val Leu Glu Ile Ser Val Arg Gly Val Lys Ile Gly Val Lys Ala
    610                 615                 620

Asp Asp Ser Gln Glu Ala Lys Gly Asn Lys Cys Ser His Phe Phe Gln
625                 630                 635                 640

Leu Lys Asn Ile Ser Phe Cys Gly Tyr His Pro Lys Asn Asn Lys Tyr
                645                 650                 655

Phe Gly Phe Ile Thr Lys His Pro Ala Asp His Arg Phe Ala Cys His
            660                 665                 670

Val Phe Val Ser Glu Asp Ser Thr Lys Ala Leu Ala Glu Ser Val Gly
        675                 680                 685

Arg Ala Phe Gln Gln Phe Tyr Lys Gln Phe Val Glu Tyr Thr Cys Pro
    690                 695                 700

Thr Glu Asp Ile Tyr Leu Glu
705                 710
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<210> 140
<211> 2136

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> description of sequence: nucleic acid sequence encoding human IB1 protein

<400> 140
atggcggagc gagaaagcgg cggcctggga ggggggggccg cgtccccgcc cgccgcctcc 60

ccgttcctgg ggctgcacat cgcttcgcct cccaatttca ggctcaccca tgacatcagc 120

ctggaggagt ttgaggatga agacctctcg gagatcactg atgagtgtgg catcagctta 180

cagtgcaaag acaccctgtc cttacggccc ccgcgcgccg ggctgctctc tgcgggcggc 240

ggcggcgcgg ggagccggtt gcaggccgag atgctgcaga tggacctgat cgacgcgacg 300

ggggacactc ccggggccga ggacgacgag gaggacgacg acgaggagcg cgcggcccgg 360

cggccgggag cggggccgcc caaggccgag tccggccagg agccggcgtc ccgcggccag 420

ggccagagcc aaggccagag ccagggcccg ggcagcgggg acacgtaccg gcccaagcgg 480

cccaccacgc tcaacctctt tccgcaggtg ccgcggtctc aggacacact gaataataat 540

tctctgggca aaaagcacag ttggcaggat cgggtgtctc gatcatcctc acccctgaag 600

acaggggagc agacaccacc gcatgaacac atctgcctga gcgatgagct gccccccccag 660

agcggccccg cccccaccac agatcgaggc acctccaccg acagcccttg ccgccgcagc 720

acagccaccc agatggcacc tccgggtggt ccccctgctg ccccgcctgg gggtcggggc 780

cactcgcatc gagaccgaat ccactaccag gccgatgtgc gactagaggc cactgaggag 840

atctacctga ccccagtgca gaggccccca gacgctgcag agcccacctc cgccttcctg 900

ccgcccactg agagccggat gtcagtcagc tccgatccag accctgccgc ctacccctcc 960

acggcagggc ggccgcaccc ctccatcagt gaagaggaag agggcttcga ctgcctgtcg 1020

tccccagagc gggctgagcc cccaggcgga gggtggcggg ggagcctggg ggagccgccg 1080

ccacctccac gggcctctct gagctcggac accagcgccc tgtcctatga ctctgtcaag 1140

tacacgctgg tggtagatga gcatgcacag ctggagctgg tgagcctgcg gccgtgcttc 1200

ggagactaca gtgacgagag tgactctgcc accgtctatg acaactgtgc ctccgtctcc 1260

tcgccctatg agtcggccat cggagaggaa tatgaggagg ccccgcggcc ccagcccccct 1320

gcctgcctct ccgaggactc cacgcctgat gaacccgacg tccatttctc caagaaattc 1380

ctgaacgtct tcatgagtgg ccgctcccgc tcctccagtg ctgagtcctt cgggctgttc 1440

tcctgcatca tcaacgggga ggagcaggag cagacccacc gggccatatt caggtttgtg 1500

cctcgacacg aagacgaact tgagctggaa gtggatgacc ctctgctagt ggagctccag 1560

gctgaagact actggtacga ggcctacaac atgcgcactg gtgcccgggg tgtctttcct 1620

gcctattacg ccatcgaggt caccaaggag cccgagcaca tggcagccct ggccaaaaac 1680

agtgactggg tggaccagtt ccgggtgaag ttcctgggct cagtccaggt tccctatcac 1740

aagggcaatg acgtcctctg tgctgctatg caaaagattg ccaccacccg ccggctcacc 1800

gtgcacttta acccgccctc cagctgtgtc ctggagatca gcgtgcgggg tgtgaagata 1860

ggcgtcaagg ccgatgactc ccaggaggcc aaggggaata aatgtagcca ctttttccag 1920

ttaaaaaaca tctctttctg cggatatcat ccaaagaaca acaagtactt tgggttcatc 1980

accaagcacc ccgccgacca ccggtttgcc tgccacgtct ttgtgtctga agactccacc 2040

aaagccctgg cagagtccgt ggggagagca ttccagcagt tctacaagca gtttgtggag 2100

tacacctgcc ccacagaaga tatctacctg gagtag 2136

<210> 141
<211> 19
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: Peptide L-IB1(s) (see Table 3)

<400> 141

Arg Pro Lys Arg Pro Thr Thr Leu Asn Leu Phe Pro Gln Val Pro Arg
1 5 10 15

Ser Gln Asp

<210> 142
<211> 19
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: Peptide D-IB1(s) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(19)
<223> all amino acids are D-amino acids

<400> 142

Asp Gln Ser Arg Pro Val Gln Pro Phe Leu Asn Leu Thr Thr Pro Arg
1 5 10 15

Lys Pro Arg

<210> 143
<211> 19
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: Peptide L-IB (generic) (s) (see Table 3)

<220>
<221> misc_feature

<223> Description of sequence: Description of sequence: general formula: NH2-Xnb-Xna-RPTTLXLXXXXXXXQD-Xnb-COOH (see Table 1)

<220>
<221> VARIANT
<222> (1)..(1)
<223> Xaa is Xnb as defined in the general formula, wherein Xaa represents an amino acid residue, preferably selected from any (native) amino acid residue;

<220>
<221> REPEAT
<222> (1)..(1)
<223> Xaa is Xnb as defined in the general formula, wherein n is 0-5, 5-10, 10-15, 15-20, 20-30 or more for Xnb

<220>
<221> VARIANT
<222> (2)..(2)
<223> Xaa is Xna as defined in the general formula, wherein Xaa represents an amino acid residue, preferably selected from any (native) amino acid residue residue except serine and threonine

<220>
<221> REPEAT
<222> (2)..(2)
<223> Xaa is Xna as defined in the general formula, wherein n is 0 or 1

<220>
<221> VARIANT
<222> (8)..(8)
<223> Xaa represents an amino acid residue, preferably selected from any (native) amino acid residue;

<220>
<221> VARIANT
<222> (10)..(16)
<223> Xaa represents an amino acid residue, preferably selected from any (native) amino acid residue;

<220>
<221> REPEAT
<222> (19)..(19)
<223> Xaa is Xnb as defined in the general formula, wherein n is 0-5, 5-10, 10-15, 15-20, 20-30 or more for Xnb

<220>
<221> VARIANT
<222> (19)..(19)
<223> Xaa is Xnb as defined in the general formula, wherein Xaa represents an amino acid residue, preferably selected from any (native) amino acid residue;

<400> 143

Xaa Xaa Arg Pro Thr Thr Leu Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Gln Asp Xaa

<210> 144
<211> 19
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: Peptide D-IB (generic) (s) (see Table 3)

<220>
<221> misc_feature
<223> Description of sequence: general formula:
NH2-Xnb-DQXXXXXXXLXLTTPR-Xna-Xnb-COOH,

<220>
<221> MUTAGEN
<222> (1)..(19)
<223> all amino acids are D-amino acids

<220>
<221> VARIANT
<222> (1)..(11)
<223> Xaa is Xnb as defined in the general formula, wherein Xaa represents an amino acid residue, preferably selected from any (native) amino acid residue;

<220>
<221> REPEAT
<222> (1)..(1)
<223> Xaa is Xnb as defined in the general formula, wherein n is 0-5, 5-10, 10-15, 15-20, 20-30 or more for Xnb

<220>
<221> VARIANT
<222> (4)..(10)
<223> Xaa represents an amino acid residue, preferably selected from any (native) amino acid residue;

<220>
<221> VARIANT
<222> (12)..(12)
<223> Xaa represents an amino acid residue, preferably selected from any (native) amino acid residue;

<220>
<221> REPEAT
<222> (18)..(18)
<223> Xaa is Xna as defined in the general formula, wherein n is 0 or 1

<220>
<221> VARIANT
<222> (18)..(18)
<223> Xaa is Xna as defined in the general formula, wherein Xaa represents an amino acid residue, preferably selected from any (native) amino acid residue residue except serine and Threonine

<220>
<221> VARIANT
<222> (18)..(18)
<223> Xaa is Xna as defined in the general formula, wherein Xaa represents an amino acid residue, preferably selected from any (native) amino acid residue residue except serine and threonine

<220>
<221> REPEAT
<222> (19)..(19)
<223> Xaa is Xnb as defined in the general formula, wherein n is 0-5, 5-10, 10-15, 15-20, 20-30 or more for Xnb

<220>
<221> VARIANT
<222> (19)..(19)
<223> Xaa is Xnb as defined in the general formula, wherein Xaa

represents an amino acid residue, preferably selected from any (native) amino acid residue;

<400> 144

Xaa Asp Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Leu Thr Thr Pro
1 5 10 15

Arg Xaa Xaa

<210> 145
<211> 29
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: peptide IB1-long (see Table 3)

<400> 145

Pro Gly Thr Gly Cys Gly Asp Thr Tyr Arg Pro Lys Arg Pro Thr Thr
1 5 10 15

Leu Asn Leu Phe Pro Gln Val Pro Arg Ser Gln Asp Thr
20 25

<210> 146
<211> 27
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: Peptide IB2-long (see Table 3)

<400> 146

Ile Pro Ser Pro Ser Val Glu Glu Pro His Lys His Arg Pro Thr Thr
1 5 10 15

Leu Arg Leu Thr Thr Leu Gly Ala Gln Asp Ser
20 25

<210> 147
<211> 29
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: Peptide derived from c-Jun (see Table 3)

<400> 147

Gly Ala Tyr Gly Tyr Ser Asn Pro Lys Ile Leu Lys Gln Ser Met Thr
1 5 10 15

Leu Asn Leu Ala Asp Pro Val Gly Asn Leu Lys Pro His
20 25

<210> 148

<211> 29
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: Peptide derived from ATF2 (see Table 3)

<400> 148

Thr Asn Glu Asp His Leu Ala Val His Lys His Lys His Glu Met Thr
1 5 10 15

Leu Lys Phe Gly Pro Ala Arg Asn Asp Ser Val Ile Val
20 25

<210> 149
<211> 23
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: Peptide L-IB1 (see Table 3)

<400> 149

Asp Thr Tyr Arg Pro Lys Arg Pro Thr Thr Leu Asn Leu Phe Pro Gln
1 5 10 15

Val Pro Arg Ser Gln Asp Thr
20

<210> 150
<211> 23
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: Peptide D-IB1 (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(23)
<223> all amino acids are D-amino acids

<400> 150

Thr Asp Gln Ser Arg Pro Val Gln Pro Phe Leu Asn Leu Thr Thr Pro
1 5 10 15

Arg Lys Pro Arg Tyr Thr Asp
20

<210> 151
<211> 19
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: Peptide L-IB (generic) (see Table 3)

<220>
<221> VARIANT
<222> (1)..(1)
<223> Xaa is selected from any amino acid residue,

<220>
<221> VARIANT
<222> (7)..(7)
<223> Xaa is selected from any amino acid residue,

<220>
<221> VARIANT
<222> (9)..(15)
<223> Xaa is selected from any amino acid residue,

<220>
<221> VARIANT
<222> (18)..(18)
<223> Xaa is selected from serine or threonine,

<220>
<221> VARIANT
<222> (19)..(19)
<223> Xaa is selected from any amino acid residue,

<400> 151

Xaa Arg Pro Thr Thr Leu Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln
1 5 10 15

Asp Xaa Xaa

<210> 152
<211> 19
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: Peptide D-IB (generic) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(19)
<223> all amino acids are D-amino acids

<220>
<221> VARIANT
<222> (1)..(1)
<223> Xaa is selected from any amino acid residue

<220>
<221> VARIANT
<222> (2)..(2)
<223> Xaa is selected from serine or threonine

<220>
<221> VARIANT
<222> (5)..(11)
<223> Xaa is selected from any amino acid residue

<220>
<221> VARIANT
<222> (13)..(13)
<223> Xaa is selected from any amino acid residue

<220>
<221> VARIANT
<222> (19)..(19)
<223> Xaa is selected from any amino acid residue

<400> 152

Xaa Xaa Asp Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Leu Thr Thr
1 5 10 15

Pro Arg Xaa

<210> 153
<211> 13
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s1) (see Table 3)

<400> 153

Thr Leu Asn Leu Phe Pro Gln Val Pro Arg Ser Gln Asp
1 5 10

<210> 154
<211> 13
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s2) (see Table 3)

<400> 154

Thr Thr Leu Asn Leu Phe Pro Gln Val Pro Arg Ser Gln
1 5 10

<210> 155
<211> 13
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s3) (see Table 3)

<400> 155

Pro Thr Thr Leu Asn Leu Phe Pro Gln Val Pro Arg Ser
1 5 10

<210> 156
<211> 13
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s4) (see Table 3)

<400> 156

Arg Pro Thr Thr Leu Asn Leu Phe Pro Gln Val Pro Arg
1 5 10

<210> 157
<211> 13
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s5) (see Table 3)

<400> 157

Lys Arg Pro Thr Thr Leu Asn Leu Phe Pro Gln Val Pro
1 5 10

<210> 158
<211> 13
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s6) (see Table 3)

<400> 158

Pro Lys Arg Pro Thr Thr Leu Asn Leu Phe Pro Gln Val
1 5 10

<210> 159
<211> 13
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s7) (see Table 3)

<400> 159

Arg Pro Lys Arg Pro Thr Thr Leu Asn Leu Phe Pro Gln
1 5 10

<210> 160
<211> 12
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s8) (see Table 3)

<400> 160

Leu Asn Leu Phe Pro Gln Val Pro Arg Ser Gln Asp
1 5 10

<210> 161
<211> 12
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s9) (see Table 3)

<400> 161

Thr Leu Asn Leu Phe Pro Gln Val Pro Arg Ser Gln
1 5 10

<210> 162
<211> 12
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s10) (see Table 3)

<400> 162

Thr Thr Leu Asn Leu Phe Pro Gln Val Pro Arg Ser
1 5 10

<210> 163
<211> 12
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s11) (see Table 3)

<400> 163

Pro Thr Thr Leu Asn Leu Phe Pro Gln Val Pro Arg
1 5 10

<210> 164
<211> 12
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s12) (see Table 3)

<400> 164

Arg Pro Thr Thr Leu Asn Leu Phe Pro Gln Val Pro
1 5 10

<210> 165
<211> 12
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s13) (see Table 3)

<400> 165

Lys Arg Pro Thr Thr Leu Asn Leu Phe Pro Gln Val
1 5 10

<210> 166
<211> 12
<212> PRT
<213> Artificial

<220>

<223> Description of sequence: L-IB1(s14) (see Table 3)

<400> 166

Pro Lys Arg Pro Thr Thr Leu Asn Leu Phe Pro Gln
1 5 10

<210> 167
<211> 12
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s15) (see Table 3)

<400> 167

Arg Pro Lys Arg Pro Thr Thr Leu Asn Leu Phe Pro
1 5 10

<210> 168
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s16) (see Table 3)

<400> 168

Asn Leu Phe Pro Gln Val Pro Arg Ser Gln Asp
1 5 10

<210> 169
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s17) (see Table 3)

<400> 169

Leu Asn Leu Phe Pro Gln Val Pro Arg Ser Gln
1 5 10

<210> 170
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s18) (see Table 3)

<400> 170

Thr Leu Asn Leu Phe Pro Gln Val Pro Arg Ser
1 5 10

<210> 171
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s19) (see Table 3)

<400> 171

Thr Thr Leu Asn Leu Phe Pro Gln Val Pro Arg
1   5   10

<210> 172
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s20) (see Table 3)

<400> 172

Pro Thr Thr Leu Asn Leu Phe Pro Gln Val Pro
1   5   10

<210> 173
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s21) (see Table 3)

<400> 173

Arg Pro Thr Thr Leu Asn Leu Phe Pro Gln Val
1   5   10

<210> 174
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s22) (see Table 3)

<400> 174

Lys Arg Pro Thr Thr Leu Asn Leu Phe Pro Gln
1   5   10

<210> 175
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s23) (see Table 3)

<400> 175

Pro Lys Arg Pro Thr Thr Leu Asn Leu Phe Pro
1   5   10

<210> 176
<211> 11

<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s24) (see Table 3)

<400> 176

Arg Pro Lys Arg Pro Thr Thr Leu Asn Leu Phe
1 5 10

<210> 177
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s25) (see Table 3)

<400> 177

Leu Phe Pro Gln Val Pro Arg Ser Gln Asp
1 5 10

<210> 178
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s26) (see Table 3)

<400> 178

Asn Leu Phe Pro Gln Val Pro Arg Ser Gln
1 5 10

<210> 179
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s27) (see Table 3)

<400> 179

Leu Asn Leu Phe Pro Gln Val Pro Arg Ser
1 5 10

<210> 180
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s28) (see Table 3)

<400> 180

Thr Leu Asn Leu Phe Pro Gln Val Pro Arg
1 5 10

<210> 181
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s29) (see Table 3)

<400> 181

Thr Thr Leu Asn Leu Phe Pro Gln Val Pro
1 5 10

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

<220>
<223> Description of sequence: L-IB1(s30) (see Table 3)

<400> 182

Pro Thr Thr Leu Asn Leu Phe Pro Gln Val
1 5 10

<210> 183
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s31) (see Table 3)

<400> 183

Arg Pro Thr Thr Leu Asn Leu Phe Pro Gln
1 5 10

<210> 184
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s32) (see Table 3)

<400> 184

Lys Arg Pro Thr Thr Leu Asn Leu Phe Pro
1 5 10

<210> 185
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s33) (see Table 3)

<400> 185

Pro Lys Arg Pro Thr Thr Leu Asn Leu Phe
1 5 10

<210> 186
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s34) (see Table 3)

<400> 186

Arg Pro Lys Arg Pro Thr Thr Leu Asn Leu
1 5 10

<210> 187
<211> 13
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s1) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(13)
<223> all amino acids are D-amino acids

<400> 187

Gln Pro Phe Leu Asn Leu Thr Thr Pro Arg Lys Pro Arg
1 5 10

<210> 188
<211> 13
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s2) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(13)
<223> all amino acids are D-amino acids

<400> 188

Val Gln Pro Phe Leu Asn Leu Thr Thr Pro Arg Lys Pro
1 5 10

<210> 189
<211> 13
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s3) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(13)

<223> all amino acids are D-amino acids

<400> 189

Pro Val Gln Pro Phe Leu Asn Leu Thr Thr Pro Arg Lys
1 5 10

<210> 190
<211> 13
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s4) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(13)
<223> all amino acids are D-amino acids

<400> 190

Arg Pro Val Gln Pro Phe Leu Asn Leu Thr Thr Pro Arg
1 5 10

<210> 191
<211> 13
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s5) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(13)
<223> all amino acids are D-amino acids

<400> 191

Ser Arg Pro Val Gln Pro Phe Leu Asn Leu Thr Thr Pro
1 5 10

<210> 192
<211> 13
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s6) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(13)
<223> all amino acids are D-amino acids

<400> 192

Gln Ser Arg Pro Val Gln Pro Phe Leu Asn Leu Thr Thr
1 5 10

<210> 193
<211> 13
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s7) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(13)
<223> all amino acids are D-amino acids

<400> 193

Asp Gln Ser Arg Pro Val Gln Pro Phe Leu Asn Leu Thr
1 5 10

<210> 194
<211> 12
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s8) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(12)
<223> all amino acids are D-amino acids

<400> 194

Pro Phe Leu Asn Leu Thr Thr Pro Arg Lys Pro Arg
1 5 10

<210> 195
<211> 12
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s9) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(12)
<223> all amino acids are D-amino acids

<400> 195

Gln Pro Phe Leu Asn Leu Thr Thr Pro Arg Lys Pro
1 5 10

<210> 196
<211> 12
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s10) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(12)
<223> all amino acids are D-amino acids

<400> 196

Val Gln Pro Phe Leu Asn Leu Thr Thr Pro Arg Lys
1 5 10

<210> 197
<211> 12
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s11) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(12)
<223> all amino acids are D-amino acids

<400> 197

Pro Val Gln Pro Phe Leu Asn Leu Thr Thr Pro Arg
1 5 10

<210> 198
<211> 12
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s12) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(12)
<223> all amino acids are D-amino acids

<400> 198

Arg Pro Val Gln Pro Phe Leu Asn Leu Thr Thr Pro
1 5 10

<210> 199
<211> 12
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s13) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(12)
<223> all amino acids are D-amino acids

<400> 199

Ser Arg Pro Val Gln Pro Phe Leu Asn Leu Thr Thr
1 5 10

<210> 200
<211> 12
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s14) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(12)
<223> all amino acids are D-amino acids

<400> 200

Gln Ser Arg Pro Val Gln Pro Phe Leu Asn Leu Thr
1 5 10

<210> 201
<211> 12
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s15) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(12)
<223> all amino acids are D-amino acids

<400> 201

Asp Gln Ser Arg Pro Val Gln Pro Phe Leu Asn Leu
1 5 10

<210> 202
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s16) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(11)
<223> all amino acids are D-amino acids

<400> 202

Phe Leu Asn Leu Thr Thr Pro Arg Lys Pro Arg
1 5 10

<210> 203
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s17) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(11)
<223> all amino acids are D-amino acids

<400> 203

Pro Phe Leu Asn Leu Thr Thr Pro Arg Lys Pro
1 5 10

<210> 204
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s18) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(11)
<223> all amino acids are D-amino acids

<400> 204

Gln Pro Phe Leu Asn Leu Thr Thr Pro Arg Lys
1 5 10

<210> 205
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s19) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(11)
<223> all amino acids are D-amino acids

<400> 205

Val Gln Pro Phe Leu Asn Leu Thr Thr Pro Arg
1 5 10

<210> 206
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s20) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(11)

<223> all amino acids are D-amino acids

<400> 206

Pro Val Gln Pro Phe Leu Asn Leu Thr Thr Pro
1 5 10

<210> 207
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s21) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(11)
<223> all amino acids are D-amino acids

<400> 207

Arg Pro Val Gln Pro Phe Leu Asn Leu Thr Thr
1 5 10

<210> 208
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s22) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(11)
<223> all amino acids are D-amino acids

<400> 208

Ser Arg Pro Val Gln Pro Phe Leu Asn Leu Thr
1 5 10

<210> 209
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s23) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(11)
<223> all amino acids are D-amino acids

<400> 209

Gln Ser Arg Pro Val Gln Pro Phe Leu Asn Leu
1 5 10

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

<220>
<223> Description of sequence: D-IB1(s24) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(11)
<223> all amino acids are D-amino acids

<400> 210

Asp Gln Ser Arg Pro Val Gln Pro Phe Leu Asn
1 5 10

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

<220>
<223> Description of sequence: D-IB1(s25) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(10)
<223> all amino acids are D-amino acids

<400> 211

Asp Gln Ser Arg Pro Val Gln Pro Phe Leu
1 5 10

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

<220>
<223> Description of sequence: D-IB1(s26) (see Table 1)

<220>
<221> MUTAGEN
<222> (1)..(10)
<223> all amino acids are D-amino acids

<400> 212

Gln Ser Arg Pro Val Gln Pro Phe Leu Asn
1 5 10

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

<220>
<223> Description of sequence: D-IB1(s27) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(10)
<223> all amino acids are D-amino acids

<400> 213

Ser Arg Pro Val Gln Pro Phe Leu Asn Leu
1 5 10

<210> 214
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s28) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(10)
<223> all amino acids are D-amino acids

<400> 214

Arg Pro Val Gln Pro Phe Leu Asn Leu Thr
1 5 10

<210> 215
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s29) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(10)
<223> all amino acids are D-amino acids

<400> 215

Pro Val Gln Pro Phe Leu Asn Leu Thr Thr
1 5 10

<210> 216
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s30) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(10)
<223> all amino acids are D-amino acids

<400> 216

Val Gln Pro Phe Leu Asn Leu Thr Thr Pro
1 5 10

<210> 217
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s31) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(10)
<223> all amino acids are D-amino acids

<400> 217

Gln Pro Phe Leu Asn Leu Thr Thr Pro Arg
1 5 10

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

<220>
<223> Description of sequence: D-IB1(s32) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(10)
<223> all amino acids are D-amino acids

<400> 218

Pro Phe Leu Asn Leu Thr Thr Pro Arg Lys
1 5 10

<210> 219
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s33) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(10)
<223> all amino acids are D-amino acids

<400> 219

Phe Leu Asn Leu Thr Thr Pro Arg Lys Pro
1 5 10

<210> 220
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s34) (see Table 3)

<220>
<221> MUTAGEN
<222> (1)..(10)
<223> all amino acids are D-amino acids

<400> 220

Leu Asn Leu Thr Thr Pro Arg Lys Pro Arg
1 5 10

<210> 221
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Description of sequence: amino acid sequence of Bid (human) (transcript variant 1)

<400> 221

Met Cys Ser Gly Ala Gly Val Met Met Ala Arg Trp Ala Ala Arg Gly
1 5 10 15

Arg Ala Gly Trp Arg Ser Thr Val Arg Ile Leu Ser Pro Leu Gly His
20 25 30

Cys Glu Pro Gly Val Ser Arg Ser Cys Arg Ala Ala Gln Ala Met Asp
35 40 45

Cys Glu Val Asn Asn Gly Ser Ser Leu Arg Asp Glu Cys Ile Thr Asn
50 55 60

Leu Leu Val Phe Gly Phe Leu Gln Ser Cys Ser Asp Asn Ser Phe Arg
65 70 75 80

Arg Glu Leu Asp Ala Leu Gly His Glu Leu Pro Val Leu Ala Pro Gln
85 90 95

Trp Glu Gly Tyr Asp Glu Leu Gln Thr Asp Gly Asn Arg Ser Ser His
100 105 110

Ser Arg Leu Gly Arg Ile Glu Ala Asp Ser Glu Ser Gln Glu Asp Ile
115 120 125

Ile Arg Asn Ile Ala Arg His Leu Ala Gln Val Gly Asp Ser Met Asp
130 135 140

Arg Ser Ile Pro Pro Gly Leu Val Asn Gly Leu Ala Leu Gln Leu Arg
145 150 155 160

```
Asn Thr Ser Arg Ser Glu Glu Asp Arg Asn Arg Asp Leu Ala Thr Ala
                165                 170                 175

Leu Glu Gln Leu Leu Gln Ala Tyr Pro Arg Asp Met Glu Lys Glu Lys
            180                 185                 190

Thr Met Leu Val Leu Ala Leu Leu Leu Ala Lys Lys Val Ala Ser His
        195                 200                 205

Thr Pro Ser Leu Leu Arg Asp Val Phe His Thr Thr Val Asn Phe Ile
    210                 215                 220

Asn Gln Asn Leu Arg Thr Tyr Val Arg Ser Leu Ala Arg Asn Gly Met
225                 230                 235                 240

Asp
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<210> 222
<211> 168
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Description of sequence: amino acid sequence of Bad (human)

<400> 222

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Met Phe Gln Ile Pro Glu Phe Glu Pro Ser Glu Gln Glu Asp Ser Ser
1               5                   10                  15

Ser Ala Glu Arg Gly Leu Gly Pro Ser Pro Ala Gly Asp Gly Pro Ser
            20                  25                  30

Gly Ser Gly Lys His His Arg Gln Ala Pro Gly Leu Leu Trp Asp Ala
        35                  40                  45

Ser His Gln Gln Glu Gln Pro Thr Ser Ser Ser His His Gly Gly Ala
    50                  55                  60

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

Glu Asp Asp Glu Gly Met Gly Glu Glu Pro Ser Pro Phe Arg Gly Arg
                85                  90                  95

Ser Arg Ser Ala Pro Pro Asn Leu Trp Ala Ala Gln Arg Tyr Gly Arg
            100                 105                 110

Glu Leu Arg Arg Met Ser Asp Glu Phe Val Asp Ser Phe Lys Lys Gly
        115                 120                 125
```

```
Leu Pro Arg Pro Lys Ser Ala Gly Thr Ala Thr Gln Met Arg Gln Ser
    130                 135                 140

Ser Ser Trp Thr Arg Val Phe Gln Ser Trp Trp Asp Arg Asn Leu Gly
145                 150                 155                 160

Arg Gly Ser Ser Ala Pro Ser Gln
                165
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<210> 223
<211> 483
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Description of sequence: amino acid sequence of Noxa1 (human)

<400> 223

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Met Ala Ser Leu Gly Asp Leu Val Arg Ala Trp His Leu Gly Ala Gln
1               5                   10                  15

Ala Val Asp Arg Gly Asp Trp Ala Arg Ala Leu His Leu Phe Ser Gly
            20                  25                  30

Val Pro Ala Pro Pro Ala Arg Leu Cys Phe Asn Ala Gly Cys Val His
        35                  40                  45

Leu Leu Ala Gly Asp Pro Glu Ala Ala Leu Arg Ala Phe Asp Gln Ala
    50                  55                  60

Val Thr Lys Asp Thr Cys Met Ala Val Gly Phe Phe Gln Arg Gly Val
65                  70                  75                  80

Ala Asn Phe Gln Leu Ala Arg Phe Gln Glu Ala Leu Ser Asp Phe Trp
                85                  90                  95

Leu Ala Leu Glu Gln Leu Arg Gly His Ala Ala Ile Asp Tyr Thr Gln
            100                 105                 110

Leu Gly Leu Arg Phe Lys Leu Gln Ala Trp Glu Val Leu His Asn Val
        115                 120                 125

Ala Ser Ala Gln Cys Gln Leu Gly Leu Trp Thr Glu Ala Ala Ser Ser
    130                 135                 140

Leu Arg Glu Ala Met Ser Lys Trp Pro Glu Gly Ser Leu Asn Gly Leu
145                 150                 155                 160

Asp Ser Ala Leu Asp Gln Val Gln Arg Arg Gly Ser Leu Pro Pro Arg
                165                 170                 175
```

```
Gln Val Pro Arg Gly Glu Val Phe Arg Pro His Arg Trp His Leu Lys
            180                 185                 190

His Leu Glu Pro Val Asp Phe Leu Gly Lys Ala Lys Val Val Ala Ser
        195                 200                 205

Ala Ile Pro Asp Asp Gln Gly Trp Gly Val Arg Pro Gln Gln Pro Gln
    210                 215                 220

Gly Pro Gly Ala Asn His Asp Ala Arg Ser Leu Ile Met Asp Ser Pro
225                 230                 235                 240

Arg Ala Gly Thr His Gln Gly Pro Leu Asp Ala Glu Thr Glu Val Gly
                245                 250                 255

Ala Asp Arg Cys Thr Ser Thr Ala Tyr Gln Glu Gln Arg Pro Gln Val
            260                 265                 270

Glu Gln Val Gly Lys Gln Ala Pro Leu Ser Pro Gly Leu Pro Ala Met
        275                 280                 285

Gly Gly Pro Gly Pro Gly Pro Cys Glu Asp Pro Ala Gly Ala Gly Gly
    290                 295                 300

Ala Gly Ala Gly Gly Ser Glu Pro Leu Val Thr Val Thr Val Gln Cys
305                 310                 315                 320

Ala Phe Thr Val Ala Leu Arg Ala Arg Arg Gly Ala Asp Leu Ser Ser
                325                 330                 335

Leu Arg Ala Leu Leu Gly Gln Ala Leu Pro His Gln Ala Gln Leu Gly
            340                 345                 350

Gln Leu Ser Tyr Leu Ala Pro Gly Glu Asp Gly His Trp Val Pro Ile
        355                 360                 365

Pro Glu Glu Glu Ser Leu Gln Arg Ala Trp Gln Asp Ala Ala Ala Cys
    370                 375                 380

Pro Arg Gly Leu Gln Leu Gln Cys Arg Gly Ala Gly Gly Arg Pro Val
385                 390                 395                 400

Leu Tyr Gln Val Val Ala Gln His Ser Tyr Ser Ala Gln Gly Pro Glu
                405                 410                 415

Asp Leu Gly Phe Arg Gln Gly Asp Thr Val Asp Val Leu Cys Glu Glu
            420                 425                 430

Pro Asp Val Pro Leu Ala Val Asp Gln Ala Trp Leu Glu Gly His Cys
        435                 440                 445
```

```
Asp Gly Arg Ile Gly Ile Phe Pro Lys Cys Phe Val Val Pro Ala Gly
    450                 455                 460

Pro Arg Met Ser Gly Ala Pro Gly Arg Leu Pro Arg Ser Gln Gln Gly
465                 470                 475                 480

Asp Gln Pro
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<210> 224
<211> 193
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Description of sequence: amino acid sequence of Puma (human)

<400> 224

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Met Ala Arg Ala Arg Gln Glu Gly Ser Ser Pro Glu Pro Val Glu Gly
1               5                   10                  15

Leu Ala Arg Asp Gly Pro Arg Pro Phe Pro Leu Gly Arg Leu Val Pro
            20                  25                  30

Ser Ala Val Ser Cys Gly Leu Cys Glu Pro Gly Leu Ala Ala Ala Pro
        35                  40                  45

Ala Ala Pro Thr Leu Leu Pro Ala Ala Tyr Leu Cys Ala Pro Thr Ala
    50                  55                  60

Pro Pro Ala Val Thr Ala Ala Leu Gly Gly Ser Arg Trp Pro Gly Gly
65                  70                  75                  80

Pro Arg Ser Arg Pro Arg Gly Pro Arg Pro Asp Gly Pro Gln Pro Ser
                85                  90                  95

Leu Ser Leu Ala Glu Gln His Leu Glu Ser Pro Val Pro Ser Ala Pro
            100                 105                 110

Gly Ala Leu Ala Gly Gly Pro Thr Gln Ala Ala Pro Gly Val Arg Gly
        115                 120                 125

Glu Glu Glu Gln Trp Ala Arg Glu Ile Gly Ala Gln Leu Arg Arg Met
    130                 135                 140

Ala Asp Asp Leu Asn Ala Gln Tyr Glu Arg Arg Arg Gln Glu Glu Gln
145                 150                 155                 160

Gln Arg His Arg Pro Ser Pro Trp Arg Val Leu Tyr Asn Leu Ile Met
                165                 170                 175
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Gly Leu Leu Pro Leu Pro Arg Gly His Arg Ala Pro Glu Met Glu Pro
180 185 190

Asn

<210> 225
<211> 198
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Description of sequence: amino acid sequence of Bim (human) (transcript variant 1)

<400> 225

Met Ala Lys Gln Pro Ser Asp Val Ser Ser Glu Cys Asp Arg Glu Gly
1 5 10 15

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

Pro Thr Ser Leu Gln Thr Glu Pro Gln Gly Asn Pro Glu Gly Asn His
35 40 45

Gly Gly Glu Gly Asp Ser Cys Pro His Gly Ser Pro Gln Gly Pro Leu
50 55 60

Ala Pro Pro Ala Ser Pro Gly Pro Phe Ala Thr Arg Ser Pro Leu Phe
65 70 75 80

Ile Phe Met Arg Arg Ser Ser Leu Leu Ser Arg Ser Ser Ser Gly Tyr
85 90 95

Phe Ser Phe Asp Thr Asp Arg Ser Pro Ala Pro Met Ser Cys Asp Lys
100 105 110

Ser Thr Gln Thr Pro Ser Pro Pro Cys Gln Ala Phe Asn His Tyr Leu
115 120 125

Ser Ala Met Ala Ser Met Arg Gln Ala Glu Pro Ala Asp Met Arg Pro
130 135 140

Glu Ile Trp Ile Ala Gln Glu Leu Arg Arg Ile Gly Asp Glu Phe Asn
145 150 155 160

Ala Tyr Tyr Ala Arg Arg Val Phe Leu Asn Asn Tyr Gln Ala Ala Glu
165 170 175

Asp His Pro Arg Met Val Ile Leu Arg Leu Leu Arg Tyr Ile Val Arg
180 185 190

Leu Val Trp Arg Met His
195

<210> 226
<211> 160
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Description of sequence: amino acid sequence of Bik (human)

<400> 226

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

Leu Tyr Glu Gln Leu Leu Glu Pro Pro Thr Met Glu Val Leu Gly Met
20 25 30

Thr Asp Ser Glu Glu Asp Leu Asp Pro Met Glu Asp Phe Asp Ser Leu
35 40 45

Glu Cys Met Glu Gly Ser Asp Ala Leu Ala Leu Arg Leu Ala Cys Ile
50 55 60

Gly Asp Glu Met Asp Val Ser Leu Arg Ala Pro Arg Leu Ala Gln Leu
65 70 75 80

Ser Glu Val Ala Met His Ser Leu Gly Leu Ala Phe Ile Tyr Asp Gln
85 90 95

Thr Glu Asp Ile Arg Asp Val Leu Arg Ser Phe Met Asp Gly Phe Thr
100 105 110

Thr Leu Lys Glu Asn Ile Met Arg Phe Trp Arg Ser Pro Asn Pro Gly
115 120 125

Ser Trp Val Ser Cys Glu Gln Val Leu Leu Ala Leu Leu Leu Leu Leu
130 135 140

Ala Leu Leu Leu Pro Leu Leu Ser Gly Gly Leu His Leu Leu Leu Lys
145 150 155 160

<210> 227
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Description of sequence: native L-amino acid sequence of the BH3-domain of Bik (Bik BH3)

<400> 227

Ala Leu Ala Leu Arg Leu Ala Cys Ile Gly Asp Glu Met Asp Val Ser
1 5 10 15

Leu Arg

<210> 228
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Description of sequence: native L-amino acid sequence of the BH3-domain of Bad (Bad BH3)

<400> 228

Arg Tyr Gly Arg Glu Leu Arg Arg Met Ser Asp Glu Phe Val Asp Ser
1 5 10 15

Phe Lys

<210> 229
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Description of sequence: native L-amino acid sequence of the BH3-domain of Bid (Bid BH3)

<400> 229

Asn Ile Ala Arg His Leu Ala Gln Val Gly Asp Ser Met Asp Arg Ser
1 5 10 15

Ile Pro

<210> 230
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Description of sequence: native L-amino acid sequence of the BH3-domain of Bmf (Bmf BH3)

<400> 230

Gln Ile Ala Arg Lys Leu Gln Cys Ile Ala Asp Gln Phe His Arg Leu
1 5 10 15

His Val

<210> 231
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Description of sequence: native L-amino acid sequence of the BH3-domain of DP5/Hrk (DP5Hrk BH3)

<400> 231

Leu Thr Ala Ala Arg Leu Lys Ala Ile Gly Asp Glu Leu His Gln Arg
1 5 10 15

Thr Met

<210> 232
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Description of sequence: native L-amino acid sequence of the BH3-domain of Bim (Bim BH3)

<400> 232

Trp Ile Ala Gln Glu Leu Arg Arg Ile Gly Asp Glu Phe Asn Ala Tyr
1 5 10 15

Tyr Ala

<210> 233
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Description of sequence: native L-amino acid sequence of the BH3-domain of Noxa (Noxa BH3)

<400> 233

Glu Cys Ala Thr Gln Leu Arg Arg Phe Gly Asp Lys Leu Asn Phe Arg
1 5 10 15

Gln Lys

<210> 234
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Description of sequence: native L-amino acid sequence of the BH3-domain of PUMA (PUMA BH3)

<400> 234

Glu Ile Gly Ala Gln Leu Arg Arg Met Ala Asp Asp Leu Asn Ala Gln
1 5 10 15

Tyr Glu

<210> 235
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Description of sequence: native L-amino acid sequence of the BH3-domain of Bax (Bax BH3)

<400> 235

Lys Leu Ser Glu Cys Leu Lys Arg Ile Gly Asp Glu Leu Asp Ser Asn
1 5 10 15

Met Glu

<210> 236
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Description of sequence: native L-amino acid sequence of the BH3-domain of Bak (Bak BH3)

<400> 236

Gln Val Gly Arg Gln Leu Ala Ile Ile Gly Asp Asp Ile Asn Arg Arg
1 5 10 15

Tyr Asp

<210> 237
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Description of sequence: native L-amino acid sequence of the BH3-domain of Bok (Bok BH3)

<400> 237

Glu Val Cys Thr Val Leu Leu Arg Leu Gly Asp Glu Leu Glu Gln Ile
1 5 10 15

Arg Pro

<210> 238
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: signal sequence or localisation sequence

<400> 238

Lys Asp Glu Leu
1

<210> 239
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: signal sequence or localisation sequence

<400> 239

Asp Asp Glu Leu
1

<210> 240
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: signal sequence or localisation sequence

<400> 240

Asp Glu Glu Leu
1

<210> 241
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: signal sequence or localisation sequence

<400> 241

Gln Glu Asp Leu
1

<210> 242
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: signal sequence or localisation sequence

<400> 242

Arg Asp Glu Leu
1

<210> 243
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: signal sequence or localisation sequence

<400> 243

Pro Lys Lys Lys Arg Lys Val
1 5

<210> 244
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: signal sequence or localisation sequence

<400> 244

Pro Gln Lys Lys Ile Lys Ser
1 5

<210> 245
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: signal sequence or localisation sequence

<400> 245

Gln Pro Lys Lys Pro
1 5

<210> 246
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: signal sequence or localisation sequence

<400> 246

Arg Lys Lys Arg
1

<210> 247
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: signal sequence or localisation sequence

<400> 247

Arg Lys Lys Arg Arg Gln Arg Arg Arg Ala His Gln
1 5 10

<210> 248
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: signal sequence or localisation sequence

<400> 248

Arg Gln Ala Arg Arg Asn Arg Arg Arg Arg Trp Arg Glu Arg Gln Arg
1 5 10 15

<210> 249
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: signal sequence or localisation sequence

<400> 249

Met Pro Leu Thr Arg Arg Arg Pro Ala Ala Ser Gln Ala Leu Ala Pro
1 5 10 15

Pro Thr Pro

<210> 250
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of sequence: signal sequence or localisation sequence

<400> 250

Met Asp Asp Gln Arg Asp Leu Ile Ser Asn Asn Glu Gln Leu Pro
1 5 10 15

<210> 251

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

<220>
<223> Description of artificial sequence: D-TAT

<220>
<221> VARIANT
<222> (1)..(9)
<223> all amino acids are D-enantiomeric amino acids

<400> 251

Arg Arg Arg Gln Arg Arg Lys Lys Arg
1 5

<210> 252
<211> 9
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: consensus sequence rXXXrXXXr

<220>
<221> misc_feature
<222> (1)..(1)
<223> Arg is D-enantiomeric Arg

<220>
<221> misc_feature
<222> (2)..(4)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (5)..(5)
<223> Arg is D-enantiomeric Arg

<220>
<221> misc_feature
<222> (6)..(8)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (9)..(9)
<223> Arg is D-enantiomeric Arg

<400> 252

Arg Xaa Xaa Xaa Arg Xaa Xaa Xaa Arg
1 5

<210> 253
<211> 5
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: Conserved sequence motif
Trp-Ser-X-Trp-Ser/cytokines of class I of the family of cytokines

<220>
<221> misc_feature
<222> (3)..(3)
<223> Xaa can be any naturally occurring amino acid

<400> 253

Trp Ser Xaa Trp Ser
1 5

<210> 254
<211> 4
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: Positionally conserved cystein residues cytokines of class I of the family of cytokines

<400> 254

Cys Cys Cys Cys
1

<210> 255
<211> 5
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: Peptidic linker sequence

<400> 255

Gly Gly Gly Gly Gly
1 5

<210> 256
<211> 4
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: Peptidic linker sequence

<400> 256

Gly Gly Gly Gly
1

<210> 257
<211> 9
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: all D transporter construct (all amino acid residues are D-amino acids)

<400> 257

Arg Arg Arg Arg Arg Arg Arg Arg Arg
1 5

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

<220>
<223> Description of sequence: D/L transporter construct (D and L amino acid residues alternate, beginning wit D amino acids)

<400> 258

Arg Arg Arg Arg Arg Arg Arg Arg Arg
1 5

<210> 259
<211> 9
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: DD/LL transporter construct

<400> 259

Arg Arg Arg Arg Arg Arg Arg Arg Arg
1 5

<210> 260
<211> 9
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: DDD/LLL (r6R3) transporter construct

<400> 260

Arg Arg Arg Arg Arg Arg Arg Arg Arg
1 5

<210> 261
<211> 9
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: DDDD/LLLL transporter construct

<400> 261

Arg Arg Arg Arg Arg Arg Arg Arg Arg
1 5

<210> 262
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Description of sequence: AP-1 doubled labeled probe

<400> 262

cgcttgatga gtcagccgga a 21