

2009006763
SEQUENCE LISTING

<110> xigen S.A.

<120> Use of cell-permeable peptide inhibitors of the JNK signal transduction pathway for the treatment of various diseases

<130> CX01P022W01

<160> 105

<170> PatentIn version 3.3

<210> 1

<211> 19

<212> PRT

<213> Artificial

<220>

<223> Description of sequence: Peptide L-IB1(s) (see Table 1)

<400> 1

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

Ser Gln Asp

<210> 2

<211> 19

<212> PRT

<213> Artificial

<220>

<223> Description of sequence: Peptide D-IB1(s) (see Table 1)

<220>

<221> MUTAGEN

<222> (1)..(19)

<223> all amino acids are D-amino acids

<400> 2

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

Lys Pro Arg

<210> 3

<211> 19

<212> PRT

<213> Artificial

<220>

<223> Description of sequence: Peptide L-IB (generic) (s) (see Table 1)

<220>

<221> misc_feature

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

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<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 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>
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<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> 3

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

Gln Asp Xaa

<210> 4
<211> 19
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: Peptide D-IB (generic) (s) (see Table 1)
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<220>
 <221> misc_feature
 <223> Description of sequence: general formula:
 NH₂-Xnb-DQXXXXXXXXLXLTPR-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 except serine and Threonine

<220>
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 <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 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> 4

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

Arg Xaa Xaa

<210> 5
 <211> 10
 <212> PRT
 <213> Artificial

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

<400> 5

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

<210> 6
 <211> 10
 <212> PRT
 <213> Artificial

<220>
 <223> Description of sequence: Peptide D-TAT (see Table 1)

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

<400> 6

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

<210> 7
 <211> 11
 <212> PRT
 <213> Artificial

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

<220>
 <221> misc_feature
 <223> General formula: NH₂-Xnb-RKKRRQRRR-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)

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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

<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

<222> (11)..(11)

<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> 7

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

<210> 8

<211> 11

<212> PRT

<213> Artificial

<220>

<223> Description of sequence: Peptide D-generic-TAT (s) (see Table 1)

<220>

<221> misc_feature

<223> General formula: NH₂-Xnb-RRRQRRKKR-Xnb-COOH

<220>

<221> MUTAGEN

<222> (1)..(10)

<223> all amino acids are D-amino acids

<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

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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

<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

<222> (11)..(11)

<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> 8

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

<210> 9
<211> 31
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-TAT-IB1 (s) (see Table 1)
<400> 9

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

Pro Thr Thr Leu Asn Leu Phe Pro Gln Val Pro Arg Ser Gln Asp
20 25 30

<210> 10
<211> 29
<212> PRT
<213> Artificial

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

<220>
<221> misc_feature
<223> Description of sequence: General formula:
NH2-Xnb-RKKRRQRRR-Xnb-Xna-RPTTLXLXXXXXXXXXQD-Xnb-COOH

<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>
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<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
<222> (11)..(11)
<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> (12)..(12)
<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 except serine and Threonine

<220>
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 <222> (12)..(12)
 <223> Xaa is Xna as defined in the general formula, wherein n is 0 or 1

<220>
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 <222> (18)..(18)
 <223> Xaa represents an amino acid residue, preferably selected from any (native) amino acid residue;

<220>
 <221> VARIANT
 <222> (20)..(26)
 <223> Xaa represents an amino acid residue, preferably selected from any (native) amino acid residue;

<220>
 <221> VARIANT
 <222> (29)..(29)
 <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> (29)..(29)
 <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> 10

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

Leu Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Gln Asp Xaa
 20 25

<210> 11
 <211> 31
 <212> PRT
 <213> Artificial

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

<220>
 <221> MUTAGEN
 <222> (1)..(31)
 <223> all amino acids are D-amino acids

<400> 11

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

Lys Pro Arg Pro Pro Arg Arg Arg Gln Arg Arg Lys Lys Arg Gly
 20 25 30

<210> 12
 <211> 29

<212> PRT
 <213> Artificial

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

<220>
 <221> misc_feature
 <223> General formula:
 NH₂-Xnb-DQXXXXXXXXLXLTPR-Xna-Xnb-RRRQRRKKR-Xnb-COOH,

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

<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> (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> 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 except serine and threonine

<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> (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;

<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

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<220>
<221> VARIANT
<222> (29)..(29)
<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> (29)..(29)
<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> 12

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

Arg Xaa Xaa Arg Arg Arg Gln Arg Arg Lys Lys Arg Xaa
20 25

<210> 13
<211> 29
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: peptide IB1-long (see Table 1)

<400> 13

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> 14
<211> 27
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: Peptide IB2-long (see Table 1)

<400> 14

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> 15
<211> 29
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: Peptide derived from c-Jun (see Table 1)

<400> 15

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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> 16
<211> 29
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: Peptide derived from ATF2 (see Table 1)

<400> 16

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> 17
<211> 23
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: Peptide L-IB1 (see Table 1)

<400> 17

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> 18
<211> 23
<212> PRT
<213> Artificial

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

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

<400> 18

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

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

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

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<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> 19

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

Asp Xaa Xaa

<210> 20
<211> 19
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: Peptide D-IB (generic) (see Table 1)

<220>
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<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

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<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> 20

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

Pro Arg Xaa

<210> 21
<211> 17
<212> PRT
<213> Artificial

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

<220>
<221> VARIANT
<222> (1)..(17)
<223> Xaa is selected from any amino acid residue

<400> 21

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

Xaa

<210> 22
<211> 17
<212> PRT
<213> Artificial

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

<220>
<221> MUTAGEN
<222> (1)..(17)
<223> all amino acids are D-amino acids

<220>
<221> VARIANT
<222> (1)..(17)
<223> Xaa is selected from any amino acid residue

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<400> 22

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

Xaa

<210> 23

<211> 35

<212> PRT

<213> Artificial

<220>

<223> Description of sequence: Peptide L-TAT-IB1 (see Table 1)

<400> 23

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

Pro Lys Arg Pro Thr Thr Leu Asn Leu Phe Pro Gln Val Pro Arg Ser
20 25 30

Gln Asp Thr
35

<210> 24

<211> 42

<212> PRT

<213> Artificial

<220>

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

<220>

<221> VARIANT

<222> (1)..(40)

<223> Xaa is selected from any amino acid residue

<220>

<221> VARIANT

<222> (41)..(41)

<223> Xaa is selected from serine or threonine

<220>

<221> VARIANT

<222> (42)..(42)

<223> Xaa is selected from any amino acid residue

<400> 24

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

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Pro Thr Thr Leu Xaa Leu Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Gln Asp Xaa Xaa

35

40

<210> 25
 <211> 35
 <212> PRT
 <213> Artificial

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

<220>
 <221> MUTAGEN
 <222> (1)..(35)
 <223> all amino acids are D-amino acids

<400> 25

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 Pro Pro Arg Arg Arg Gln Arg Arg Lys
 20 25 30

Lys Arg Gly
 35

<210> 26
 <211> 42
 <212> PRT
 <213> Artificial

<220>
 <223> Description of sequence: Peptide D-TAT IB (generic) (see Table 1)

<220>
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 <222> (1)..(42)
 <223> all amino acids are D-amino acids

<220>
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 <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> (3)..(42)
 <223> Xaa is selected from any amino acid residue

<400> 26

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

Pro Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Arg Arg Gln Arg Arg
 20 25 30

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Lys Lys Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40

<210> 27
<211> 30
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: chimeric peptide sequence L-TAT-IB1(s1)
(see Table 1)

<400> 27

Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Arg Pro Lys Arg Pro
1 5 10 15

Thr Thr Leu Asn Leu Phe Pro Gln Val Pro Arg Ser Gln Asp
20 25 30

<210> 28
<211> 30
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: chimeric peptide sequence L-TAT-IB1(s2)
(see Table 1)

<220>
<221> VARIANT
<222> (11)..(11)
<223> Xaa is selected from glycine or proline

<220>
<221> REPEAT
<222> (11)..(11)
<223> Xaa is Xnc as defined in the general formula, wherein n is 0-5,
5-10, 10-15, 15-20, 20-30 or more for Xnc

<400> 28

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

Thr Thr Leu Asn Leu Phe Pro Gln Val Pro Arg Ser Gln Asp
20 25 30

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

<220>
<223> Description of sequence: chimeric peptide sequence L-TAT-IB1(s3)
(see Table 1)

<220>
<221> VARIANT

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<222> (10)..(10)

<223> xaa is selected from glycine or proline

<220>

<221> REPEAT

<222> (10)..(10)

<223> xaa is Xnc as defined in the general formula, wherein n is 0-5, 5-10, 10-15, 15-20, 20-30 or more for Xnc

<400> 29

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

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

<210> 30

<211> 30

<212> PRT

<213> Artificial

<220>

<223> Description of sequence: chimeric peptide sequence D-TAT-IB1(s1)
(see Table 1)

<220>

<221> MUTAGEN

<222> (1)..(30)

<223> all amino acids are D-amino acids

<400> 30

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

Lys Pro Arg Pro Pro Arg Arg Arg Gln Arg Arg Lys Lys Arg
20 25 30

<210> 31

<211> 30

<212> PRT

<213> Artificial

<220>

<223> Description of sequence: chimeric peptide sequence D-TAT-IB1(s2)
(see Table 1)

<220>

<221> MUTAGEN

<222> (1)..(30)

<223> all amino acids are D-amino acids

<220>

<221> VARIANT

<222> (20)..(20)

<223> xaa is selected from glycine or proline

<220>

<221> REPEAT

<222> (20)..(20)

<223> xaa is Xnc as defined in the general formula, wherein n is 0-5,
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5-10, 10-15, 15-20, 20-30 or more for Xnc

<400> 31

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

Lys Pro Arg Xaa Arg Arg Arg Gln Arg Arg Lys Lys Arg Gly
20 25 30

<210> 32

<211> 29

<212> PRT

<213> Artificial

<220>

<223> Description of sequence: chimeric peptide sequence D-TAT-IB1(s3)
(see Table 1)

<220>

<221> MUTAGEN

<222> (1)..(29)

<223> all amino acids are D-amino acids

<220>

<221> VARIANT

<222> (20)..(20)

<223> Xaa is selected from glycine or proline

<220>

<221> REPEAT

<222> (20)..(20)

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

<400> 32

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

Lys Pro Arg Xaa Arg Arg Arg Gln Arg Arg Lys Lys Arg
20 25

<210> 33

<211> 13

<212> PRT

<213> Artificial

<220>

<223> Description of sequence: L-IB1(s1) (see Table 1)

<400> 33

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

<210> 34

<211> 13

<212> PRT

<213> Artificial

<220>

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<223> Description of sequence: L-IB1(s2) (see Table 1)

<400> 34

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

<210> 35

<211> 13

<212> PRT

<213> Artificial

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<223> Description of sequence: L-IB1(s3) (see Table 1)

<400> 35

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

<210> 36

<211> 13

<212> PRT

<213> Artificial

<220>

<223> Description of sequence: L-IB1(s4) (see Table 1)

<400> 36

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

<210> 37

<211> 13

<212> PRT

<213> Artificial

<220>

<223> Description of sequence: L-IB1(s5) (see Table 1)

<400> 37

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

<210> 38

<211> 13

<212> PRT

<213> Artificial

<220>

<223> Description of sequence: L-IB1(s6) (see Table 1)

<400> 38

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

<210> 39

<211> 13

<212> PRT

<213> Artificial

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<220>

<223> Description of sequence: L-IB1(s7) (see Table 1)

<400> 39

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

<210> 40

<211> 12

<212> PRT

<213> Artificial

<220>

<223> Description of sequence: L-IB1(s8) (see Table 1)

<400> 40

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

<210> 41

<211> 12

<212> PRT

<213> Artificial

<220>

<223> Description of sequence: L-IB1(s9) (see Table 1)

<400> 41

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

<210> 42

<211> 12

<212> PRT

<213> Artificial

<220>

<223> Description of sequence: L-IB1(s10) (see Table 1)

<400> 42

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

<210> 43

<211> 12

<212> PRT

<213> Artificial

<220>

<223> Description of sequence: L-IB1(s11) (see Table 1)

<400> 43

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

<210> 44

<211> 12

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<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s12) (see Table 1)

<400> 44

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

<210> 45
<211> 12
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s13) (see Table 1)

<400> 45

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

<210> 46
<211> 12
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s14) (see Table 1)

<400> 46

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

<210> 47
<211> 12
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s15) (see Table 1)

<400> 47

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

<210> 48
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s16) (see Table 1)

<400> 48

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

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<210> 49
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s17) (see Table 1)

<400> 49

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

<210> 50
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s18) (see Table 1)

<400> 50

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

<210> 51
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s19) (see Table 1)

<400> 51

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

<210> 52
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s20) (see Table 1)

<400> 52

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

<210> 53
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s21) (see Table 1)

<400> 53

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

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<210> 54
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s22) (see Table 1)

<400> 54

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

<210> 55
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s23) (see Table 1)

<400> 55

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

<210> 56
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s24) (see Table 1)

<400> 56

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

<210> 57
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: L-IB1(s25) (see Table 1)

<400> 57

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

<210> 58
<211> 10
<212> PRT
<213> Artificial

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

<400> 58

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

<210> 59
 <211> 10
 <212> PRT
 <213> Artificial

<220>
 <223> Description of sequence: L-IB1(s27) (see Table 1)

<400> 59

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

<210> 60
 <211> 10
 <212> PRT
 <213> Artificial

<220>
 <223> Description of sequence: L-IB1(s28) (see Table 1)

<400> 60

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

<210> 61
 <211> 10
 <212> PRT
 <213> Artificial

<220>
 <223> Description of sequence: L-IB1(s29) (see Table 1)

<400> 61

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

<210> 62
 <211> 10
 <212> PRT
 <213> Artificial

<220>
 <223> Description of sequence: L-IB1(s30) (see Table 1)

<400> 62

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

<210> 63
 <211> 10
 <212> PRT
 <213> Artificial

<220>
 <223> Description of sequence: L-IB1(s31) (see Table 1)

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<400> 63

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

<210> 64

<211> 10

<212> PRT

<213> Artificial

<220>

<223> Description of sequence: L-IB1(s32) (see Table 1)

<400> 64

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

<210> 65

<211> 10

<212> PRT

<213> Artificial

<220>

<223> Description of sequence: L-IB1(s33) (see Table 1)

<400> 65

Pro Lys Arg Pro Thr Thr Leu Asn Leu Phe
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<210> 66

<211> 10

<212> PRT

<213> Artificial

<220>

<223> Description of sequence: L-IB1(s34) (see Table 1)

<400> 66

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

<210> 67

<211> 13

<212> PRT

<213> Artificial

<220>

<223> Description of sequence: D-IB1(s1) (see Table 1)

<220>

<221> MUTAGEN

<222> (1)..(13)

<223> all amino acids are D-amino acids

<400> 67

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

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<210> 68
<211> 13
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s2) (see Table 1)

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

<400> 68

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

<210> 69
<211> 13
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s3) (see Table 1)

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

<400> 69

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

<210> 70
<211> 13
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s4) (see Table 1)

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

<400> 70

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

<210> 71
<211> 13
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s5) (see Table 1)

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

<400> 71

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

<210> 72
<211> 13
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s6) (see Table 1)

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

<400> 72

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

<210> 73
<211> 13
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s7) (see Table 1)

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

<400> 73

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

<210> 74
<211> 12
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s8) (see Table 1)

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

<400> 74

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

<210> 75
<211> 12
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s9) (see Table 1)

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<222> (1)..(12)
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<400> 75

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

<210> 76
<211> 12
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s10) (see Table 1)

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

<400> 76

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

<210> 77
<211> 12
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s11) (see Table 1)

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

<400> 77

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

<210> 78
<211> 12
<212> PRT
<213> Artificial

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<220>
<223> Description of sequence: D-IB1(s12) (see Table 1)

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

<400> 78

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

<210> 79
<211> 12
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s13) (see Table 1)

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

<400> 79

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

<210> 80
<211> 12
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s14) (see Table 1)

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

<400> 80

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

<210> 81
<211> 12
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s15) (see Table 1)

<220>
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<222> (1)..(12)

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<223> all amino acids are D-amino acids

<400> 81

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

<210> 82

<211> 11

<212> PRT

<213> Artificial

<220>

<223> Description of sequence: D-IB1(s16) (see Table 1)

<220>

<221> MUTAGEN

<222> (1)..(11)

<223> all amino acids are D-amino acids

<400> 82

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

<210> 83

<211> 11

<212> PRT

<213> Artificial

<220>

<223> Description of sequence: D-IB1(s17) (see Table 1)

<220>

<221> MUTAGEN

<222> (1)..(11)

<223> all amino acids are D-amino acids

<400> 83

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

<210> 84

<211> 11

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<220>

<223> Description of sequence: D-IB1(s18) (see Table 1)

<220>

<221> MUTAGEN

<222> (1)..(11)

<223> all amino acids are D-amino acids

<400> 84

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

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<210> 85
<211> 11
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<213> Artificial

<220>
<223> Description of sequence: D-IB1(s19) (see Table 1)

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

<400> 85

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

<210> 86
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s20) (see Table 1)

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

<400> 86

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

<210> 87
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s21) (see Table 1)

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

<400> 87

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

<210> 88
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s22) (see Table 1)

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

<400> 88

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

<210> 89
 <211> 11
 <212> PRT
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<220>
 <223> Description of sequence: D-IB1(s23) (see Table 1)

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

<400> 89

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

<210> 90
 <211> 11
 <212> PRT
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<220>
 <223> Description of sequence: D-IB1(s24) (see Table 1)

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

<400> 90

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

<210> 91
 <211> 10
 <212> PRT
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<220>
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 <222> (1)..(10)
 <223> all amino acids are D-amino acids

<400> 91

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

<210> 92
<211> 10
<212> PRT
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<220>
<223> Description of sequence: D-IB1(s26) (see Table 1)

<220>
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<223> all amino acids are D-amino acids

<400> 92

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

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<211> 10
<212> PRT
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<220>
<223> Description of sequence: D-IB1(s27) (see Table 1)

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

<400> 93

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

<210> 94
<211> 10
<212> PRT
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<220>
<223> Description of sequence: D-IB1(s28) (see Table 1)

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

<400> 94

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

<210> 95
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s29) (see Table 1)

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

<400> 95

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

<210> 96
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s30) (see Table 1)

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

<400> 96

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

<210> 97
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s31) (see Table 1)

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

<400> 97

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

<210> 98
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Description of sequence: D-IB1(s32) (see Table 1)

<220>
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<222> (1)..(10)

<223> all amino acids are D-amino acids

<400> 98

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

<210> 99

<211> 10

<212> PRT

<213> Artificial

<220>

<223> Description of sequence: D-IB1(s33) (see Table 1)

<220>

<221> MUTAGEN

<222> (1)..(10)

<223> all amino acids are D-amino acids

<400> 99

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

<210> 100

<211> 10

<212> PRT

<213> Artificial

<220>

<223> Description of sequence: D-IB1(s34) (see Table 1)

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<221> MUTAGEN

<222> (1)..(10)

<223> all amino acids are D-amino acids

<400> 100

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

<210> 101

<211> 21

<212> DNA

<213> Artificial

<220>

<223> Description of sequence: ap-1 doubled labeled probe (see p. 66)

<400> 101

cgcttgatga gtcagccgga a

21

<210> 102

<211> 2953

<212> DNA

<213> Artificial

<220>

<223> description of sequence: rat IB1 cDNA sequence and its predicted
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amino acid sequence (see Figure 1)

<220>
<221> CDS
<222> (108)..(2252)

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cgccgcccgc gccgcccgc ccgcctcccc cgccgctctc cgcccgg atg gcc agg      116
                                   Met Ala Arg
                                   1

ctg agc ccg gga atg gcg gag cga gag agc ggc ctg agc ggg ggt gcc      164
Leu Ser Pro Gly Met Ala Glu Arg Glu Ser Gly Leu Ser Gly Gly Ala
5                               10                               15

gcg tcc cca ccg gcc gct tcc cca ttc ctg gga ctg cac atc gcg tcg      212
Ala Ser Pro Pro Ala Ala Ser Pro Phe Leu Gly Leu His Ile Ala Ser
20                               25                               30                               35

cct ccc aat ttc agg ctc acc cat gat atc agc ctg gag gag ttt gag      260
Pro Pro Asn Phe Arg Leu Thr His Asp Ile Ser Leu Glu Glu Phe Glu
40                               45                               50

gat gaa gac ctt tcg gag atc act gat gag tgt ggc atc agc ctg cag      308
Asp Glu Asp Leu Ser Glu Ile Thr Asp Glu Cys Gly Ile Ser Leu Gln
55                               60                               65

tgc aaa gac acc ttg tct ctc cgg ccc ccg cgc gcc ggg cta ctg tct      356
Cys Lys Asp Thr Leu Ser Leu Arg Pro Pro Arg Ala Gly Leu Leu Ser
70                               75                               80

gcg ggt agc agc ggt agc gcg ggg agc cgg ctg cag gcg gag atg ctg      404
Ala Gly Ser Ser Gly Ser Ala Gly Ser Arg Leu Gln Ala Glu Met Leu
85                               90                               95

cag atg gac ctg atc gac gcg gca agt gac act ccg ggc gcc gag gac      452
Gln Met Asp Leu Ile Asp Ala Ala Ser Asp Thr Pro Gly Ala Glu Asp
100                               105                               110                               115

gac gaa gag gac gac gac gag ctc gct gcc caa cgg cca gga gtg ggg      500
Asp Glu Glu Asp Asp Asp Glu Leu Ala Ala Gln Arg Pro Gly Val Gly
120                               125                               130

cct tcc aaa gcc gag tct ggc cag gag ccg gcg tct cgc agc cag ggt      548
Pro Ser Lys Ala Glu Ser Gly Gln Glu Pro Ala Ser Arg Ser Gln Gly
135                               140                               145

cag ggc cag ggc ccc ggc aca ggc tgc gga gac acc tac cgg ccc aag      596
Gln Gly Gln Gly Pro Gly Thr Gly Cys Gly Asp Thr Tyr Arg Pro Lys
150                               155                               160

agg cct acc acg ctc aac ctt ttc ccg cag gtg ccg cgg tct cag gac      644
Arg Pro Thr Thr Leu Asn Leu Phe Pro Gln Val Pro Arg Ser Gln Asp
165                               170                               175

acg ctg aat aat aac tct tta ggc aaa aag cac agt tgg cag gac cgt      692
Thr Leu Asn Asn Asn Ser Leu Gly Lys Lys His Ser Trp Gln Asp Arg
180                               185                               190                               195

gtg tct cga tca tcc tcc cct ctg aag aca ggg gag cag acg cct cca      740
Val Ser Arg Ser Ser Ser Pro Leu Lys Thr Gly Glu Gln Thr Pro Pro
200                               205                               210

cat gaa cat atc tgc ctg agt gat gag ctg ccg ccc cag ggc agt cct      788
His Glu His Ile Cys Leu Ser Asp Glu Leu Pro Pro Gln Gly Ser Pro
215                               220                               225

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gtt Val	ccc Pro	acc Thr 230	cag Gln	gat Asp	cgt Arg	ggc Gly	act Thr 235	tcc Ser	acc Thr	gac Asp	agc Ser	cct Pro 240	tgt Cys	cgc Arg	cgt Arg	836
act Thr	gca Ala 245	gcc Ala	acc Thr	cag Gln	atg Met	gca Ala 250	cct Pro	cca Pro	agt Ser	ggg Gly	ccc Pro 255	cct Pro	gcc Ala	act Thr	gca Ala	884
cct Pro 260	ggg Gly	ggc Gly	cgg Arg	ggc Gly	cac His 265	tcc Ser	cat His	cga Arg	gat Asp	cgg Arg 270	tcc Ser	ata Ile	tca Ser	gca Ala	gat Asp 275	932
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ccc Pro	cca Pro	gac Asp	cct Pro 295	gca Ala	gaa Glu	ccc Pro	acc Thr	tcc Ser 300	acc Thr	ttc Phe	ttg Leu	cca Pro	ccc Pro 305	act Thr	gag Glu	1028
agc Ser	cgg Arg	atg Met 310	tct Ser	gtc Val	agc Ser	tcg Ser	gat Asp 315	cct Pro	gac Asp	cct Pro	gcc Ala	gct Ala 320	tac Tyr	tct Ser	gta Val	1076
act Thr	gca Ala 325	ggg Gly	cga Arg	ccg Pro	cac His	cct Pro 330	tcc Ser	atc Ile	agt Ser	gaa Glu	gag Glu 335	gat Asp	gag Glu	ggc Gly	ttc Phe	1124
gac Asp 340	tgt Cys	ctg Leu	tca Ser	tcc Ser	cca Pro 345	gag Glu	caa Gln	gct Ala	gag Glu	cca Pro 350	cca Pro	ggg Gly	gga Gly	ggg Gly	tgg Trp 355	1172
cgg Arg	gga Gly	agc Ser	ctc Leu	ggg Gly 360	gag Glu	cca Pro	cca Pro	ccg Pro	cct Pro 365	cca Pro	cgg Arg	gcc Ala	tca Ser	ctg Leu 370	agc Ser	1220
tcg Ser	gac Asp	acc Thr	agc Ser 375	gca Ala	ctg Leu	tcc Ser	tac Tyr	gac Asp 380	tct Ser	gtc Val	aag Lys	tac Tyr	aca Thr 385	ctg Leu	gtg Val	1268
gtg Val	gat Asp	gag Glu 390	cat His	gcc Ala	cag Gln	ctt Leu	gag Glu 395	ttg Leu	gtg Val	agc Ser	ctg Leu	cgg Arg 400	cca Pro	tgt Cys	ttt Phe	1316
gga Gly 405	gat Asp	tac Tyr	agt Ser	gac Asp	gaa Glu	agc Ser 410	gac Asp	tct Ser	gcc Ala	act Thr	gtc Val 415	tat Tyr	gac Asp	aac Asn	tgt Cys	1364
gcc Ala 420	tct Ser	gcc Ala	tcc Ser	tcg Ser	ccc Pro 425	tac Tyr	gag Glu	tca Ser	gcc Ala	att Ile 430	ggg Gly	gag Glu	gaa Glu	tat Tyr	gag Glu 435	1412
gag Glu	gcc Ala	cct Pro	caa Gln	ccc Pro 440	cgg Arg	cct Pro	ccc Pro	acc Thr	tgc Cys 445	ctg Leu	tca Ser	gag Glu	gac Asp	tcc Ser 450	aca Thr	1460
ccg Pro	gat Asp	gag Glu	cct Pro 455	gac Asp	gtc Val	cac His	ttc Phe	tct Ser 460	aag Lys	aag Lys	ttt Phe	ctg Leu	aat Asn 465	gtc Val	ttc Phe	1508
atg Met	agt Ser	ggc Gly 470	cgc Arg	tct Ser	cgt Arg	tcc Ser	tcc Ser 475	agt Ser	gcc Ala	gag Glu	tcc Ser	ttt Phe 480	ggg Gly	ctg Leu	ttc Phe	1556
tcc Ser	tgt Cys 485	gtc Val	atc Ile	aat Asn	ggg Gly	gag Glu 490	gag Glu	cat His	gag Glu	caa Gln	acc Thr 495	cat His	cgg Arg	gct Ala	ata Ile	1604

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ttc agg ttt gtg cct cgg cat gaa gat gaa ctt gag ctg gaa gtg gac Phe Arg Phe Val Pro Arg His Glu Asp Glu Leu Glu Leu Glu Val Asp 500 505 510 515	1652
gac cct ctg ctg gtg gag ctg cag gca gaa gac tat tgg tat gag gcc Asp Pro Leu Leu Val Glu Leu Gln Ala Glu Asp Tyr Trp Tyr Glu Ala 520 525 530	1700
tat aac atg cgc act gga gcc cgt ggt gtc ttt cct gcc tac tat gcc Tyr Asn Met Arg Thr Gly Ala Arg Gly Val Phe Pro Ala Tyr Tyr Ala 535 540 545	1748
att gag gtc acc aag gag cct gag cac atg gca gcc ctt gcc aaa aac Ile Glu Val Thr Lys Glu Pro Glu His Met Ala Ala Leu Ala Lys Asn 550 555 560	1796
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gtt cct tat cac aag ggc aat gat gtc ctc tgt gct gct atg caa aag Val Pro Tyr His Lys Gly Asn Asp Val Leu Cys Ala Ala Met Gln Lys 580 585 590 595	1892
atc gcc acc acc cgc cgg ctc acc gtg cac ttt aac ccg ccc tcc agc Ile Ala Thr Thr Arg Arg Leu Thr Val His Phe Asn Pro Pro Ser Ser 600 605 610	1940
tgt gtc ctt gaa atc agc gtt agg ggt gtc aag ata ggt gtc aaa gct Cys Val Leu Glu Ile Ser Val Arg Gly Val Lys Ile Gly Val Lys Ala 615 620 625	1988
gat gaa gct cag gag gcc aag gga aat aaa tgt agc cac ttt ttc cag Asp Glu Ala Gln Glu Ala Lys Gly Asn Lys Cys Ser His Phe Phe Gln 630 635 640	2036
cta aaa aac atc tct ttc tgt ggg tac cat cca aag aac aac aag tac Leu Lys Asn Ile Ser Phe Cys Gly Tyr His Pro Lys Asn Asn Lys Tyr 645 650 655	2084
ttt ggg ttt atc act aag cac cct gct gac cac cgg ttt gcc tgc cat Phe Gly Phe Ile Thr Lys His Pro Ala Asp His Arg Phe Ala Cys His 660 665 670 675	2132
gtc ttt gtg tct gaa gat tcc acc aaa gcc ctg gca gag tct gtg ggg Val Phe Val Ser Glu Asp Ser Thr Lys Ala Leu Ala Glu Ser Val Gly 680 685 690	2180
cgt gca ttt cag cag ttc tac aag caa ttt gtg gaa tat acc tgt cct Arg Ala Phe Gln Gln Phe Tyr Lys Gln Phe Val Glu Tyr Thr Cys Pro 695 700 705	2228
aca gaa gat atc tac ttg gag tag cagcaacccc cctctctgca gcccctcagc Thr Glu Asp Ile Tyr Leu Glu 710	2282
cccaggccag tactaggaca gctgactgct gacaggatgt tgtactgcca cgagagaatg	2342
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<210> 103
 <211> 714
 <212> PRT
 <213> Artificial

<220>
 <223> description of sequence: Protein encoded by Exon-Intron Boundary
 of the rIB1 Gene - Splice donor

<400> 103

Met Ala Arg Leu Ser Pro Gly Met Ala Glu Arg Glu Ser Gly Leu Ser
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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 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

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

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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

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

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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

Thr Cys Pro Thr Glu Asp Ile Tyr Leu Glu
705 710

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<210> 104
<211> 711
<212> PRT
<213> Homo sapiens

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

<400> 104

Met Ala Glu Arg Glu Ser Gly Gly Leu Gly Gly Gly Ala Ala Ser Pro
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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

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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 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

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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

<210> 105
<211> 2136
<212> DNA
<213> Homo sapiens

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

<400> 105

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