

2015007907
SEQUENCE LISTING

<110> Xigen Inflammation Ltd.
<120> Use of cell-permeable peptide inhibitors of the JNK signal transduction pathway for the treatment of various diseases
<130> CX01P048W01
<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-RPTTLXLLLLXXXXXQD-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 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> 3

Xaa	Xaa	Arg	Pro	Thr	Thr	Leu	Xaa	Leu	Xaa	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)

<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>
 <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> (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 Xaa Leu Xaa Leu Thr Thr Pro

2015007907

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)

<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

<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

<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

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-RPTTLXLXXXXXXQD-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>
 <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

<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>
 <221> REPEAT
 <222> (12)..(12)
 <223> Xaa is Xna as defined in the general formula, wherein n is 0 or 1

<220>

2015007907

<221> VARIANT
<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	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

<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

2015007907

<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

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

2015007907

<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

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

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

<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> 19

Xaa	Arg	Pro	Thr	Thr	Leu	Xaa	Leu	Xaa	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>

<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> 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>

2015007907

<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

<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

2015007907

<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>
 <221> MUTAGEN
 <222> (1)..(42)
 <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

2015007907

<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		

Lys	Lys	Arg	Xaa	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>

2015007907

<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
<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

2015007907

<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,
5-10, 10-15, 15-20, 20-30 or more for Xnc

<400> 31

2015007907

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)

2015007907

<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>

<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

<220>

<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

<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		

2015007907

<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
<212> PRT
<213> Artificial

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

<400> 44

2015007907

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>

2015007907

<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	

<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

2015007907

<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	

<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)

<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
1				5				10	

<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	

2015007907

<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

<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)

2015007907

<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)

<220>

<221> MUTAGEN

<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

2015007907

<220>

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

<220>

<221> MUTAGEN

<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>

<221> MUTAGEN

<222> (1)..(12)

<223> all amino acids are D-amino acids

<400> 74

2015007907

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)

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

<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)

2015007907

<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

<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

2015007907

<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>
<221> MUTAGEN
<222> (1)..(12)
<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)

2015007907

<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

<212> PRT

<213> Artificial

<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

<210> 85

<211> 11

<212> PRT

<213> Artificial

2015007907

<220>

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

<220>

<221> MUTAGEN

<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)

<220>

<221> MUTAGEN

<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)

<220>

<221> MUTAGEN

<222> (1)..(11)

<223> all amino acids are D-amino acids

<400> 87

2015007907

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)

<220>
<221> MUTAGEN
<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
<213> Artificial

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

<220>
<221> MUTAGEN
<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
<213> Artificial

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

<220>
 <221> MUTAGEN
 <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
 <213> Artificial

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

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

<400> 91

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

<210> 92
 <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> 92

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

2015007907

<210> 93
<211> 10
<212> PRT
<213> Artificial

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

<220>
<221> MUTAGEN
<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
<213> Artificial

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

<220>
<221> MUTAGEN
<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)

2015007907

<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>

<221> MUTAGEN

<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>
 <221> MUTAGEN
 <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)

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

<400> 100

2015007907

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 amino acid sequence (see Figure 1)

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

<400> 102
ccgccccagc tcagtccgaa ccccgcggcg gcggcggcct cctccacacg cctccacctc 60
cgccgccgcc gccgccgcc cgccctcccg cgccgctctc cgcccg 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			
gtt	ccc	acc	cag	gat	cgt	ggc	act	tcc	acc	gac	agc	cct	tgt	cgc	cgt	836
Val	Pro	Thr	Gln	Asp	Arg	Gly	Thr	Ser	Thr	Asp	Ser	Pro	Cys	Arg	Arg	
		230					235					240				
act	gca	gcc	acc	cag	atg	gca	cct	cca	agt	ggt	ccc	cct	gcc	act	gca	884
Thr	Ala	Ala	Thr	Gln	Met	Ala	Pro	Pro	Ser	Gly	Pro	Pro	Ala	Thr	Ala	
	245					250					255					
cct	ggt	ggc	cgg	ggc	cac	tcc	cat	cga	gat	cgg	tcc	ata	tca	gca	gat	932
Pro	Gly	Gly	Arg	Gly	His	Ser	His	Arg	Asp	Arg	Ser	Ile	Ser	Ala	Asp	
260					265					270					275	

2015007907

gtg cgg ctc gag gcg act gag gag atc tac ctg acc cca gtg cag agg	980
Val Arg Leu Glu Ala Thr Glu Glu Ile Tyr Leu Thr Pro Val Gln Arg	
280 285 290	
ccc cca gac cct gca gaa ccc acc tcc acc ttc ttg cca ccc act gag	1028
Pro Pro Asp Pro Ala Glu Pro Thr Ser Thr Phe Leu Pro Pro Thr Glu	
295 300 305	
agc cgg atg tct gtc agc tcg gat cct gac cct gcc gct tac tct gta	1076
Ser Arg Met Ser Val Ser Ser Asp Pro Asp Pro Ala Ala Tyr Ser Val	
310 315 320	
act gca ggg cga ccg cac cct tcc atc agt gaa gag gat gag ggc ttc	1124
Thr Ala Gly Arg Pro His Pro Ser Ile Ser Glu Glu Asp Glu Gly Phe	
325 330 335	
gac tgt ctg tca tcc cca gag caa gct gag cca cca ggt gga ggg tgg	1172
Asp Cys Leu Ser Ser Pro Glu Gln Ala Glu Pro Pro Gly Gly Gly Trp	
340 345 350 355	
cgg gga agc ctc ggg gag cca cca ccg cct cca cgg gcc tca ctg agc	1220
Arg Gly Ser Leu Gly Glu Pro Pro Pro Pro Pro Arg Ala Ser Leu Ser	
360 365 370	
tcg gac acc agc gca ctg tcc tac gac tct gtc aag tac aca ctg gtg	1268
Ser Asp Thr Ser Ala Leu Ser Tyr Asp Ser Val Lys Tyr Thr Leu Val	
375 380 385	
gtg gat gag cat gcc cag ctt gag ttg gtg agc ctg cgg cca tgt ttt	1316
Val Asp Glu His Ala Gln Leu Glu Leu Val Ser Leu Arg Pro Cys Phe	
390 395 400	
gga gat tac agt gac gaa agc gac tct gcc act gtc tat gac aac tgt	1364
Gly Asp Tyr Ser Asp Glu Ser Asp Ser Ala Thr Val Tyr Asp Asn Cys	
405 410 415	
gcc tct gcc tcc tcg ccc tac gag tca gcc att ggt gag gaa tat gag	1412
Ala Ser Ala Ser Ser Pro Tyr Glu Ser Ala Ile Gly Glu Glu Tyr Glu	
420 425 430 435	
gag gcc cct caa ccc cgg cct ccc acc tgc ctg tca gag gac tcc aca	1460
Glu Ala Pro Gln Pro Arg Pro Pro Thr Cys Leu Ser Glu Asp Ser Thr	
440 445 450	
ccg gat gag cct gac gtc cac ttc tct aag aag ttt ctg aat gtc ttc	1508
Pro Asp Glu Pro Asp Val His Phe Ser Lys Lys Phe Leu Asn Val Phe	
455 460 465	
atg agt ggc cgc tct cgt tcc tcc agt gcc gag tcc ttt ggg ctg ttc	1556
Met Ser Gly Arg Ser Arg Ser Ser Ala Glu Ser Phe Gly Leu Phe	
470 475 480	

2015007907

tcc tgt gtc atc aat ggg gag gag cat gag caa acc cat cgg gct ata	1604
Ser Cys Val Ile Asn Gly Glu Glu His Glu Gln Thr His Arg Ala Ile	
485 490 495	
ttc agg ttt gtg cct cgg cat gaa gat gaa ctt gag ctg gaa gtg gac	1652
Phe Arg Phe Val Pro Arg His Glu Asp Glu Leu Glu Leu Glu Val Asp	
500 505 510 515	
gac cct ctg ctg gtg gag ctg cag gca gaa gac tat tgg tat gag gcc	1700
Asp Pro Leu Leu Val Glu Leu Gln Ala Glu Asp Tyr Trp Tyr Glu Ala	
520 525 530	
tat aac atg cgc act gga gcc cgt ggt gtc ttt cct gcc tac tat gcc	1748
Tyr Asn Met Arg Thr Gly Ala Arg Gly Val Phe Pro Ala Tyr Tyr Ala	
535 540 545	
att gag gtc acc aag gag cct gag cac atg gca gcc ctt gcc aaa aac	1796
Ile Glu Val Thr Lys Glu Pro Glu His Met Ala Ala Leu Ala Lys Asn	
550 555 560	
agc gac tgg att gac cag ttc cgg gtg aag ttc ctg ggc tct gtc cag	1844
Ser Asp Trp Ile Asp Gln Phe Arg Val Lys Phe Leu Gly Ser Val Gln	
565 570 575	
gtt cct tat cac aag ggc aat gat gtc ctc tgt gct gct atg caa aag	1892
Val Pro Tyr His Lys Gly Asn Asp Val Leu Cys Ala Ala Met Gln Lys	
580 585 590 595	
atc gcc acc acc cgc cgg ctc acc gtg cac ttt aac ccg ccc tcc agc	1940
Ile Ala Thr Thr Arg Arg Leu Thr Val His Phe Asn Pro Pro Ser Ser	
600 605 610	
tgt gtc ctt gaa atc agc gtt agg ggt gtc aag ata ggt gtc aaa gct	1988
Cys Val Leu Glu Ile Ser Val Arg Gly Val Lys Ile Gly Val Lys Ala	
615 620 625	
gat gaa gct cag gag gcc aag gga aat aaa tgt agc cac ttt ttc cag	2036
Asp Glu Ala Gln Glu Ala Lys Gly Asn Lys Cys Ser His Phe Phe Gln	
630 635 640	
cta aaa aac atc tct ttc tgt ggg tac cat cca aag aac aac aag tac	2084
Leu Lys Asn Ile Ser Phe Cys Gly Tyr His Pro Lys Asn Asn Lys Tyr	
645 650 655	
ttt ggg ttt atc act aag cac cct gct gac cac cgg ttt gcc tgc cat	2132
Phe Gly Phe Ile Thr Lys His Pro Ala Asp His Arg Phe Ala Cys His	
660 665 670 675	
gtc ttt gtg tct gaa gat tcc acc aaa gcc ctg gca gag tct gtg ggg	2180
Val Phe Val Ser Glu Asp Ser Thr Lys Ala Leu Ala Glu Ser Val Gly	
680 685 690	

2015007907

```

cgt gca ttt cag cag ttc tac aag caa ttt gtg gaa tat acc tgt cct 2228
Arg Ala Phe Gln Gln Phe Tyr Lys Gln Phe Val Glu Tyr Thr Cys Pro
          695                700                705

aca gaa gat atc tac ttg gag tag cagcaacccc cctctctgca gcccctcagc 2282
Thr Glu Asp Ile Tyr Leu Glu
          710

cccaggccag tactaggaca gctgactgct gacaggatgt tgtactgcca cgagagaatg 2342

ggggagtgag ggctgttggg gtcgggggggc aggggttttg ggagaggcag atgcagttta 2402

ttgtaatata tgggggttaga ttaatctatg gaggacagta caggctctct cggggctggg 2462

gaagggcagg gctgggggtgg gggtcaggca tctggccaca aaggggtccc ctagggacag 2522

aggcgctgca ccacctctggg cttgtttcat actagaggcc ctggctttct ggctcttggg 2582

tcctgccttg acaaagccca gccacctgga agtgtcacct tcccttgtcc acctcaccca 2642

gtgccctgag ctcatgctga gccaagcac ctccgaagga ctttccagta aggaaatggc 2702

aacatgtgac agtgagaccc tgttctcatc tgtggggctc cggcagctcc gacccccagc 2762

ctggccagca cgctgaccct ggcaagcttg tgtgttcaaa gaaggagagg gccacagcaa 2822

gccctgcctg ccagggaagg ttccctctca gctggcccca gccaaactggt cactgtcttg 2882

tcacctggct actactatta aagtgccatt tcttgtctga aaaaaaaaaa aaaaaaaaaa 2942

aaaaactcga g 2953

```

<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
1          5                10                15

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

```

2015007907

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

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

2015007907

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

2015007907

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

2015007907

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

<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
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

2015007907

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

2015007907

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

2015007907

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

2015007907

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

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

<400> 105
atggcggagc gagaaagcgg cggcctggga gggggggccg cgtccccgcc cgccgcctcc 60
ccgttcctgg ggctgcacat cgcttcgcct cccaatttca ggctcaccca tgacatcagc 120
ctggaggagt ttgaggatga agacctctcg gagatcactg atgagtgtgg catcagctta 180
cagtgcaaag acaccctgtc cttacggccc ccgcgcgccg ggctgtcttc 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 ccaggggccc ggacgcgggg acacgtaccg gcccagcgg 480
cccaccacgc tcaacctctt tccgcagggt ccgcggtctc aggacacact gaataataat 540
tctctgggca aaaagcacag ttggcaggat cgggtgtctc gatcatcctc acccctgaag 600
acaggggagc agacaccacc gcatgaacac atctgcctga gcgatgagct gccccccag 660
agcggccccg cccccaccac agatcgaggc acctccaccg acagcccttg ccgccgcagc 720
acagccaccc agatggcacc tccgggtggt cccctgtctg cccgccttg gggtcggggc 780
cactcgcata gagaccgaat ccactaccag gccgatgtgc gactagaggc cactgaggag 840
atctacctga cccagtgca gaggcccca gacgtgcag agcccacctc cgccttcctg 900
ccgcccactg agagccggat gtcagtcagc tccgatccag accctgccgc ctaccctcc 960
acggcagggc ggccgcaccc ctccatcagt gaagaggaag agggcttcga ctgcctgtcg 1020
tccccagagc gggctgagcc ccaggcgga ggggtggcggg ggagcctggg ggagccgccg 1080
ccacctccac gggcctctct gagctcggac accagcgccc tgtcctatga ctctgtcaag 1140
tacacgctgg tggtagatga gcatgcacag ctggagctgg tgagcctgcg gccgtgcttc 1200

2015007907

ggagactaca gtagcgagag tgactctgcc accgtctatg acaactgtgc ctccgtctcc	1260
tcgccctatg agtcggccat cggagaggaa tatgaggagg ccccgcggcc ccagccccct	1320
gcctgcctct ccgaggactc cacgcctgat gaacccgacg tccatttctc caagaaattc	1380
ctgaacgtct tcatgagtgg cgcctccgc tcctccagtg ctgagtcctt cgggctgttc	1440
tcctgcatca tcaacgggga ggagcaggag cagaccacc 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 cggggtgaag ttcttgggct cagtccaggt tccctatcac	1740
aagggaatg acgtcctctg tgctgctatg caaaagattg ccaccacccg ccggctcacc	1800
gtgcacttta acccgccctc cagctgtgtc ctggagatca gcgtgcgggg tgtgaagata	1860
ggcgtcaagg ccgatgactc ccaggaggcc aagggaata aatgtagcca ctttttccag	1920
ttaaaaaaca tctctttctg cggatatcat ccaaagaaca acaagtactt tgggttcac	1980
accaagcacc ccgccacca ccggtttgcc tgccacgtct ttgtgtctga agactccacc	2040
aaagccctgg cagagtcctg ggggagagca ttccagcagt tctacaagca gtttgtggag	2100
tacacctgcc ccacagaaga tatctacctg gagtag	2136