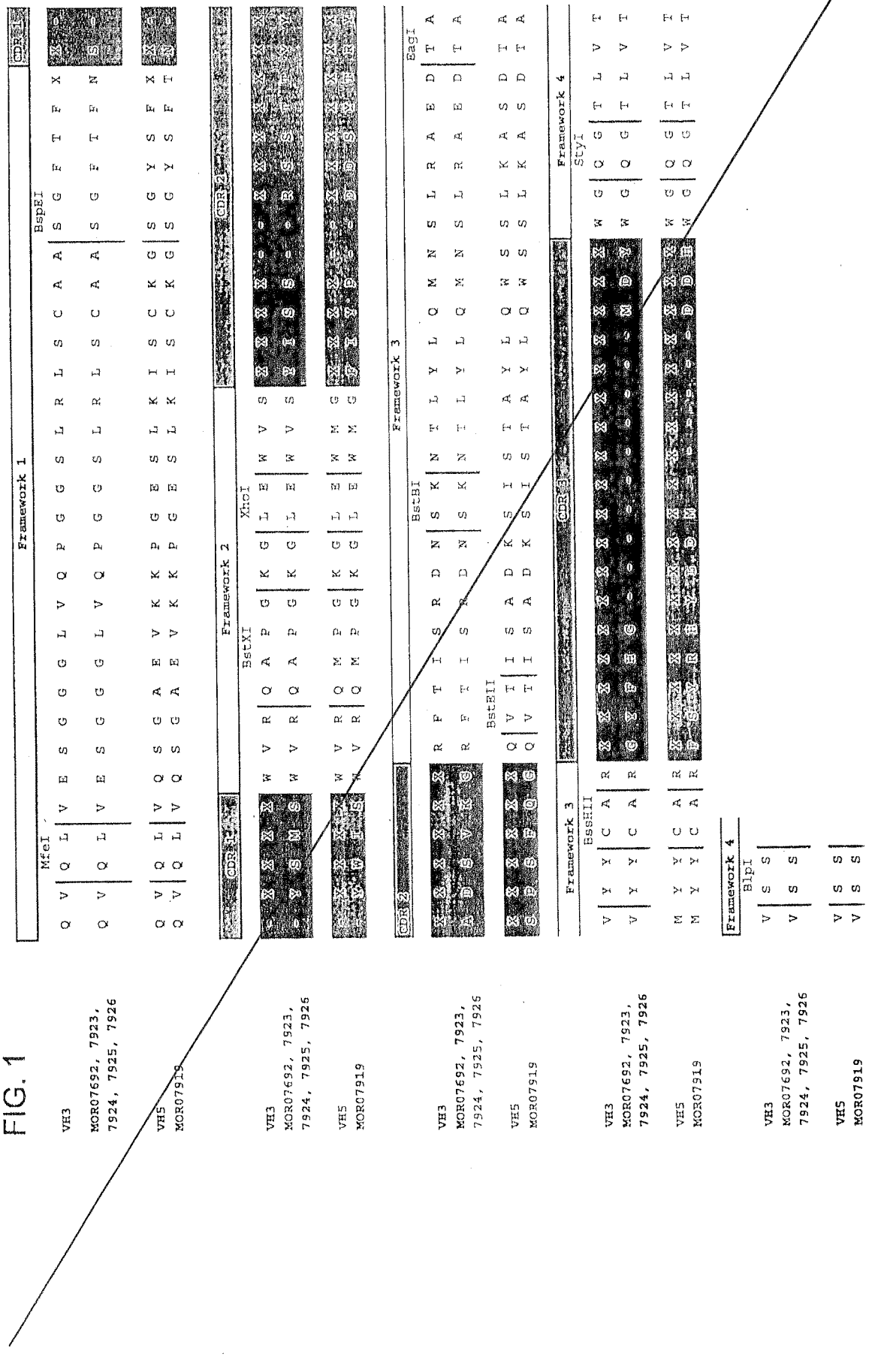
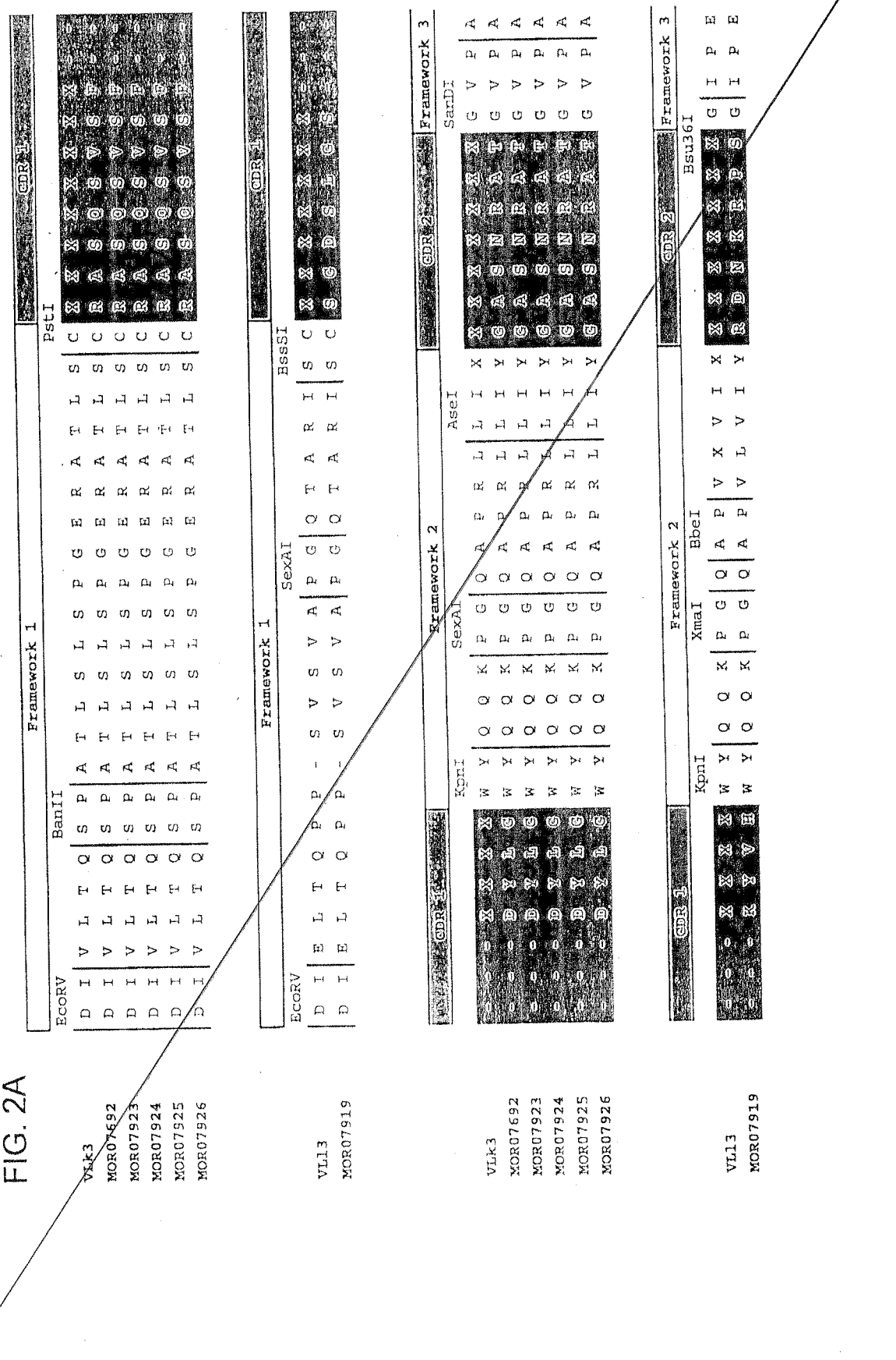
[Fig. 1]

FIG. 1


Framework 1
CDR1
Framework 2
CDR2
Framework 3
CDR3
Framework 4
MfeI
BspEI
BstXI
XhoI
BstBI
BstEII
EagI
BsmI
StyI
BsaHI
BlpI
VH3
MOR07692, 7923, 7924, 7925, 7926
VH5
MOR07919

[Fig. 2A]


FIG. 2A
Framework 1
CDR1
Framework 2
CDR2
Framework 3
CDR3
EcoRV
BanII
PstI
SexAI
BssSI
KpnI
AseI
SanDI
XmaI
BbeI
Bsu36I
VLk3
MOR07692
MOR07923
MOR07924
MOR07925
MOR07926
VL13
MOR07919

[Fig. 2B]

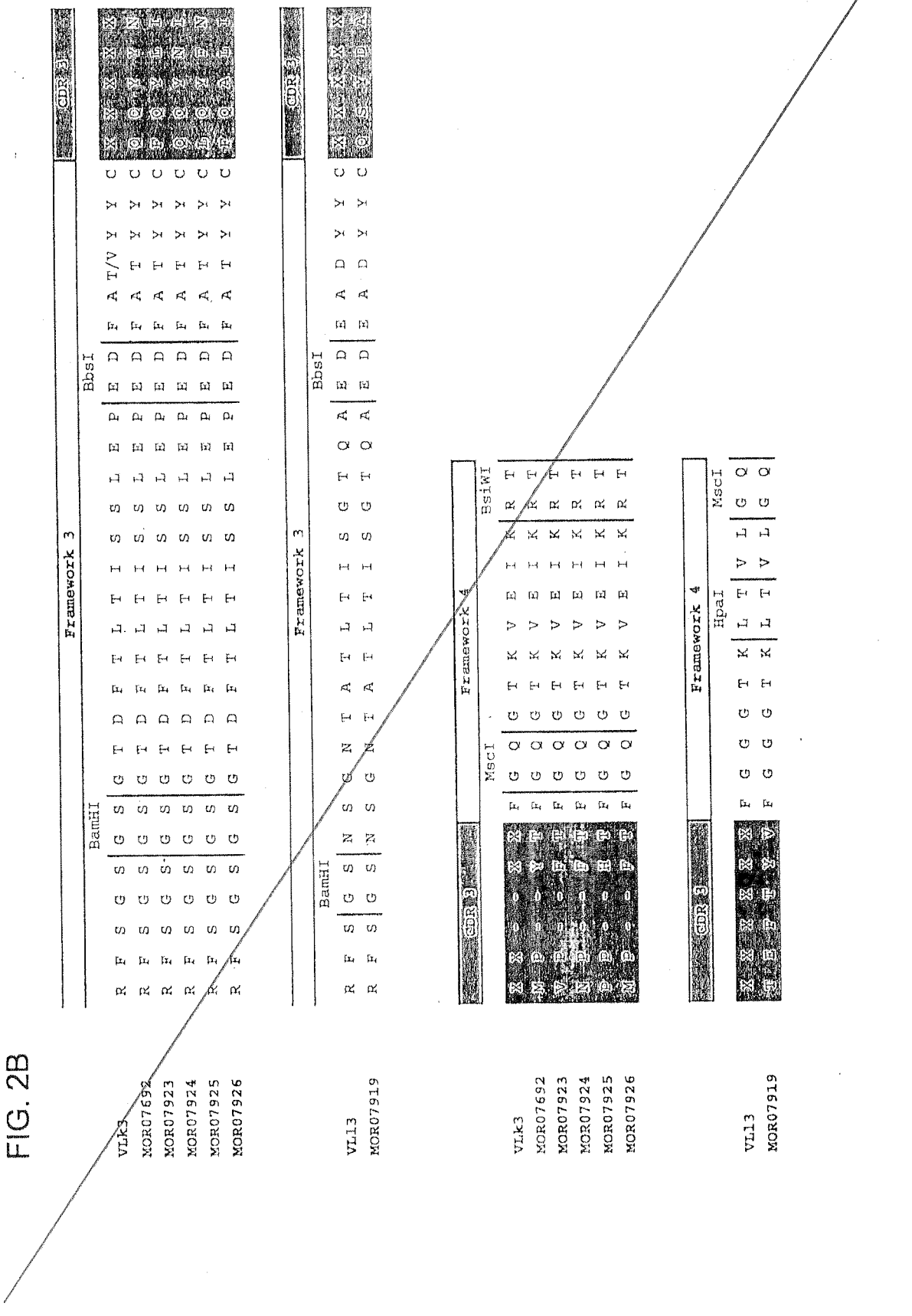

CDR3
Framework 3
BamHI
BbsI
VLk3
MOR07692
MOR07923
MOR07924
MOR07925
MOR07926
VL13
MOR07919
Framework 4
MscI
BsiWI
HpaI

FIG. 2B

[Fig. 5]

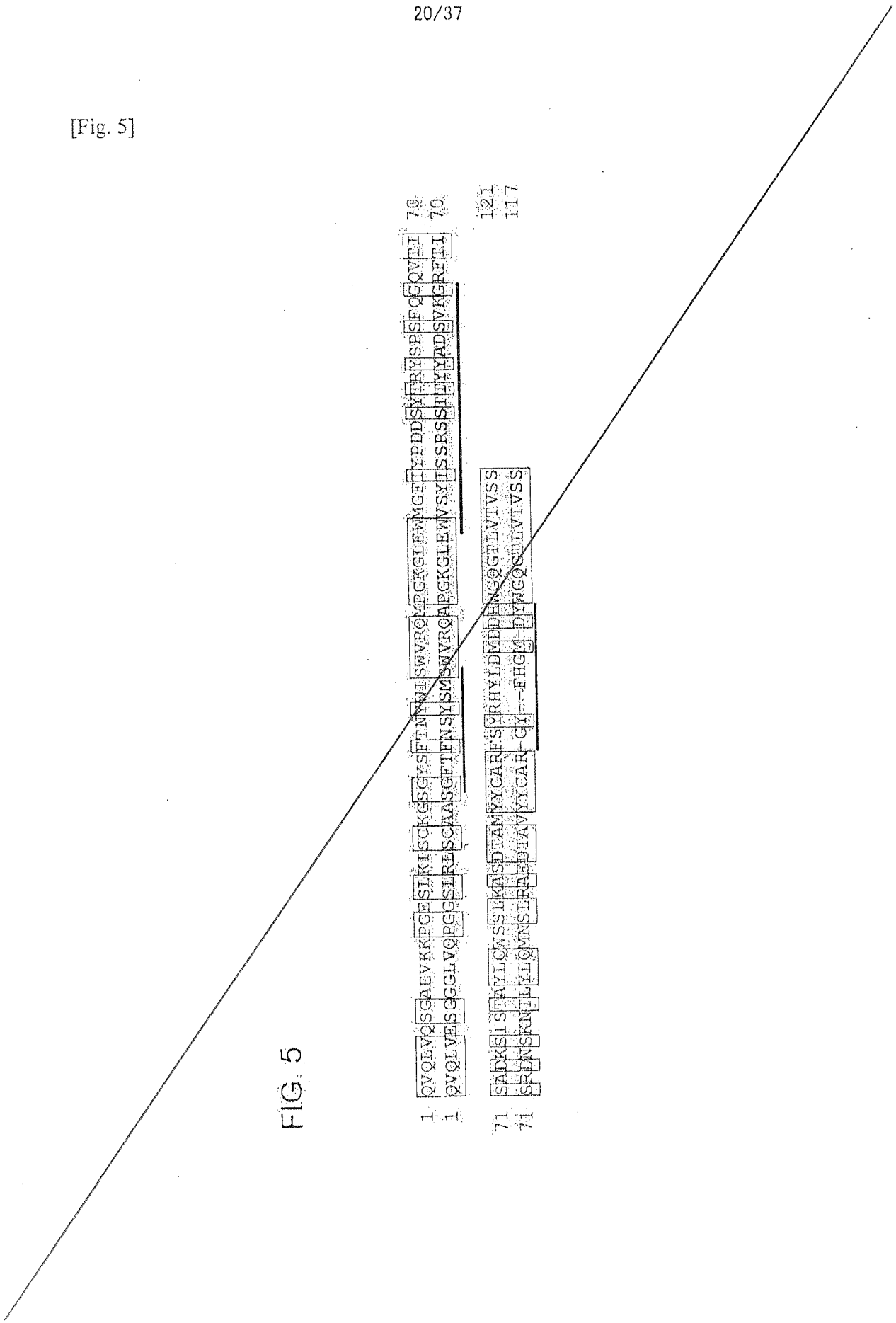


FIG. 5

[Fig. 6]

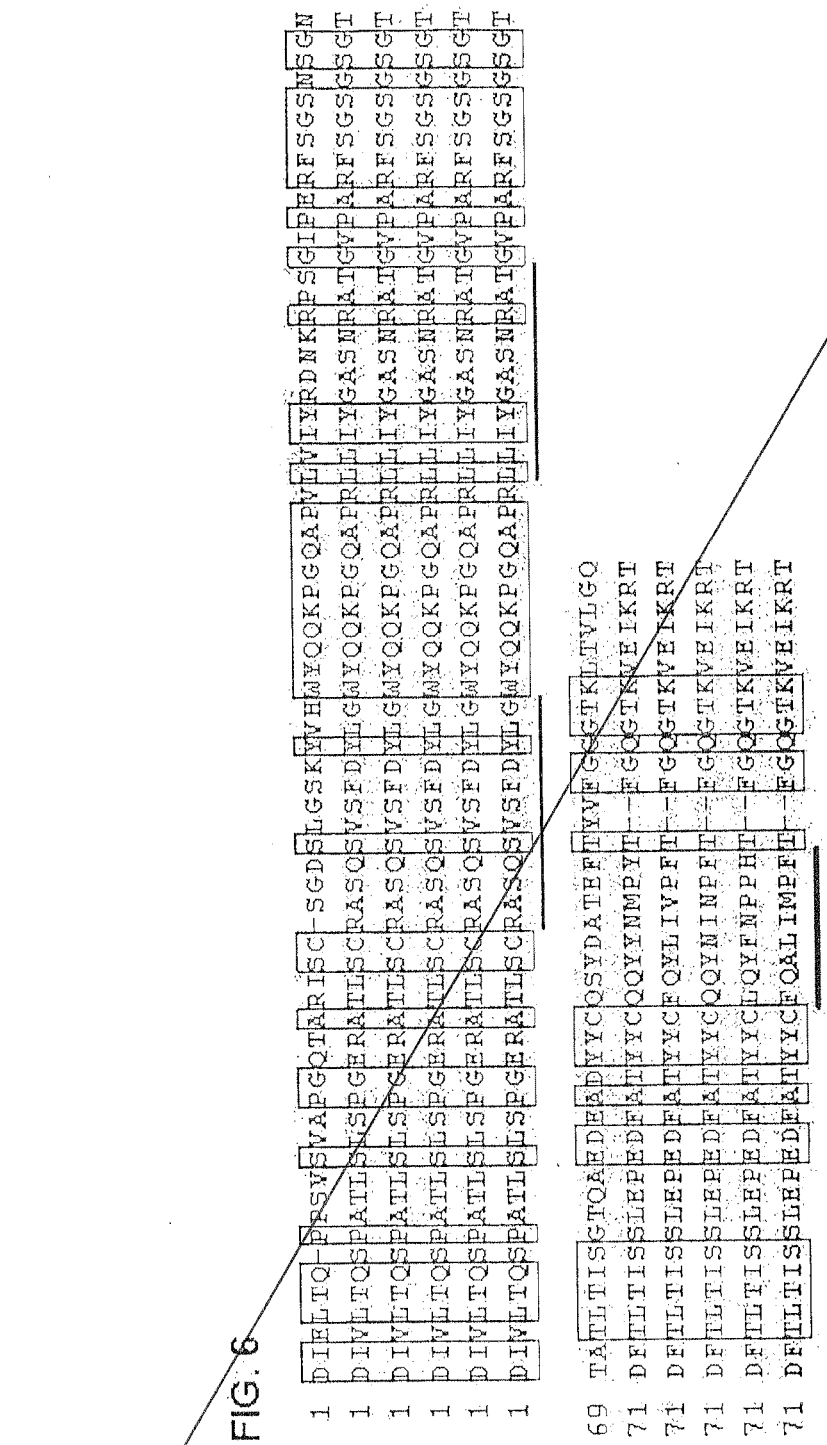
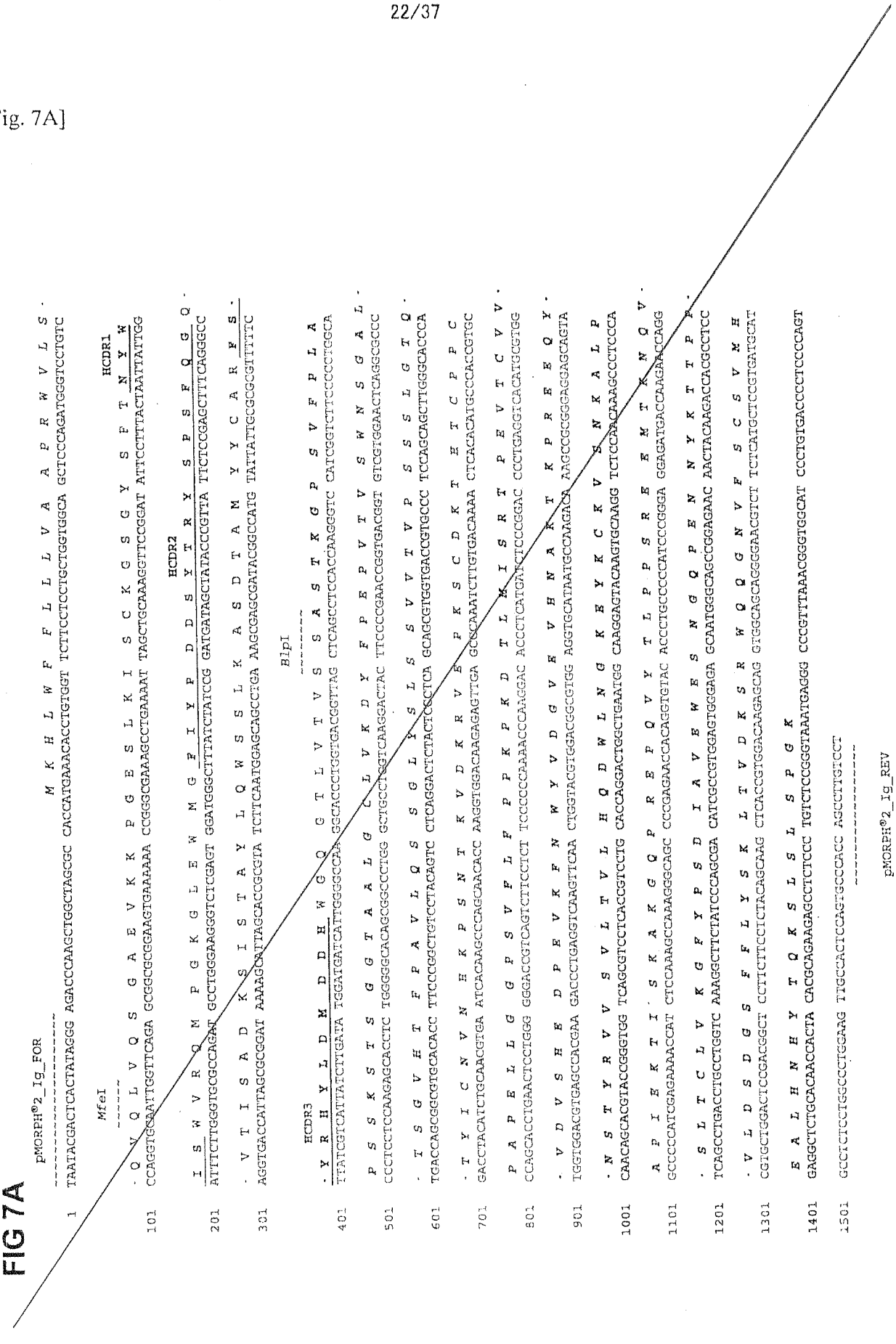


FIG. 6

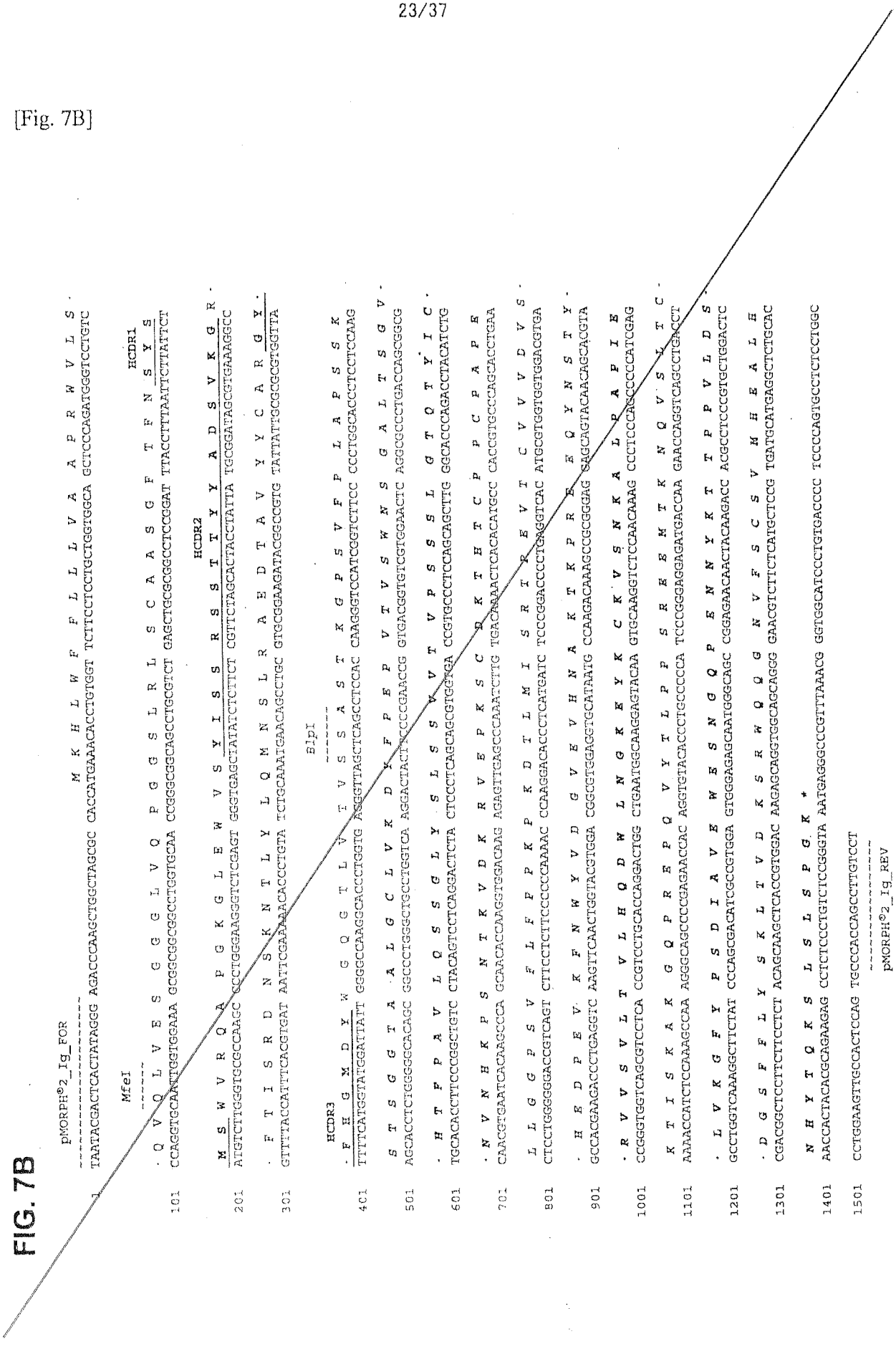
[Fig. 7A]

FIG 7A



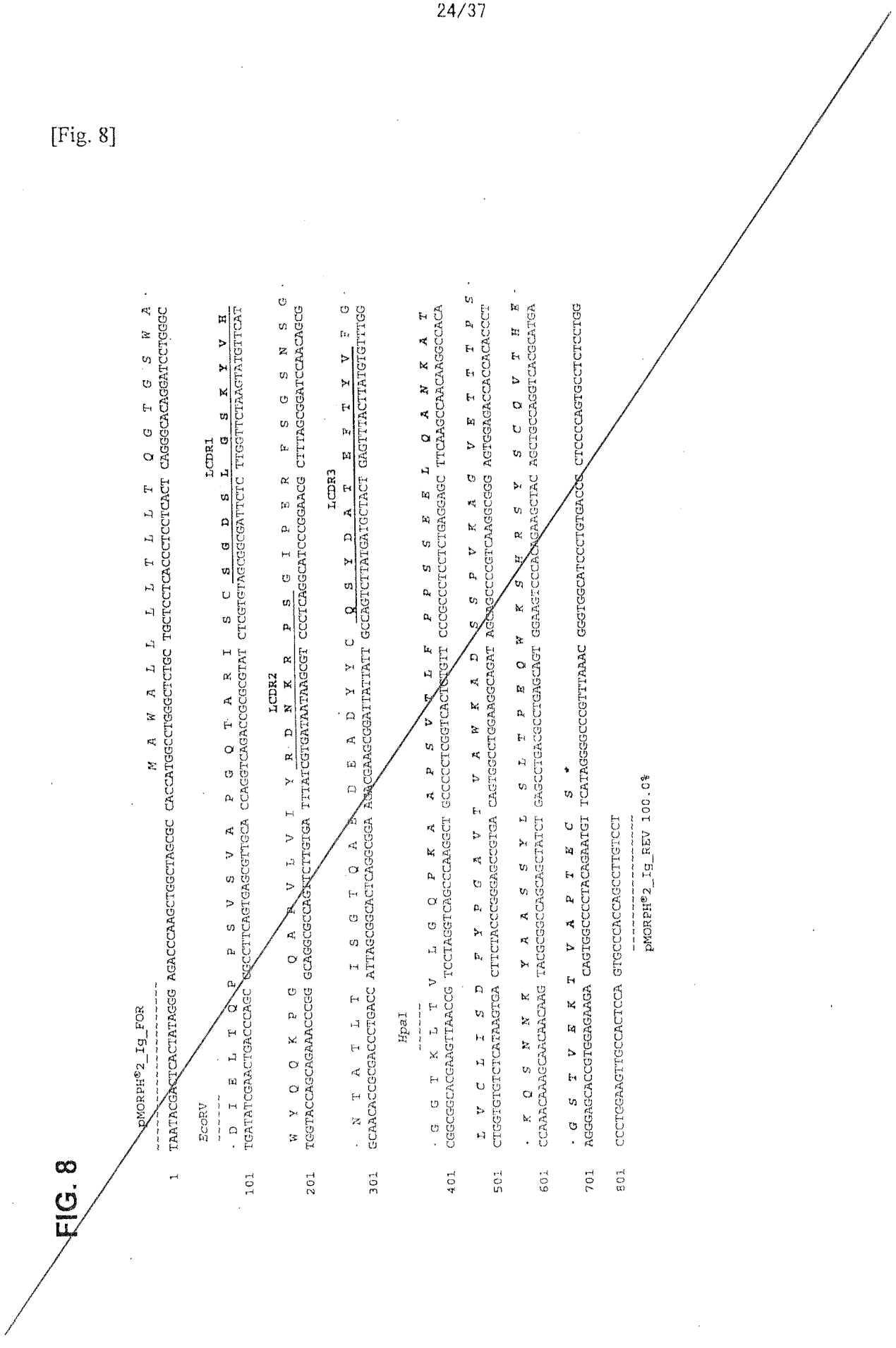
[Fig. 7B]

FIG. 7B



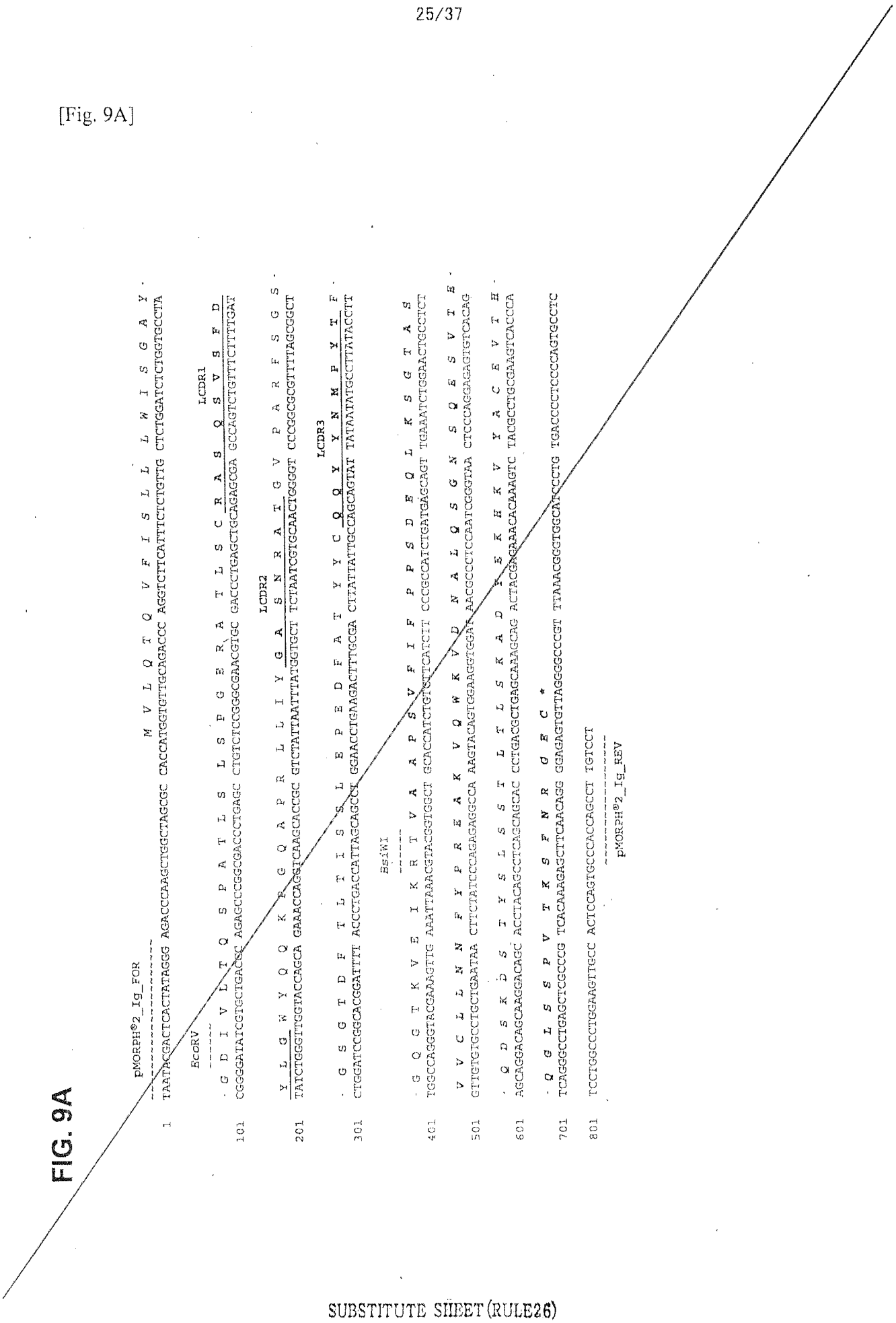
[Fig. 8]

FIG. 8


pMORPH®2_Ig_FOR
M A W A L L L T L L L T Q G T G S W A
1 TAATACGACTCACTATAGGG AGACCCAAGCTGGCTAGCGC CACCATGGCCTGGGCTCTGC TGCTCCTCACCCTCCTCACT CAGGGCACAGGATCCTGGGC
EcoRV
LCDR1
D I E L T Q P P S V S V A P G Q T A R I S C S G D S L G S K Y V H
101 TGATATCGAACTGACCCAGC CGCCTTCAGTGAGCGTTGCA CCAGGTCAGACCGCGCGTAT CTCGTGTAGCGGCGATTCTC TTGGTTCTAACTATGTTCAT
LCDR2
W Y Q Q K P G Q A P V L V I Y R D N K R P S G I P E R F S G S N S G
201 TGGTACCAGCAGAAACCCGG GCAGGCGCCAGNNCTTGTGA TTTATCGTGATAATAAGCGT CCCTCAGGCATCCCGGAACG CTTTAGCGGATCCAACAGCG
LCDR3
N T A T L T I S G T Q A E D E A D Y Y C Q S Y D A T E F T Y V F G
301 GCAACACCGCCGACCCTGACC ATTAGCGGCACTCAGGCGGA RGACGAAGCGGATTATTATT GCCAGTCTTATGATGCTACT GAGTTTACTTATGTGTTTGG
HpaI
G G G T K L T V L G Q P K A A P S V T L F P P S S E E L Q A N K A T
401 CGGCGGCACGAAGTTAACCG TCCTAGGTCAGCCCAAGGCT GCCCCCTCGGTCACTNTGTT CCCGCCCTCCTCTGAGGAGC TTCAAGCCAACAAGGCCACA
L V C L I S D F Y P G A V T V A W K A D S S P V K A G V E T T T P S
501 CTGGTGTGTCTCATAAGTGA CTTCTACCCGGGAGCCGTGA CAGTGGCCTGGAAGGCAGAT AGCAGCCCCGTCAAGGCGGG AGTGGAGACCACCACACCCT
K Q S N N K Y A A S S Y L S L T P E Q W K S H R S Y S C Q V T H E
601 CCAACAAAGCAACAACAAG TACGCGGCCAGCTATCT GAGCCTGACGCCTGAGCAGT GGAAGTCCCACAGAGCTAC AGCTGCCAGGTCACGCATGA
G S T V E K T V A P T E C S *
701 AGGGAGCACCGTGGAGAAGA CAGTGGCCCTACAGAATGT TCATAGGGGCCCGTTTAAAC GGGTGGCATCCCTGTGACCC CTCCCCAGTGCCTCTCCTGG
801 CCCTGGAAGTTGCCACTCCA GTGCCCACCAGCCTTGTCCT
pMORPH®2_Ig_REV 100.0%

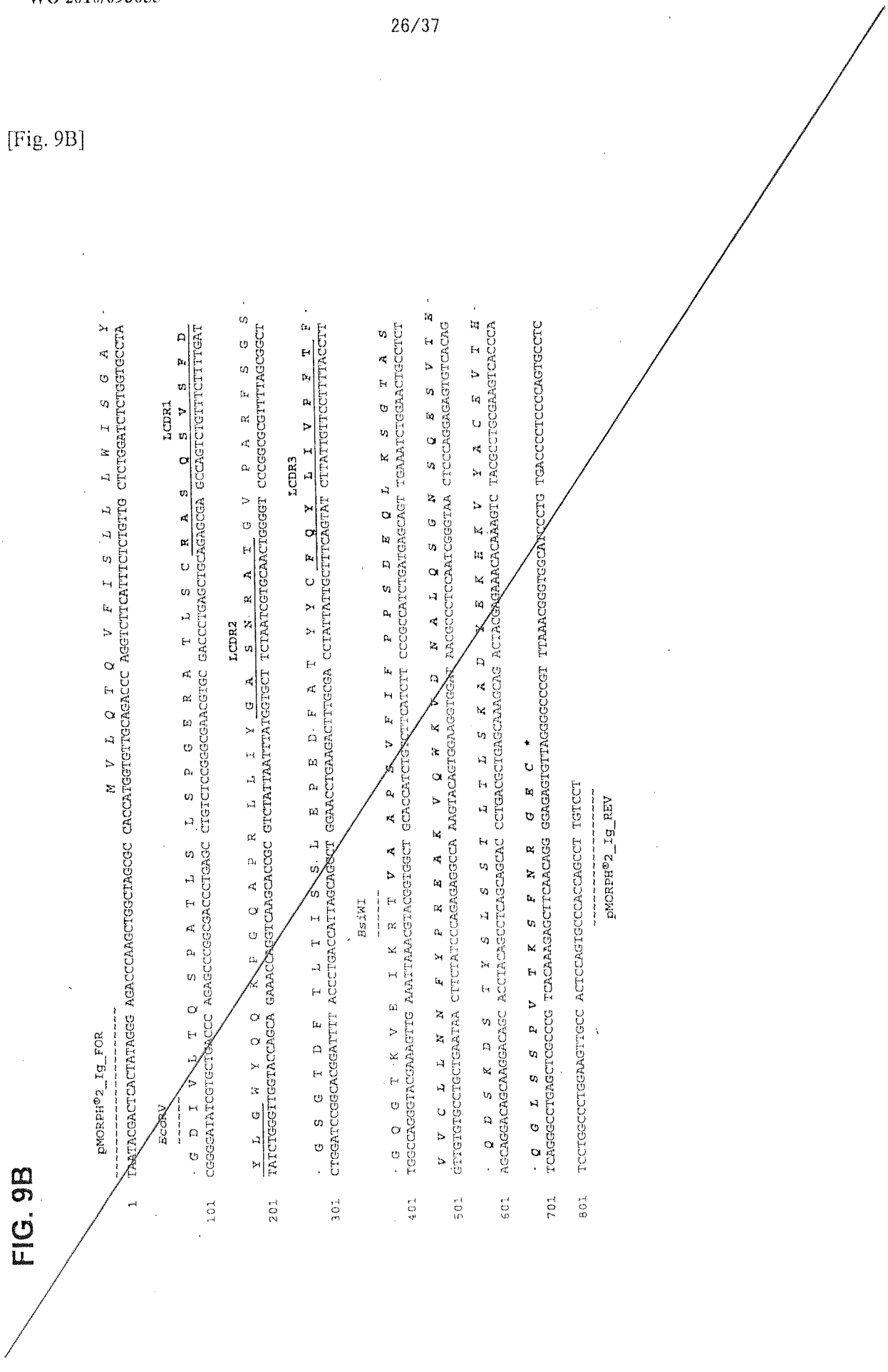
[Fig. 9A]

FIG. 9A



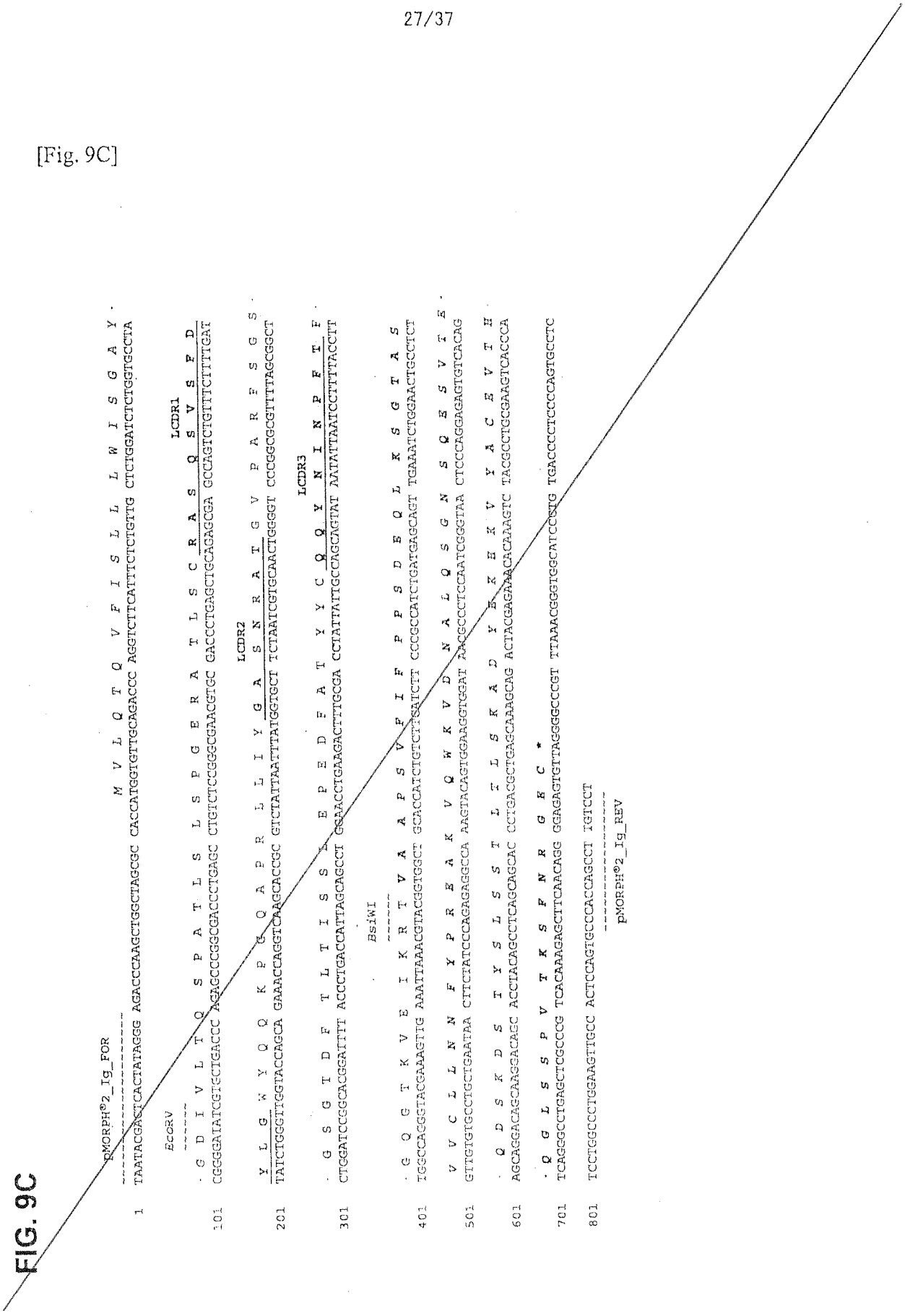
[Fig. 9B]

FIG. 9B



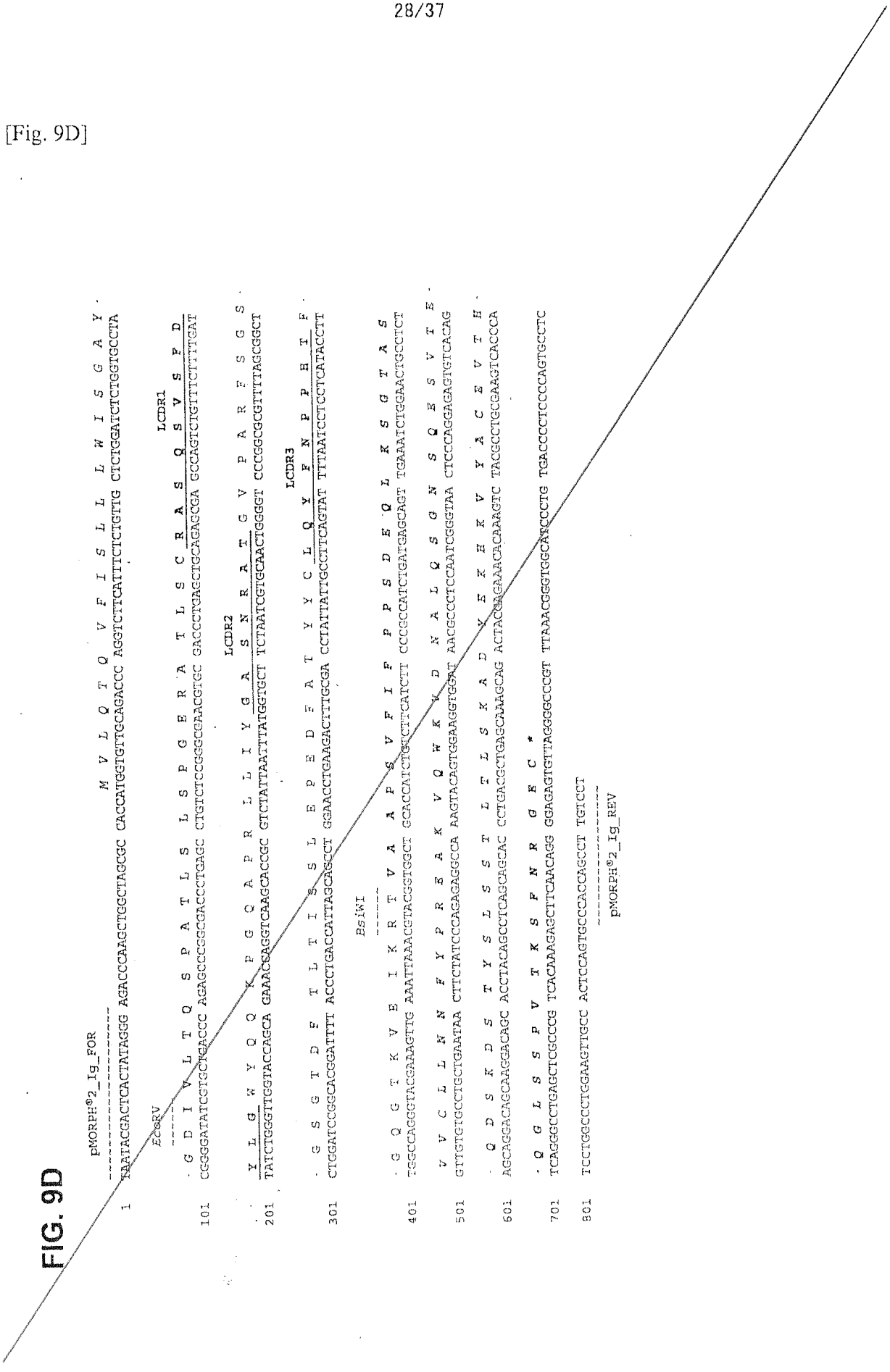
[Fig. 9C]

FIG. 9C


pMORPH®2_Ig_FOR
M V L Q T Q V F I S L L L W I S G A Y
1 TAATACGACTCACTATAGGG AGACCCAAGCTGGCTAGCGC CACCATGGTGTTGCAGACCC AGGTCTTCATTTCTCTGTTG CTCTGGATCTCTGGTGCCTA
EcoRV
G D I V L T Q S P A T L S L S P G E R A T L S C R A S Q S V S S F D
101 CGGGGATATCGTGCTGACCC AGAGCCCGGCGACCCTGAGC CTGTCTCCGGGCGAACGTGC GACCCTGAGCTGCAGAGCGA GCCAGTCTGTTTCTTTTGAT
LCDR1
LCDR2
Y L G W Y Q Q K P G Q A P R L L I Y G A S N R A T G V P A R F S G S
201 TATCTGGGTTGGTACCAGCA GAAACCAGGTCAAGCACCGC GTCTATTAATTTATGGTGCT TCTAATCGTGCAACTGGGGT CCCGGCGCGTTTTAGCGGCT
LCDR3
G S G T D F T L T I S S L E P E D F A T Y Y C Q Q Y N I N P F T F
301 CTGGATCCGGCACGGATTT ACCCTGACCATTAGCAGCCT GGAACCTGAAGACTTTGCGA CCTATTATTGCCAGCAGTAT AATATTAATCCTTTTACCTT
BsiWI
G Q G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S
401 TGGCCAGGGTACGAAAGTTG AAATTAAACGTACGGTGGCT GCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGT TGAAATCTGGAACTGCCTCT
V V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E
501 GTTGTGTGCCTGCTGAATAA CTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGAT AACGCCCTCCAATCGGGTAA CTCCCAGGAGAGTGTCACAG
Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H
601 AGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCAC CCTGACGCTGAGCAAAGCAG ACTACGAGAAACACAAAGTC TACGCCTGCGAAGTCACCCA
Q G L S S P V T K S F N R G E C *
701 TCAGGGCCTGAGCTCGCCCG TCACAAAGAGCTTCAACAGG GGAGAGTGTTAGGGGGCCGT TTAAACGGGTGGCATCCCTG TGACCCCTCCCCAGTGCCTC
801 TCCTGGCCCTGGAAGTTGCC ACTCCAGTGCCCACCAGCCT KGTCCT
pMORPH®2_Ig_REV

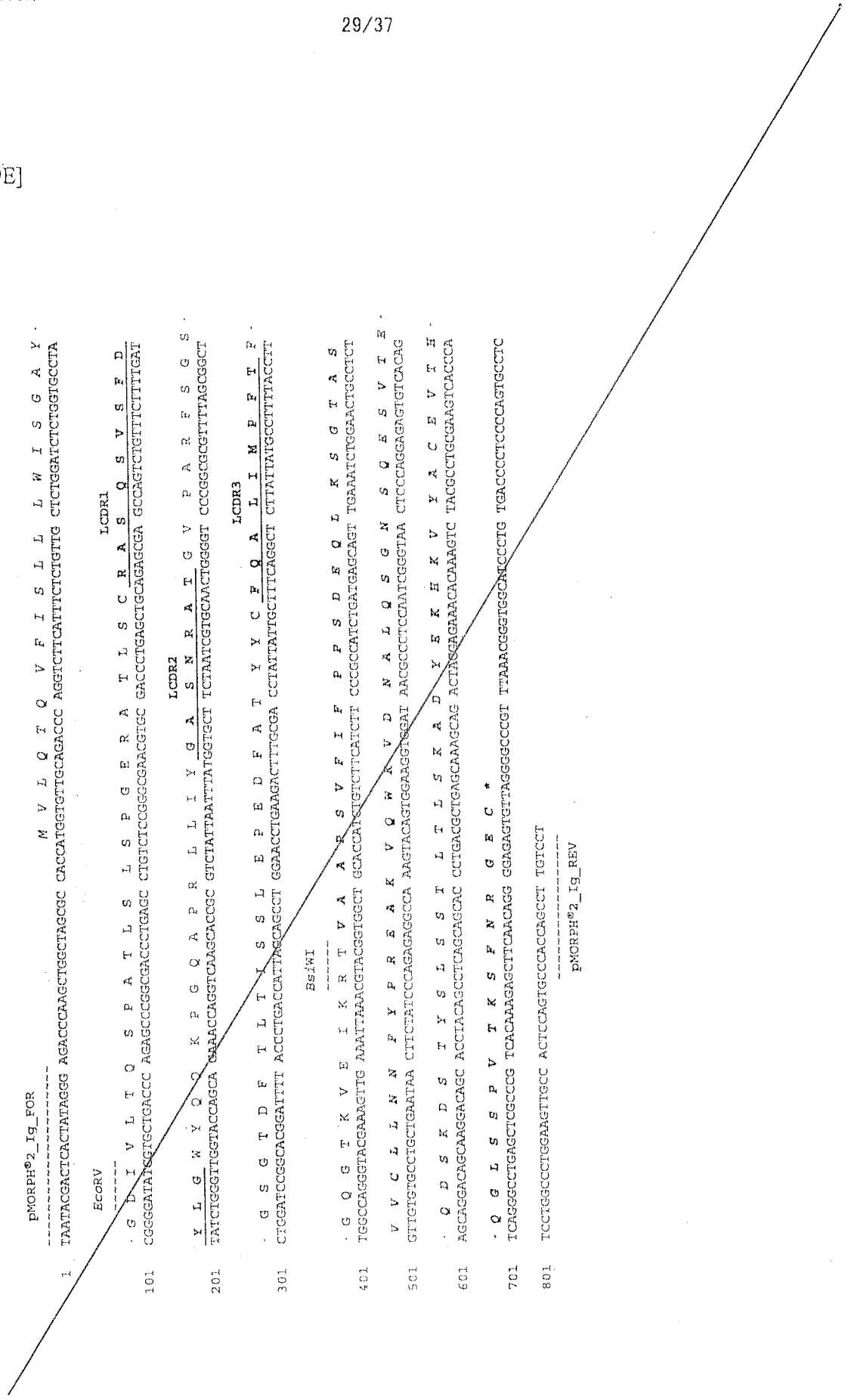
[Fig. 9D]

FIG. 9D


pMORPH®2_Ig_FOR
M V L Q T Q V F I S L L L W I S G A Y
EcoRV
LCDR1
G D I V L T Q S P A T L S L S P G E R A T L S C R A S Q S V S F D
LCDR2
Y L G W Y Q Q K P G Q A P R L L I Y G A S N R A T G V P A R F S G S
LCDR3
G S G T D F T L T I S S L E P E D F A T Y Y C L Q Y F N P P H T F
BsiWI
G Q G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S
V V C L L N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E
Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H
Q G L S S P V T K S F N R G E C *
pMORPH®2_Ig_REV

[Fig. 9E]

FIG. 9E



[Fig. 11]

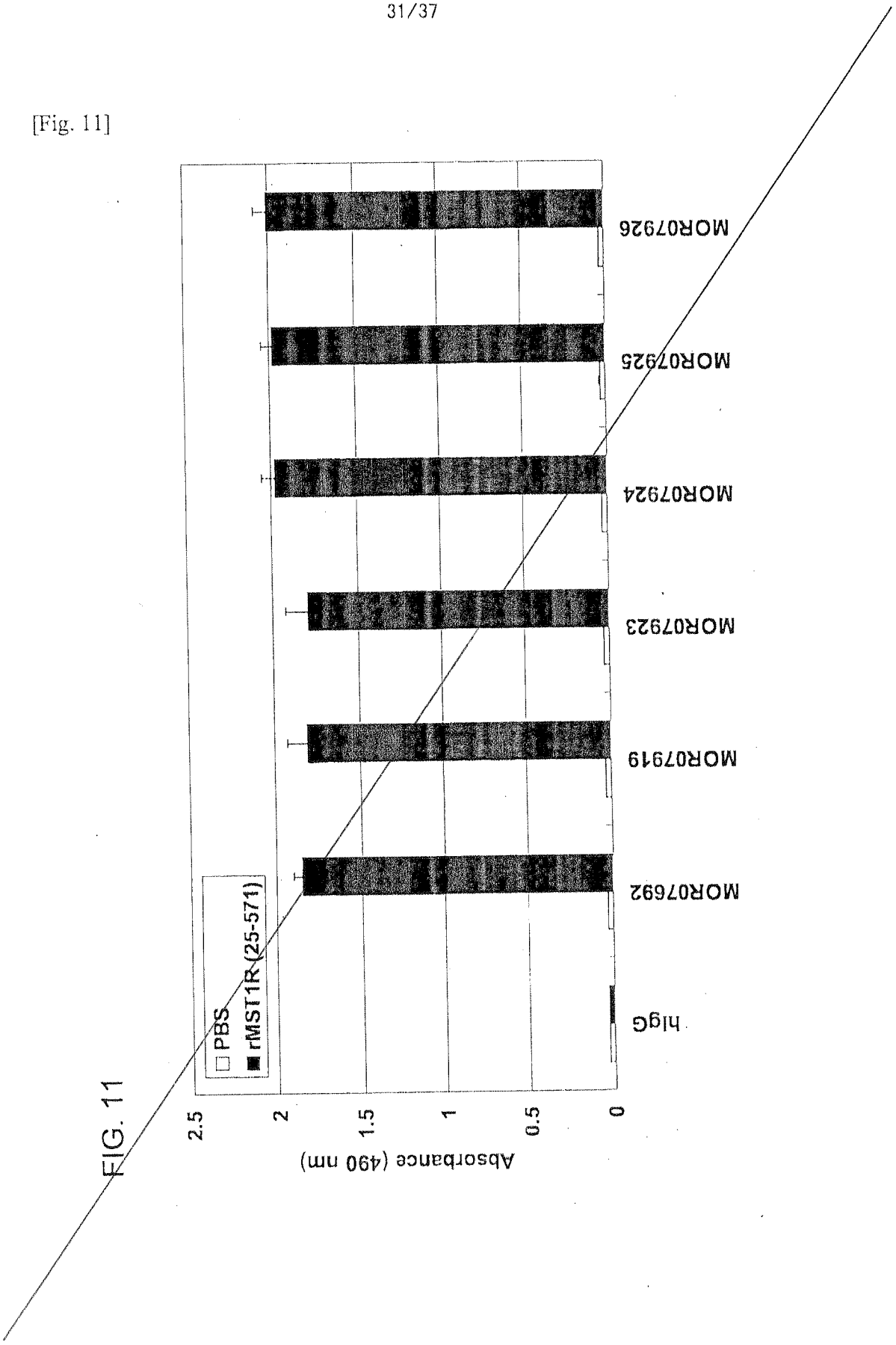

MOR07926
MOR07925
MOR07924
MOR07923
MOR07919
MOR07692
hIgG
PBS
rMST1R(25-571)
2.5
2
1.5
1
0.5
0
Absorbance (490 nm)

FIG. 11

FIG. 1

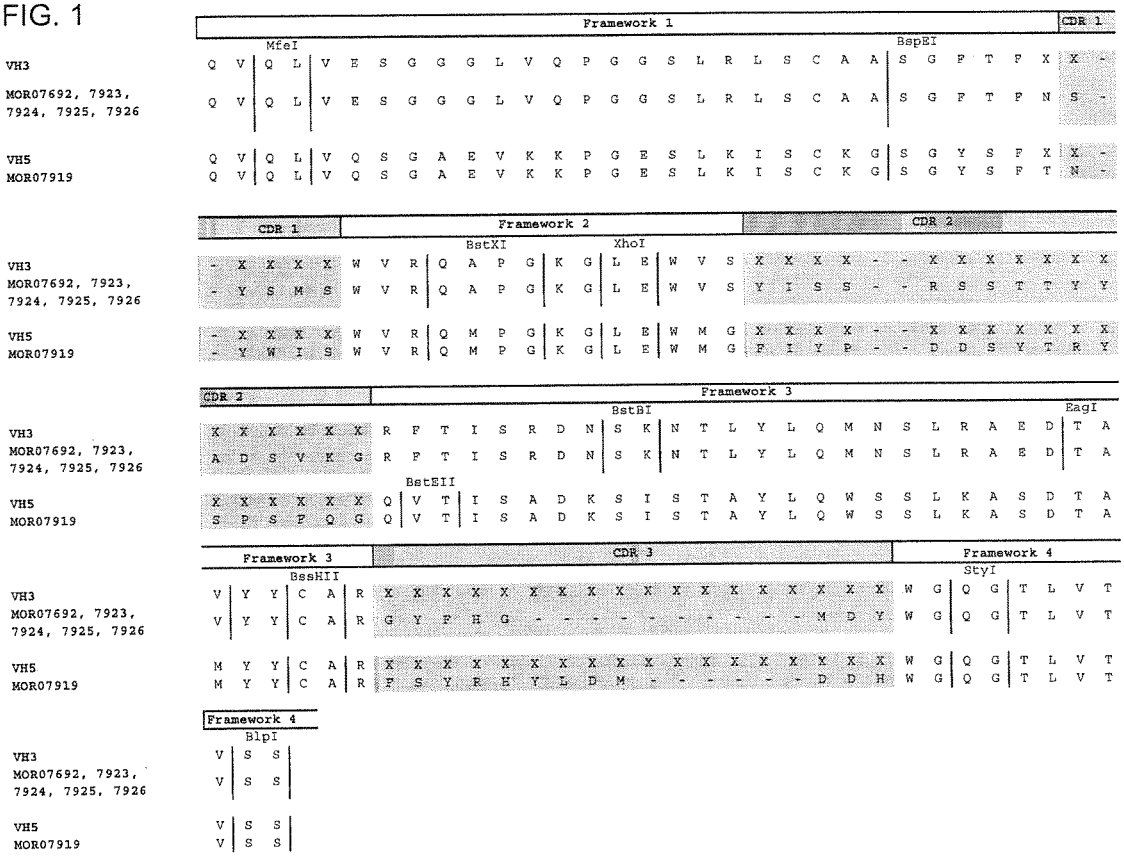

Framework 1
CDR 1
MfeI
BspEI
VH3
MOR07692, 7923, 7924, 7925, 7926
VH5
MOR07919
CDR 1
Framework 2
CDR 2
BstXI
XhoI
VH3
MOR07692, 7923, 7924, 7925, 7926
VH5
MOR07919
CDR 2
Framework 3
BstBI
EagI
BstEII
VH3
MOR07692, 7923, 7924, 7925, 7926
VH5
MOR07919
Framework 3
CDR 3
Framework 4
BssHII
StyI
VH3
MOR07692, 7923, 7924, 7925, 7926
VH5
MOR07919
Framework 4
BlpI
VH3
MOR07692, 7923, 7924, 7925, 7926
VH5
MOR07919

FIG. 2A

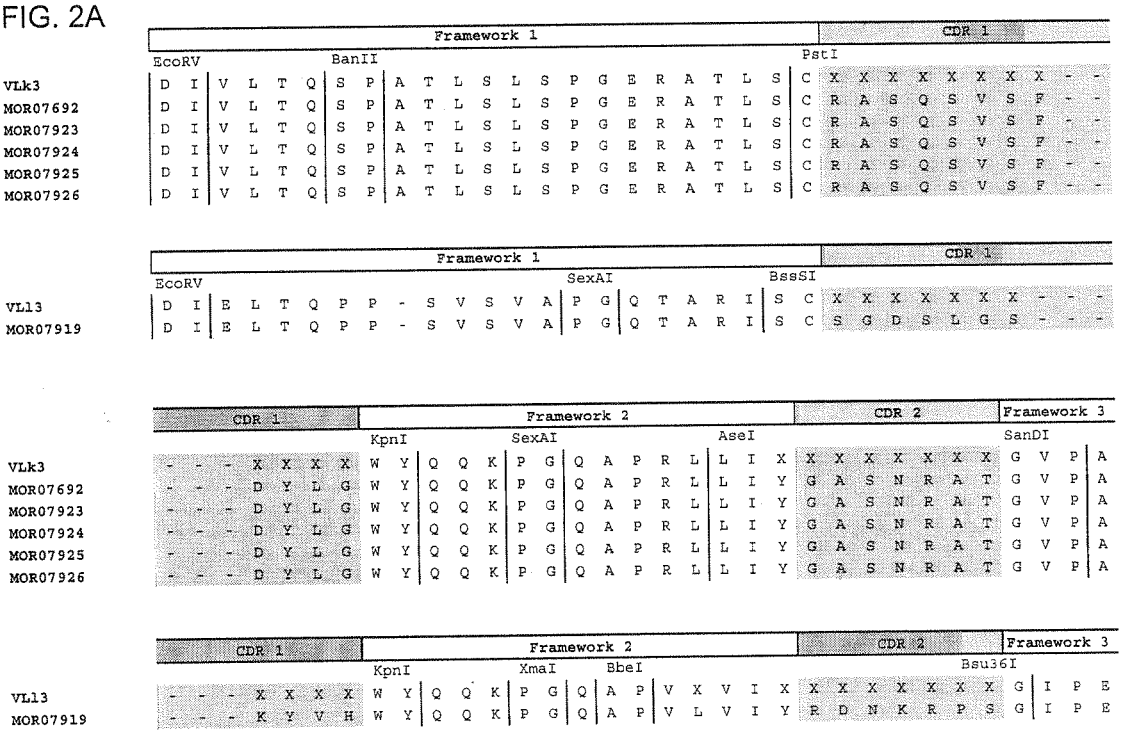

Framework 1
CDR 1
EcoRV
BanII
PstI
VLk3
MOR07692
MOR07923
MOR07924
MOR07925
MOR07926
Framework 1
CDR 1
EcoRV
SexAI
BssSI
VL13
MOR07919
CDR 1
Framework 2
CDR 2
Framework 3
KpnI
SexAI
AseI
SanDI
VLk3
MOR07692
MOR07923
MOR07924
MOR07925
MOR07926
CDR 1
Framework 2
CDR 2
Framework 3
KpnI
XmaI
BbeI
Bsu36I
VL13
MOR07919

FIG. 2B

	Framework 3																										CDR 3				
					BamHI															BbsI												
VLk3	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	S	L	E	P	E	D	F	A	T/V	Y	Y	C	X	X	X	X	X
MOR07692	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	S	L	E	P	E	D	F	A	T	Y	Y	C	Q	Q	Y	Y	N
MOR07923	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	S	L	E	P	E	D	F	A	T	Y	Y	C	F	Q	Y	L	I
MOR07924	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	S	L	E	P	E	D	F	A	T	Y	Y	C	Q	Q	Y	N	I
MOR07925	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	S	L	E	P	E	D	F	A	T	Y	Y	C	L	Q	Y	F	N
MOR07926	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	S	L	E	P	E	D	F	A	T	Y	Y	C	F	Q	A	L	I

	Framework 3																										CDR 3				
				BamHI																BbsI												
VL13	R	F	S	G	S	N	S	G	N	T	A	T	L	T	I	S	G	T	Q	A	E	D	E	A	D	Y	Y	C	X	X	X	X	X
MOR07919	R	F	S	G	S	N	S	G	N	T	A	T	L	T	I	S	G	T	Q	A	E	D	E	A	D	Y	Y	C	Q	S	Y	D	A

	CDR 3						Framework 4											
								MscI								BsiWI		
VLk3	X	X	-	-	X	X	F	G	Q	G	T	K	V	E	I	K	R	T
MOR07692	M	P	-	-	Y	T	F	G	Q	G	T	K	V	E	I	K	R	T
MOR07923	V	P	-	-	F	T	F	G	Q	G	T	K	V	E	I	K	R	T
MOR07924	N	P	-	-	F	T	F	G	Q	G	T	K	V	E	I	K	R	T
MOR07925	P	P	-	-	H	T	F	G	Q	G	T	K	V	E	I	K	R	T
MOR07926	M	P	-	-	F	T	F	G	Q	G	T	K	V	E	I	K	R	T

	CDR 3						Framework 4											
												HpaI				MscI		
VL13	X	X	X	X	X	X	F	G	G	G	T	K	L	T	V	L	G	Q
MOR07919	T	E	F	T	Y	V	F	G	G	G	T	K	L	T	V	L	G	Q

FIG. 5

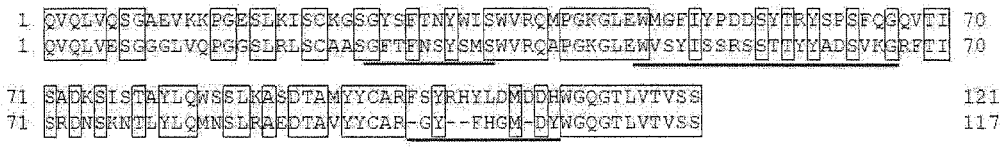

1 QVQLVQSGAEVKKPGESLKISCKGSGYSFTNYWISWVRQMPGKGLEWMGFIYPDDSYTRYSPSFQGQVTI 70
1 QVQLVESGGGLVQPGGSLRLSCAASGFTFNSYSMSWVRQAPGKGLEWVSYISSRSSTIYYADSVKGRFTI 70
71 SADKSISTAYLQWSSLKASDTAMYYCARFSYRHYLDMDDHWGQGTLVTVSS 121
71 SRDNSKNTLYLQMNSLRAEDTAVYYCAR-GY--FHGM-DYWGQGTLVTVSS 117

FIG. 6


1 DIELTQ-PPSVSVAPGQTARISC-SGDSLGSKYVHWYQQKPGQAPVLVIYRDNKRPSGIPERFSGSNSGN
1 DIVLTQSPATLSLSPGERATLSCRASQSVSFDYLGWYQQKPGQAPRLLIYGASNRATGVPARFSGSGSGT
1 DIVLTQSPATLSLSPGERATLSCRASQSVSFDYLGWYQQKPGQAPRLLIYGASNRATGVPARFSGSGSGT
1 DIVLTQSPATLSLSPGERATLSCRASQSVSFDYLGWYQQKPGQAPRLLIYGASNRATGVPARFSGSGSGT
1 DIVLTQSPATLSLSPGERATLSCRASQSVSFDYLGWYQQKPGQAPRLLIYGASNRATGVPARFSGSGSGT
1 DIVLTQSPATLSLSPGERATLSCRASQSVSFDYLGWYQQKPGQAPRLLIYGASNRATGVPARFSGSGSGT
69 TATLTISGTQAEDEADYYCQSYDATEFTYVFGGGTKLTVLGQ
71 DFTLTISSLEPEDFATYYCQQYYNMPYT--FGQGTKVEIKRT
71 DFTLTISSLEPEDFATYYCFQYLIVPFT--FGQGTKVEIKRT
71 DFTLTISSLEPEDFATYYCQQYNINPFT--FGQGTKVEIKRT
71 DFTLTISSLEPEDFATYYCLQYFNPPHT--FGQGTKVEIKRT
71 DFTLTISSLEPEDFATYYCFQALIMPFT--FGQGTKVEIKRT

FIG 7A

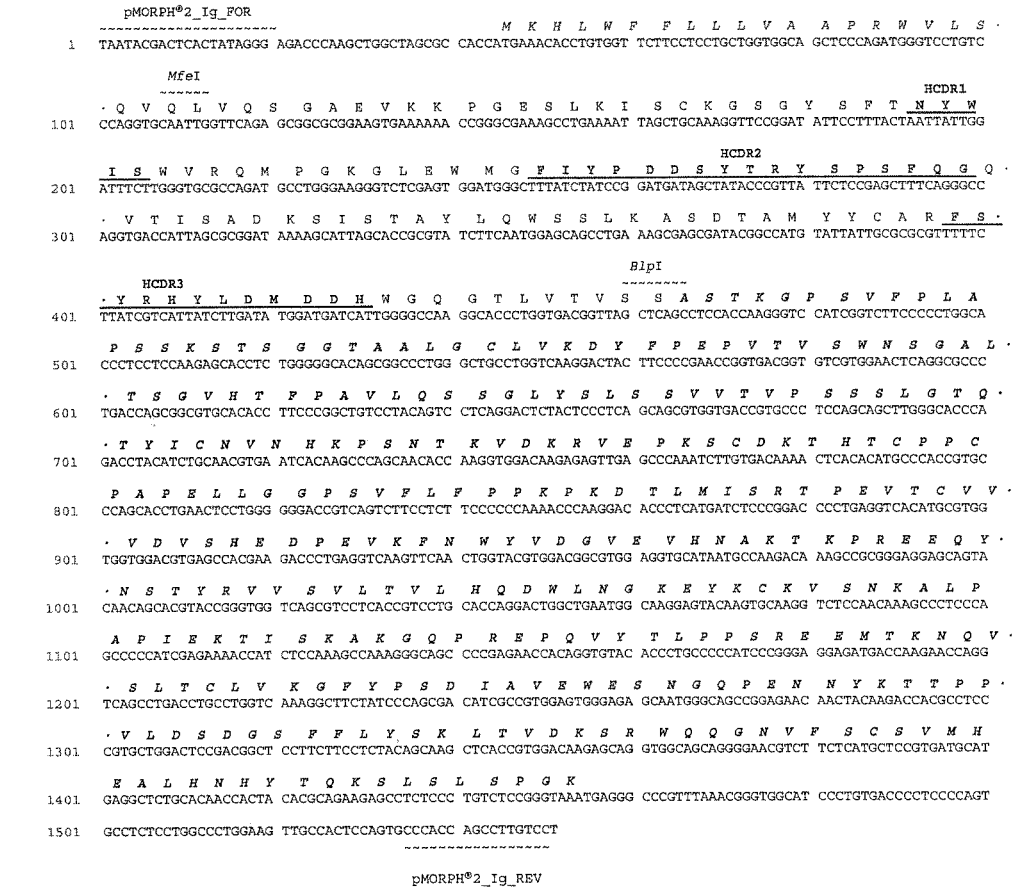


FIG. 7B

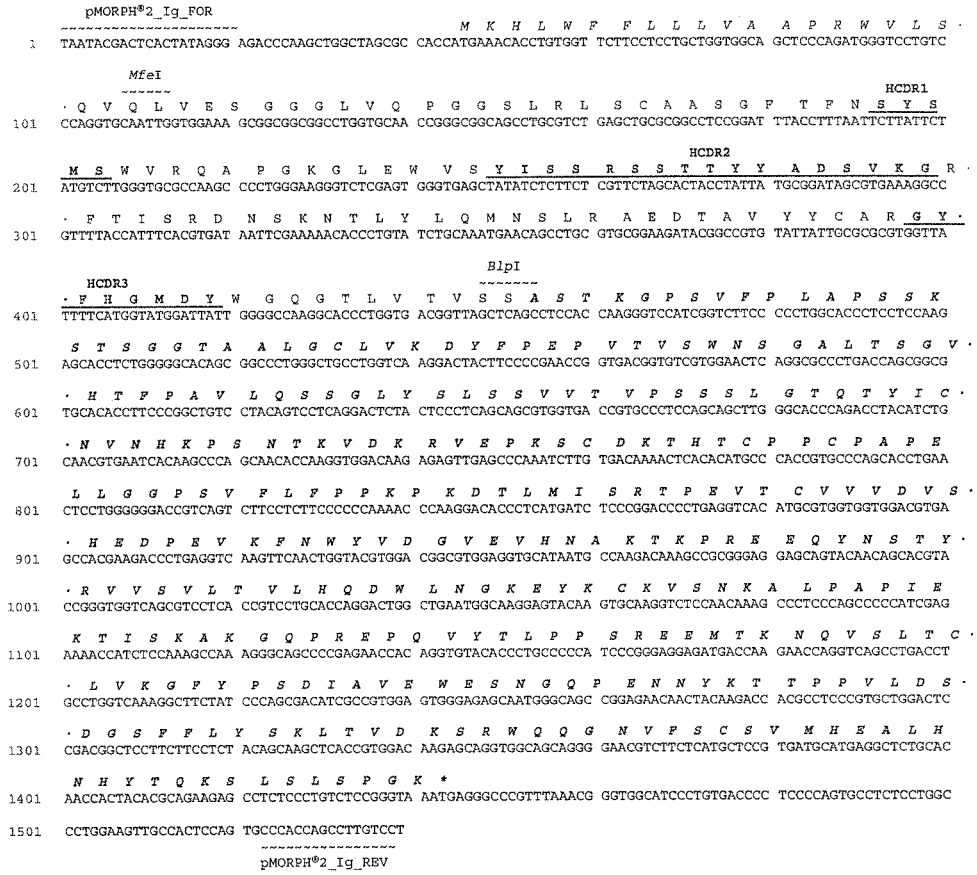


FIG. 8

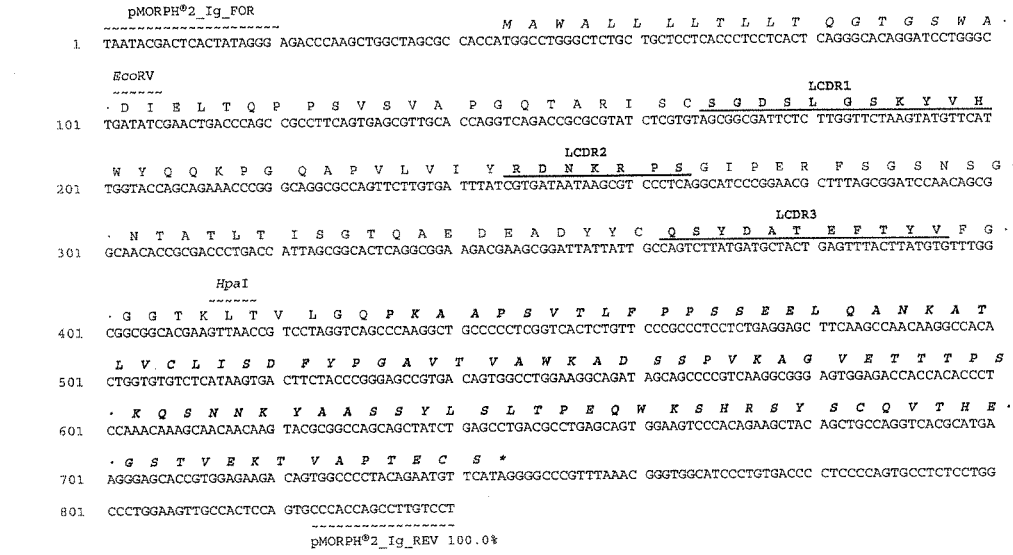

pMORPH®2_Ig_FOR
M A W A L L L L T L L T Q G T G S W A ·
1 TAATACGACTCACTATAGGG AGACCCAAGCTGGCTAGCGC CACCATGGCCTGGGCTCTGC TGCTCCTCACCCTCCTCACT CAGGGCACAGGATCCTGGGC
EcoRV
LCDR1
· D I E L T Q P P S V S V A P G Q T A R I S C S G D S L G S K Y V H
101 TGATATCGAACTGACCCAGC CGCCTTCAGTGAGCGTTGCA CCAGGTCAGACCGCGCGTAT CTCGTGTAGCGGCGATTCTC TTGGTTCTAAGTATGTTCAT
LCDR2
W Y Q Q K P G Q A P V L V I Y R D N K R P S G I P E R F S G S N S G ·
201 TGGTACCAGCAGAAACCCGG GCAGGCGCCAGTTCTTGTGA TTTATCGTGATAATAAGCGT CCCTCAGGCATCCCGGAACG CTTTAGCGGATCCAACAGCG
LCDR3
· N T A T L T I S G T Q A E D E A D Y Y C Q S Y D A T E F T Y V F G ·
301 GCAACACCGCGACCCTGACC ATTAGCGGCACTCAGGCGGA AGACGAAGCGGATTATTATT GCCAGTCTTATGATGCTACT GAGTTTACTTATGTGTTTGG
HpaI
· G G T K L T V L G Q P K A A P S V T L F P P S S E E L Q A N K A T
401 CGGCGGCACGAAGTTAACCG TCCTAGGTCAGCCCAAGGCT GCCCCCTCGGTCACTCTGTT CCCGCCCTCCTCTGAGGAGC TTCAAGCCAACAAGGCCACA
L V C L I S D F Y P G A V T V A W K A D S S P V K A G V E T T T P S ·
501 CTGGTGTGTCTCATAAGTGA CTTCTACCCGGGAGCCGTGA CAGTGGCCTGGAAGGCAGAT AGCAGCCCCGTCAAGGCGGG AGTGGAGACCACCACACCCT
· K Q S N N K Y A A S S Y L S L T P E Q W K S H R S Y S C Q V T H E ·
601 CCAAACAAAGCAACAACAAG TACGCGGCCAGCAGCTATCT GAGCCTGACGCCTGAGCAGT GGAAGTCCCACAGAAGCTAC AGCTGCCAGGTCACGCATGA
· G S T V E K T V A P T E C S *
701 AGGGAGCACCGTGGAGAAGA CAGTGGCCCCTACAGAATGT TCATAGGGGCCCGTTTAAAC GGGTGGCATCCCTGTGACCC CTCCCCAGTGCCTCTCCTGG
801 CCCTGGAAGTTGCCACTCCA GTGCCCACCAGCCTTGTCCT
pMORPH®2_Ig_REV 100.0%

FIG. 9A

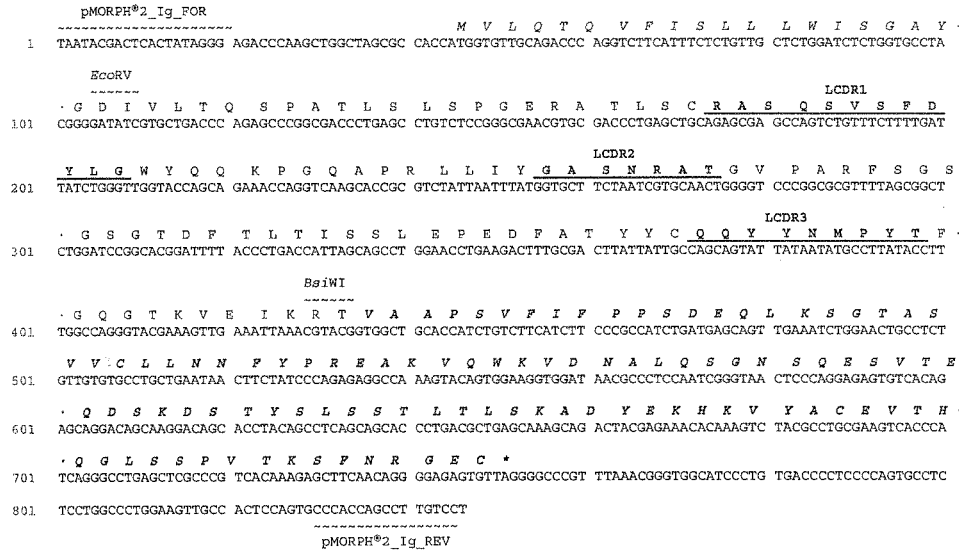

pMORPH®2_Ig_FOR
M V L Q T Q V F I S L L L W I S G A Y ·
1 TAATACGACTCACTATAGGG AGACCCAAGCTGGCTAGCGC CACCATGGTGTTGCAGACCC AGGTCTTCATTTCTCTGTTG CTCTGGATCTCTGGTGCCTA
EcoRV
LCDR1
· G D I V L T Q S P A T L S L S P G E R A T L S C R A S Q S V S F D
101 CGGGGATATCGTGCTGACCC AGAGCCCGGCGACCCTGAGC CTGTCTCCGGGCGAACGTGC GACCCTGAGCTGCAGAGCGA GCCAGTCTGTTTCTTTTGAT
LCDR2
Y L G W Y Q Q K P G Q A P R L L I Y G A S N R A T G V P A R F S G S ·
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LCDR3
· G S G T D F T L T I S S L E P E D F A T Y Y C Q Q Y Y N M P Y T F ·
301 CTGGATCCGGCACGGATTTT ACCCTGACCATTAGCAGCCT GGAACCTGAAGACTTTGCGA CTTATTATTGCCAGCAGTAT TATAATATGCCTTATACCTT
BsiWI
· G Q G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S
401 TGGCCAGGGTACGAAAGTTG AAATTAAACGTACGGTGGCT GCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGT TGAAATCTGGAACTGCCTCT
V V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E ·
501 GTTGTGTGCCTGCTGAATAA CTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGAT AACGCCCTCCAATCGGGTAA CTCCCAGGAGAGTGTCACAG
· Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H ·
601 AGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCAC CCTGACGCTGAGCAAAGCAG ACTACGAGAAACACAAAGTC TACGCCTGCGAAGTCACCCA
· Q G L S S P V T K S F N R G E C *
701 TCAGGGCCTGAGCTCGCCCG TCACAAAGAGCTTCAACAGG GGAGAGTGTTAGGGGCCCGT TTAAACGGGTGGCATCCCTG TGACCCCTCCCCAGTGCCTC
801 TCCTGGCCCTGGAAGTTGCC ACTCCAGTGCCCACCAGCCT TGTCCT
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FIG. 9B

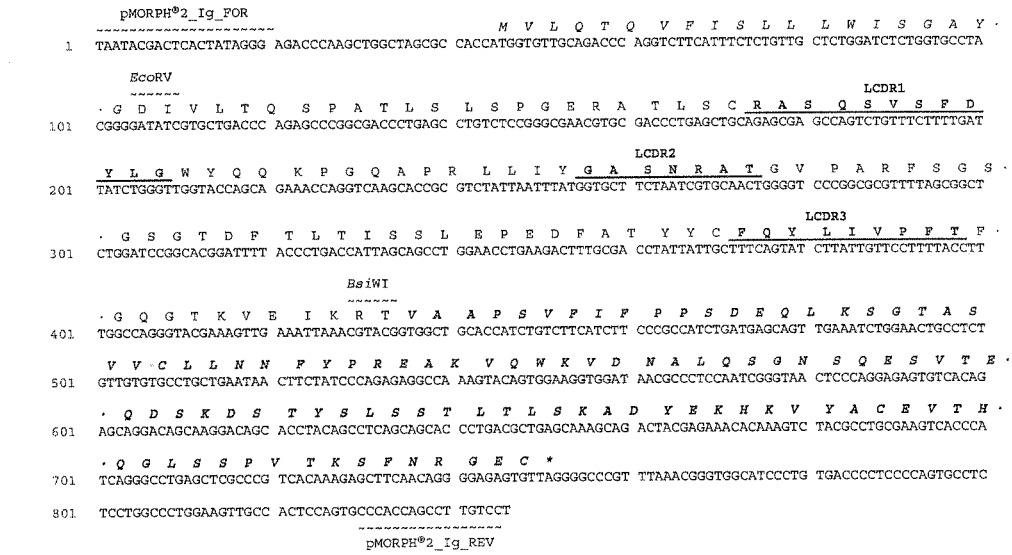

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EcoRV
LCDR1
· G D I V L T Q S P A T L S L S P G E R A T L S C R A S Q S V S F D
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LCDR2
Y L G W Y Q Q K P G Q A P R L L I Y G A S N R A T G V P A R F S G S ·
201 TATCTGGGTTGGTACCAGCA GAAACCAGGTCAAGCACCGC GTCTATTAATTTATGGTGCT TCTAATCGTGCAACTGGGGT CCCGGCGCGTTTTAGCGGCT
LCDR3
· G S G T D F T L T I S S L E P E D F A T Y Y C F Q Y L I V P F T F ·
301 CTGGATCCGGCACGGATTTT ACCCTGACCATTAGCAGCCT GGAACCTGAAGACTTTGCGA CCTATTATTGCTTTCAGTAT CTTATTGTTCCTTTTACCTT
BsiWI
· G Q G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S
401 TGGCCAGGGTACGAAAGTTG AAATTAAACGTACGGTGGCT GCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGT TGAAATCTGGAACTGCCTCT
V V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E ·
501 GTTGTGTGCCTGCTGAATAA CTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGAT AACGCCCTCCAATCGGGTAA CTCCCAGGAGAGTGTCACAG
· Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H ·
601 AGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCAC CCTGACGCTGAGCAAAGCAG ACTACGAGAAACACAAAGTC TACGCCTGCGAAGTCACCCA
· Q G L S S P V T K S F N R G E C *
701 TCAGGGCCTGAGCTCGCCCG TCACAAAGAGCTTCAACAGG GGAGAGTGTTAGGGGCCCGT TTAAACGGGTGGCATCCCTG TGACCCCTCCCCAGTGCCTC
801 TCCTGGCCCTGGAAGTTGCC ACTCCAGTGCCCACCAGCCT TGTCCT
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FIG. 9C

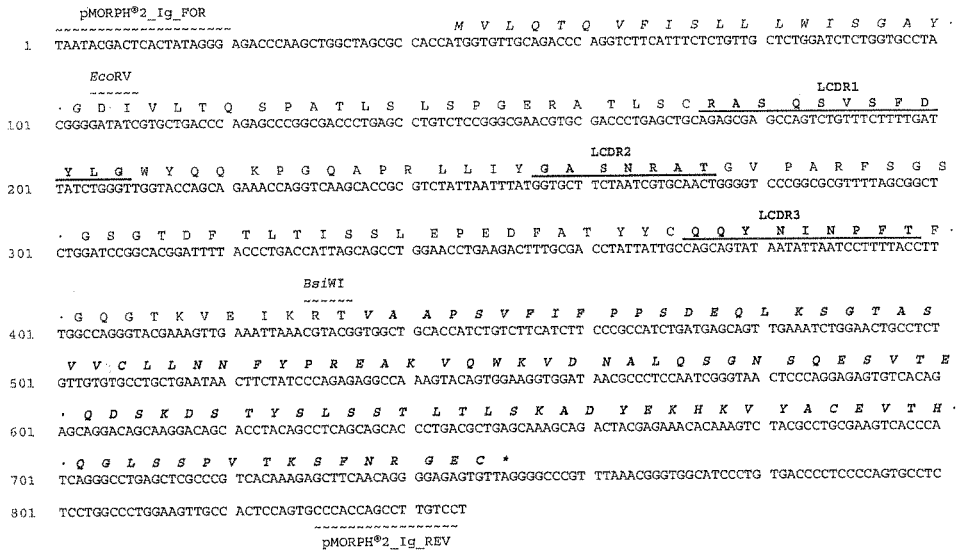

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EcoRV
LCDR1
· G D I V L T Q S P A T L S L S P G E R A T L S C R A S Q S V S F D
101 CGGGGATATCGTGCTGACCC AGAGCCCGGCGACCCTGAGC CTGTCTCCGGGCGAACGTGC GACCCTGAGCTGCAGAGCGA GCCAGTCTGTTTCTTTTGAT
LCDR2
Y L G W Y Q Q K P G Q A P R L L I Y G A S N R A T G V P A R F S G S ·
201 TATCTGGGTTGGTACCAGCA GAAACCAGGTCAAGCACCGC GTCTATTAATTTATGGTGCT TCTAATCGTGCAACTGGGGT CCCGGCGCGTTTTAGCGGCT
LCDR3
· G S G T D F T L T I S S L E P E D F A T Y Y C Q Q Y N I N P F T F ·
301 CTGGATCCGGCACGGATTTT ACCCTGACCATTAGCAGCCT GGAACCTGAAGACTTTGCGA CCTATTATTGCCAGCAGTAT AATATTAATCCTTTTACCTT
BsiWI
· G Q G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S
401 TGGCCAGGGTACGAAAGTTG AAATTAAACGTACGGTGGCT GCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGT TGAAATCTGGAACTGCCTCT
V V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E ·
501 GTTGTGTGCCTGCTGAATAA CTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGAT AACGCCCTCCAATCGGGTAA CTCCCAGGAGAGTGTCACAG
· Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H ·
601 AGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCAC CCTGACGCTGAGCAAAGCAG ACTACGAGAAACACAAAGTC TACGCCTGCGAAGTCACCCA
· Q G L S S P V T K S F N R G E C *
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FIG. 9D

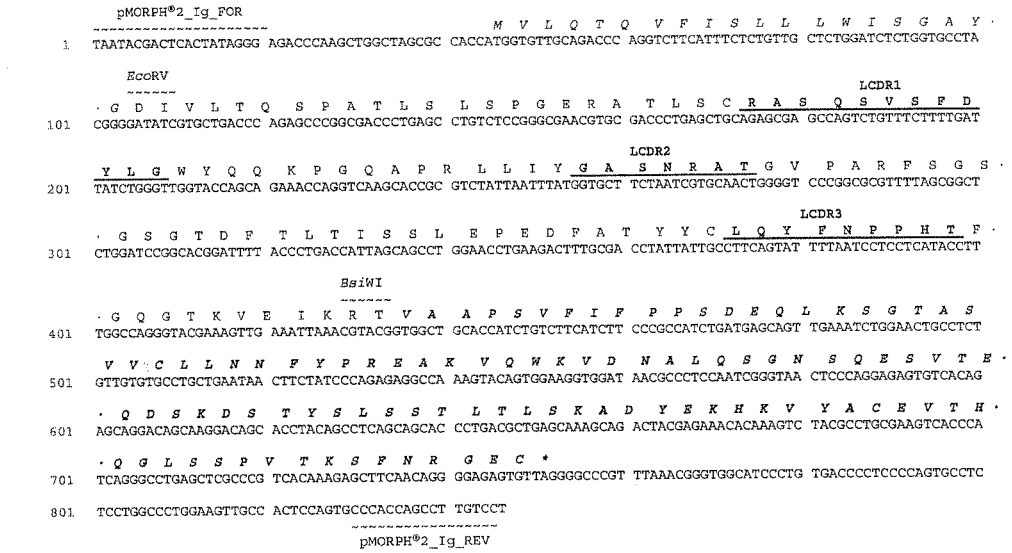

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LCDR1
· G D I V L T Q S P A T L S L S P G E R A T L S C R A S Q S V S F D
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LCDR2
Y L G W Y Q Q K P G Q A P R L L I Y G A S N R A T G V P A R F S G S ·
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LCDR3
· G S G T D F T L T I S S L E P E D F A T Y Y C L Q Y F N P P H T F ·
301 CTGGATCCGGCACGGATTTT ACCCTGACCATTAGCAGCCT GGAACCTGAAGACTTTGCGA CCTATTATTGCCTTCAGTAT TTTAATCCTCCTCATACCTT
BsiWI
· G Q G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S
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V V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E ·
501 GTTGTGTGCCTGCTGAATAA CTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGAT AACGCCCTCCAATCGGGTAA CTCCCAGGAGAGTGTCACAG
· Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H ·
601 AGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCAC CCTGACGCTGAGCAAAGCAG ACTACGAGAAACACAAAGTC TACGCCTGCGAAGTCACCCA
· Q G L S S P V T K S F N R G E C *
701 TCAGGGCCTGAGCTCGCCCG TCACAAAGAGCTTCAACAGG GGAGAGTGTTAGGGGCCCGT TTAAACGGGTGGCATCCCTG TGACCCCTCCCCAGTGCCTC
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FIG. 9E

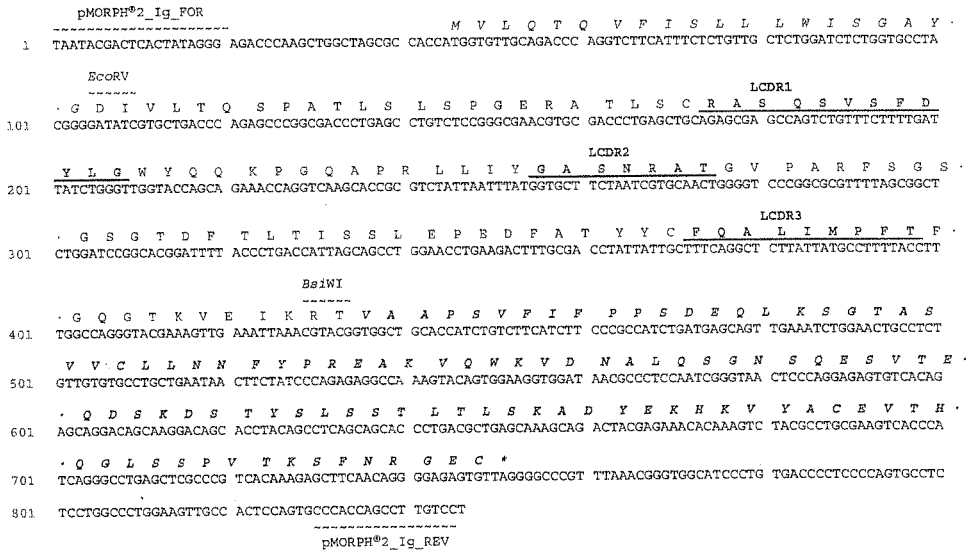
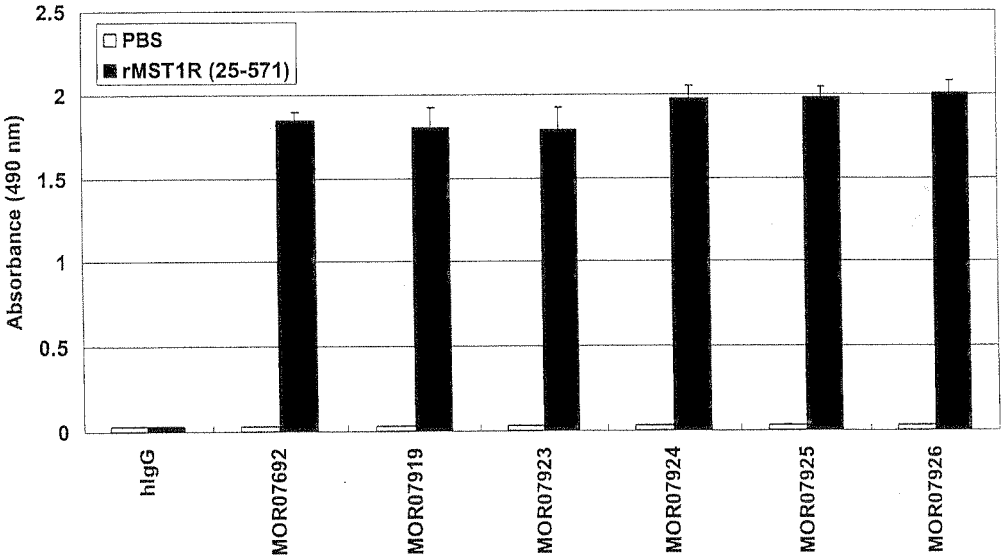

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LCDR1
G D I V L T Q S P A T L S L S P G E R A T L S C R A S Q S V S F D
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Y L G W Y Q Q K P G Q A P R L L I Y G A S N R A T G V P A R F S G S
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BsiWI
G Q G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S
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Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H
601 AGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCAC CCTGACGCTGAGCAAAGCAG ACTACGAGAAACACAAAGTC TACGCCTGCGAAGTCACCCA
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801 TCCTGGCCCTGGAAGTTGCC ACTCCAGTGCCCACCAGCCT TGTCCT
pMORPH®2_Ig_REV

FIG. 11


2.5
2
1.5
1
0.5
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<151> 2009-02-10

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35 40 45

Ala Ile Arg Asn Arg Leu His Val Leu Gly Pro Asp Leu Lys Ser Val
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Gln Ser Leu Ala Thr Gly Pro Ala Gly Asp Pro Gly Cys Gln Thr Cys
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Lys Val Leu Val Leu Asp Pro Ala Leu Pro Ala Leu Val Ser Cys Gly
100 105 110

Ser Ser Leu Gln Gly Arg Cys Phe Leu His Asp Leu Glu Pro Gln Gly
115 120 125

Thr Ala Val His Leu Ala Ala Pro Ala Cys Leu Phe Ser Ala His His
130 135 140

Asn Arg Pro Asp Asp Cys Pro Asp Cys Val Ala Ser Pro Leu Gly Thr
145 150 155 160

Arg Val Thr Val Val Glu Gln Gly Gln Ala Ser Tyr Phe Tyr Val Ala
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Ser Ile Arg Arg Leu Lys Ala Asp Ala Ser Gly Phe Ala Pro Gly Phe
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Val Ala Leu Ser Val Leu Pro Lys His Leu Val Ser Tyr Ser Ile Glu
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Tyr Val His Ser Phe His Thr Gly Ala Phe Val Tyr Phe Leu Thr Val
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Leu Ile Asp Glu Gly Val Glu Arg Cys Cys Glu Ser Pro Val His Pro
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Gly Leu Arg Arg Gly Leu Asp Phe Phe Gln Ser Pro Ser Phe Cys Pro
370 375 380

Asn Pro Pro Gly Leu Glu Ala Leu Ser Pro Asn Thr Ser Cys Arg His
385 390 395 400

Phe Pro Leu Leu Val Ser Ser Ser Phe Ser Arg Val Asp Leu Phe Asn
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Asp Asn Val Thr Val Ala His Met Gly Thr Met Asp Gly Arg Ile Leu
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Phe Ser Leu Gly Asp Ser Gly Gln Pro Val Gln Arg Asp Val Ser Arg
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Leu Gly Asp His Leu Leu Phe Ala Ser Gly Asp Gln Val Phe Gln Val
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Pro Ile Arg Gly Pro Gly Cys Arg His Phe Leu Thr Cys Gly Arg Cys
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Leu Arg Ala Trp His Phe Met Gly Cys Gly Trp Cys Gly Asn Met Cys
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20 25 30

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Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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Ser Tyr Ile Ser Ser Arg Ser Ser Thr Thr Tyr Tyr Ala Asp Ser Val
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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
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Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

gcg cgt ggt tat ttt cat ggt atg gat tat tgg ggc caa ggc acc ctg 336
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35 40 45

Ser Tyr Ile Ser Ser Arg Ser Ser Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
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Val Thr Val Ser Ser
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Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Asn Tyr
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Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
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Gly Phe Ile Tyr Pro Asp Asp Ser Tyr Thr Arg Tyr Ser Pro Ser Phe
50 55 60

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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Phe Asp
20 25 30

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65 70 75 80

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<213> Homo sapiens

<400> 23

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Phe Asp
20 25 30

Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Asn Met Pro
85 90 95

Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 24
<211> 330
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(330)

<400> 24
gat atc gaa ctg acc cag ccg cct tca gtg agc gtt gca cca ggt cag 48
Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln

1 5 10 15

acc gcg cgt atc tcg tgt agc ggc gat tct ctt ggt tct aag tat gtt 96
Thr Ala Arg Ile Ser Cys Ser Gly Asp Ser Leu Gly Ser Lys Tyr Val
20 25 30

cat tgg tac cag cag aaa ccc ggg cag gcg cca gtt ctt gtg att tat 144
His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

cgt gat aat aag cgt ccc tca ggc atc ccg gaa cgc ttt agc gga tcc 192
Arg Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

aac agc ggc aac acc gcg acc ctg acc att agc ggc act cag gcg gaa 240
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
65 70 75 80

gac gaa gcg gat tat tat tgc cag tct tat gat gct act gag ttt act 288
Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ala Thr Glu Phe Thr
85 90 95

tat gtg ttt ggc ggc ggc acg aag tta acc gtt ctt ggc cag 330
Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
100 105 110

<210> 25
<211> 110
<212> PRT
<213> Homo sapiens

<400> 25

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

Thr Ala Arg Ile Ser Cys Ser Gly Asp Ser Leu Gly Ser Lys Tyr Val
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

Arg Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ala Thr Glu Phe Thr
85 90 95

Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
100 105 110

<210> 26
<211> 330
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(330)

<400> 26
gat atc gtg ctg acc cag agc ccg gcg acc ctg agc ctg tct ccg ggc 48
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

gaa cgt gcg acc ctg agc tgc aga gcg agc cag tct gtt tct ttt gat 96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Phe Asp
20 25 30

tat ctg ggt tgg tac cag cag aaa cca ggt caa gca ccg cgt cta tta 144
Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

att tat ggt gct tct aat cgt gca act ggg gtc ccg gcg cgt ttt agc 192
Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

ggc tct gga tcc ggc acg gat ttt acc ctg acc att agc agc ctg gaa 240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

cct gaa gac ttt gcg acc tat tat tgc ttt cag tat ctt att gtt cct 288
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Tyr Leu Ile Val Pro
85 90 95

ttt acc ttt ggc cag ggt acg aaa gtt gaa att aaa cgt acg 330
Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 27
<211> 110
<212> PRT
<213> Homo sapiens

<400> 27

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Phe Asp
20 25 30

Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Tyr Leu Ile Val Pro
85 90 95

Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 28
<211> 330
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(330)

<400> 28
gat atc gtg ctg acc cag agc ccg gcg acc ctg agc ctg tct ccg ggc 48
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

gaa cgt gcg acc ctg agc tgc aga gcg agc cag tct gtt tct ttt gat 96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Phe Asp
20 25 30

tat ctg ggt tgg tac cag cag aaa cca ggt caa gca ccg cgt cta tta 144
Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

att tat ggt gct tct aat cgt gca act ggg gtc ccg gcg cgt ttt agc 192
Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

ggc tct gga tcc ggc acg gat ttt acc ctg acc att agc agc ctg gaa 240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

cct gaa gac ttt gcg acc tat tat tgc cag cag tat aat att aat cct 288
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Asn Pro
85 90 95

ttt acc ttt ggc cag ggt acg aaa gtt gaa att aaa cgt acg 330
Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 29
<211> 110
<212> PRT

<213> Homo sapiens

<400> 29

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Phe Asp
20 25 30

Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Asn Pro
85 90 95

Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 30
<211> 330
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(330)

<400> 30
gat atc gtg ctg acc cag agc ccg gcg acc ctg agc ctg tct ccg ggc 48
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

gaa cgt gcg acc ctg agc tgc aga gcg agc cag tct gtt tct ttt gat 96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Phe Asp
20 25 30

tat ctg ggt tgg tac cag cag aaa cca ggt caa gca ccg cgt cta tta 144
Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

att tat ggt gct tct aat cgt gca act ggg gtc ccg gcg cgt ttt agc 192
Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

ggc tct gga tcc ggc acg gat ttt acc ctg acc att agc agc ctg gaa 240

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

cct gaa gac ttt gcg acc tat tat tgc ctt cag tat ttt aat cct cct 288
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Tyr Phe Asn Pro Pro
85 90 95

cat acc ttt ggc cag ggt acg aaa gtt gaa att aaa cgt acg 330
His Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 31
<211> 110
<212> PRT
<213> Homo sapiens

<400> 31

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Phe Asp
20 25 30

Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Tyr Phe Asn Pro Pro
85 90 95

His Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 32
<211> 330
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(330)

<400> 32
gat atc gtg ctg acc cag agc ccg gcg acc ctg agc ctg tct ccg ggc 48
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly

1 5 10 15

gaa cgt gcg acc ctg agc tgc aga gcg agc cag tct gtt tct ttt gat 96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Phe Asp
20 25 30

tat ctg ggt tgg tac cag cag aaa cca ggt caa gca ccg cgt cta tta 144
Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

att tat ggt gct tct aat cgt gca act ggg gtc ccg gcg cgt ttt agc 192
Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

ggc tct gga tcc ggc acg gat ttt acc ctg acc att agc agc ctg gaa 240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

cct gaa gac ttt gcg acc tat tat tgc ttt cag gct ctt att atg cct 288
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Ala Leu Ile Met Pro
85 90 95

ttt acc ttt ggc cag ggt acg aaa gtt gaa att aaa cgt acg 330
Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 33
<211> 110
<212> PRT
<213> Homo sapiens

<400> 33

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Phe Asp
20 25 30

Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Ala Leu Ile Met Pro
85 90 95

Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 34
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR forward primer

<400> 34
ttggcccagt ccagacctcg agtc 24

<210> 35
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR reverse primer

<400> 35
actctgtgga gtgagggacc taatg 25

<210> 36
<211> 4200
<212> DNA
<213> Macaca fascicularis

<220>
<221> CDS
<222> (1)..(4200)

<400> 36
atg gag ctc ctc cct ccg ctg cct cag tcc ttc tta ctg ctg ctg ctg 48
Met Glu Leu Leu Pro Pro Leu Pro Gln Ser Phe Leu Leu Leu Leu Leu
1 5 10 15

ttg cct gcc aag ccc gcg gcg gcc aag gaa tgg cag tgc ccg cgc acc 96
Leu Pro Ala Lys Pro Ala Ala Ala Lys Glu Trp Gln Cys Pro Arg Thr
20 25 30

ccc tac gcg gcc tct cga gac ttt aac gtg aag tac atg gtg ccc agc 144
Pro Tyr Ala Ala Ser Arg Asp Phe Asn Val Lys Tyr Met Val Pro Ser
35 40 45

ttc tcc gcc gga ggc ctg gtg cag acc atg gtg acc tac cag ggc gac 192
Phe Ser Ala Gly Gly Leu Val Gln Thr Met Val Thr Tyr Gln Gly Asp
50 55 60

aaa aat gag agt gct gtg ttt gta gcc ata cgc aat cgc ctg cac gtg 240
Lys Asn Glu Ser Ala Val Phe Val Ala Ile Arg Asn Arg Leu His Val
65 70 75 80

ctt ggg cct gac ctg aag tct gtc cag agc ctg gcc acg ggc cct gct 288
Leu Gly Pro Asp Leu Lys Ser Val Gln Ser Leu Ala Thr Gly Pro Ala
85 90 95

ggg gac cct ggc tgc cag acg tgt gca gcc tgt ggc cca ggc ccc cac 336
Gly Asp Pro Gly Cys Gln Thr Cys Ala Ala Cys Gly Pro Gly Pro His
100 105 110

ggc cct tcc ggt gac aca gac aca aag gtg ctg gtg ctg gag ccc gcg 384
Gly Pro Ser Gly Asp Thr Asp Thr Lys Val Leu Val Leu Glu Pro Ala
115 120 125

ctg cct gcc ctg gtc agt tgt ggc tcc agc ctg cag ggc cgc tgc ttc 432
Leu Pro Ala Leu Val Ser Cys Gly Ser Ser Leu Gln Gly Arg Cys Phe
130 135 140

ctg cat gac cta gat ccc caa ggg aca gcc gtg cat ctg gca gcg cca 480
Leu His Asp Leu Asp Pro Gln Gly Thr Ala Val His Leu Ala Ala Pro
145 150 155 160

gcc tgc ctc ttc tca gcc cac cat aac cgg ccc gat gac tgc ccc gac 528
Ala Cys Leu Phe Ser Ala His His Asn Arg Pro Asp Asp Cys Pro Asp
165 170 175

tgt gtg gcc agc cca ttg ggc acc cgt gtg act gtg gtt gag caa ggc 576
Cys Val Ala Ser Pro Leu Gly Thr Arg Val Thr Val Val Glu Gln Gly
180 185 190

cag gcc tcc tat ttc tac gtg gca tcc tca ctg gac gca gcc gtg gct 624
Gln Ala Ser Tyr Phe Tyr Val Ala Ser Ser Leu Asp Ala Ala Val Ala
195 200 205

gcc agc ttc agc cca cgc tca gtg tct atc agg cgt ctc aag gcc gac 672
Ala Ser Phe Ser Pro Arg Ser Val Ser Ile Arg Arg Leu Lys Ala Asp
210 215 220

gcc tcg gga ttt gca ccg ggc ttt gtg gca ttg tca gtg ctg ccc aag 720
Ala Ser Gly Phe Ala Pro Gly Phe Val Ala Leu Ser Val Leu Pro Lys
225 230 235 240

cat ctt gtc tcc tac agt att gaa tat gtg cac agc ttc cat acg gga 768
His Leu Val Ser Tyr Ser Ile Glu Tyr Val His Ser Phe His Thr Gly
245 250 255

gcc ttc gtc tac ttc ctg act gta cag ccg gcc agc gtg act gat gct 816
Ala Phe Val Tyr Phe Leu Thr Val Gln Pro Ala Ser Val Thr Asp Ala
260 265 270

cct ggt gcc ctg cac aca cgc ctg gca cga ctt agc gcc act gag cca 864
Pro Gly Ala Leu His Thr Arg Leu Ala Arg Leu Ser Ala Thr Glu Pro
275 280 285

gag ttg ggt gac tat cgg gag ctg gtc ctc gac tgc aga ttt gct cca 912
Glu Leu Gly Asp Tyr Arg Glu Leu Val Leu Asp Cys Arg Phe Ala Pro
290 295 300

aaa cgc agg cgc cgg ggg gcc cca gag ggc gga cag ccc tac cct gtg 960
Lys Arg Arg Arg Arg Gly Ala Pro Glu Gly Gly Gln Pro Tyr Pro Val
305 310 315 320

ctg cgg gtg gcc cac tct gct cca gtg ggt gct caa ctt gcc act gag 1008
Leu Arg Val Ala His Ser Ala Pro Val Gly Ala Gln Leu Ala Thr Glu
325 330 335

ctg agc att gct gag ggc cag gaa gtg cta ttt ggg gtc ttt gtg gct 1056
Leu Ser Ile Ala Glu Gly Gln Glu Val Leu Phe Gly Val Phe Val Ala
340 345 350

ggc aag gat agt ggc cct ggc gtg ggc ccc aac tct gtc gtc tgt gcc 1104
Gly Lys Asp Ser Gly Pro Gly Val Gly Pro Asn Ser Val Val Cys Ala
355 360 365

ttc ccc att gac ctg ctg gac aca tta att gat gaa ggt gtg gag cgc 1152
Phe Pro Ile Asp Leu Leu Asp Thr Leu Ile Asp Glu Gly Val Glu Arg
370 375 380

tgt tgt gaa tcc cca gtc cat cca ggc ctc cgg cga ggc ctc gac ttc 1200
Cys Cys Glu Ser Pro Val His Pro Gly Leu Arg Arg Gly Leu Asp Phe
385 390 395 400

ttc cag tca ccc agt ttt tgc ccc aac ccg cct ggc ctg gag gcc ccc 1248
Phe Gln Ser Pro Ser Phe Cys Pro Asn Pro Pro Gly Leu Glu Ala Pro
405 410 415

agc ccc aac acc agc tgc cgc cac ttc cct ttg ctg gtc agt agc agc 1296
Ser Pro Asn Thr Ser Cys Arg His Phe Pro Leu Leu Val Ser Ser Ser
420 425 430

ttc tca cgt gtg gac cta ttc aat ggg ctg ttg gga aca gta gag gtc 1344
Phe Ser Arg Val Asp Leu Phe Asn Gly Leu Leu Gly Thr Val Glu Val
435 440 445

act gca ctg tat gtg aca cgc ctt gac aac gtc aca gtg gca cac atg 1392
Thr Ala Leu Tyr Val Thr Arg Leu Asp Asn Val Thr Val Ala His Met
450 455 460

ggc aca gcg gat ggg cgt atc ctg cag gtg gag ctg gcc agg tca ctc 1440
Gly Thr Ala Asp Gly Arg Ile Leu Gln Val Glu Leu Ala Arg Ser Leu
465 470 475 480

aac tac ttg ctg tat gtg tcc aac ttc tca ctg ggt gac agt ggg cag 1488
Asn Tyr Leu Leu Tyr Val Ser Asn Phe Ser Leu Gly Asp Ser Gly Gln
485 490 495

ccc gtg cag cgg gat gtc agt cgc ctt ggg gac cac cta ttc ttc gcc 1536
Pro Val Gln Arg Asp Val Ser Arg Leu Gly Asp His Leu Phe Phe Ala
500 505 510

tct ggg gac cag gtt ttc cag gta cct atc caa ggc cct ggc tgc cgc 1584
Ser Gly Asp Gln Val Phe Gln Val Pro Ile Gln Gly Pro Gly Cys Arg
515 520 525

cac ttc ctc acc tgt ggg cgt tgc cta agg gca cag cgt ttc atg ggc 1632
His Phe Leu Thr Cys Gly Arg Cys Leu Arg Ala Gln Arg Phe Met Gly
530 535 540

tgt ggc tgg tgt ggg aac atg tgt ggc cgg cag aag gag tgt cct ggc 1680
Cys Gly Trp Cys Gly Asn Met Cys Gly Arg Gln Lys Glu Cys Pro Gly
545 550 555 560

tcc tgg caa cag gac cac tgt ccg cct aag ctt act gag ttc cac ccc 1728
Ser Trp Gln Gln Asp His Cys Pro Pro Lys Leu Thr Glu Phe His Pro
565 570 575

cac agt gga cct tta agg ggc agt aca agg ctg acc ctg tgt ggc tcc 1776
His Ser Gly Pro Leu Arg Gly Ser Thr Arg Leu Thr Leu Cys Gly Ser
580 585 590

aac ttc tac ctg cac cct tct ggt ctg gtg cct gag gga acc cat cag 1824
Asn Phe Tyr Leu His Pro Ser Gly Leu Val Pro Glu Gly Thr His Gln
595 600 605

atc acg gtg ggc caa agt ccc tgc cgg cca ctg ccc aag gac agc tca 1872
Ile Thr Val Gly Gln Ser Pro Cys Arg Pro Leu Pro Lys Asp Ser Ser
610 615 620

aaa ctc aga cca gtg ccc cgg aaa gac ttt gta gag gag ttt gag tgt 1920
Lys Leu Arg Pro Val Pro Arg Lys Asp Phe Val Glu Glu Phe Glu Cys
625 630 635 640

gaa ctg gag ccc ttg ggc acc caa gca gtg ggg cct acc aac gtc agc 1968
Glu Leu Glu Pro Leu Gly Thr Gln Ala Val Gly Pro Thr Asn Val Ser
645 650 655

ctc acc gtg act aac atg cca ccg ggc aag cac ttc cgg gta gac ggc 2016
Leu Thr Val Thr Asn Met Pro Pro Gly Lys His Phe Arg Val Asp Gly
660 665 670

acc tcc atg ctg aga ggc ttc ttt ttc atg gag cca gtg ctg ata gca 2064
Thr Ser Met Leu Arg Gly Phe Phe Phe Met Glu Pro Val Leu Ile Ala
675 680 685

gtg caa ccc ctc ttt ggc cca cgg gca gga ggc acc tgt ctc act ctt 2112
Val Gln Pro Leu Phe Gly Pro Arg Ala Gly Gly Thr Cys Leu Thr Leu
690 695 700

gaa ggc cag agt ctg tct gta ggc acc agc cgg gct gtg ctg gtc aat 2160
Glu Gly Gln Ser Leu Ser Val Gly Thr Ser Arg Ala Val Leu Val Asn
705 710 715 720

ggg act gag tgt ctg cta gca cgg gtc agt gag ggg cag ctt tta tgt 2208
Gly Thr Glu Cys Leu Leu Ala Arg Val Ser Glu Gly Gln Leu Leu Cys
725 730 735

gcc aca ccc cct ggg gcc atg gtg gcc agt gtc ccc ctt agc ctg cag 2256
Ala Thr Pro Pro Gly Ala Met Val Ala Ser Val Pro Leu Ser Leu Gln
740 745 750

gtg ggg ggt gcc cag gta cct ggt tcc tgg acc ttc cac tac aga gaa 2304
Val Gly Gly Ala Gln Val Pro Gly Ser Trp Thr Phe His Tyr Arg Glu
755 760 765

gac cct gtc gtg cta agc atc agc ccc aac tgt ggc tac agc aac tcc 2352
Asp Pro Val Val Leu Ser Ile Ser Pro Asn Cys Gly Tyr Ser Asn Ser
770 775 780

cac atc acc atc tgt ggc cag cat cta act tca gca tgg cac tta gtg 2400
His Ile Thr Ile Cys Gly Gln His Leu Thr Ser Ala Trp His Leu Val
785 790 795 800

ctg tca ttc cat gac ggg ctt agg gca gtg gag agc agg tgt gag agg 2448
Leu Ser Phe His Asp Gly Leu Arg Ala Val Glu Ser Arg Cys Glu Arg
805 810 815

cag ctt cca gag cag cag ttg tgc cgc ctg cct gaa tat gtg gtc caa 2496
Gln Leu Pro Glu Gln Gln Leu Cys Arg Leu Pro Glu Tyr Val Val Gln
820 825 830

gac ccc cag gga tgg gtg gca gga aat ctg agt gcc tgg ggg gat gga 2544
Asp Pro Gln Gly Trp Val Ala Gly Asn Leu Ser Ala Trp Gly Asp Gly
835 840 845

gct gct ggc ttt aca ctg cct ggc ttt cgc ttc cta acc cca ccc cat 2592
Ala Ala Gly Phe Thr Leu Pro Gly Phe Arg Phe Leu Thr Pro Pro His
850 855 860

cca ccc agt gcc aac cta att cca ctg aag cct gag gag cat gcc att 2640
Pro Pro Ser Ala Asn Leu Ile Pro Leu Lys Pro Glu Glu His Ala Ile
865 870 875 880

aag ttt gag tat att ggg ctg ggt gct gtg act gac tgc gtg ggt gtc 2688
Lys Phe Glu Tyr Ile Gly Leu Gly Ala Val Thr Asp Cys Val Gly Val
885 890 895

aac gtg acc gtg ggt ggt gag agc tgc cag cac gag ttc cgg ggg gac 2736
Asn Val Thr Val Gly Gly Glu Ser Cys Gln His Glu Phe Arg Gly Asp
900 905 910

atg gtt gtc tgc ccc ctg ccc cca tcc ctg cag ctt ggc aag gat ggt 2784
Met Val Val Cys Pro Leu Pro Pro Ser Leu Gln Leu Gly Lys Asp Gly
915 920 925

gcc cca ctg cag gtc tgc gtg gat ggt gaa tgt cac atc ctg ggt aga 2832
Ala Pro Leu Gln Val Cys Val Asp Gly Glu Cys His Ile Leu Gly Arg
930 935 940

gtg gtg tgg cca ggg cca gat ggg gtc cca cag agc acg ctc ctt ggt 2880
Val Val Trp Pro Gly Pro Asp Gly Val Pro Gln Ser Thr Leu Leu Gly
945 950 955 960

atc ctg ctg cct ttg ctg ctg ctt gtg gcc gca ttg gcc act gca ctg 2928
Ile Leu Leu Pro Leu Leu Leu Leu Val Ala Ala Leu Ala Thr Ala Leu
965 970 975

gtc ttc agc tac tgg tgg cag agg aag cag cta gtt ctt cct ccc aac 2976
Val Phe Ser Tyr Trp Trp Gln Arg Lys Gln Leu Val Leu Pro Pro Asn
980 985 990

ctg gat gac ctg gca tcc ctg gac cag act act gga gcc aca ccc ctg 3024
Leu Asp Asp Leu Ala Ser Leu Asp Gln Thr Thr Gly Ala Thr Pro Leu
995 1000 1005

cct att ctc tac tcg ggc tct gac tac aga agt ggc ctt gca cgc 3069
Pro Ile Leu Tyr Ser Gly Ser Asp Tyr Arg Ser Gly Leu Ala Arg
1010 1015 1020

cct gcc act gat ggt cta gat tcc act tgt gtc cat gga gca tcc 3114
Pro Ala Thr Asp Gly Leu Asp Ser Thr Cys Val His Gly Ala Ser
1025 1030 1035

ttc tcc aat agt gaa gat gaa tcc tgt gtt cca ctg ctg cgg aaa 3159
Phe Ser Asn Ser Glu Asp Glu Ser Cys Val Pro Leu Leu Arg Lys
1040 1045 1050

gag tcc atc cag cta agg gac ctg gac tct gcg ctg ttg gct gag 3204
Glu Ser Ile Gln Leu Arg Asp Leu Asp Ser Ala Leu Leu Ala Glu
1055 1060 1065

gtc aag gat gtg ctg att ccc cat gag cgg gtg gtc gcc cac agt 3249
Val Lys Asp Val Leu Ile Pro His Glu Arg Val Val Ala His Ser
1070 1075 1080

gac cga gtc att ggc aaa ggc cac ttt gga gtt gtc tac cat gga 3294
Asp Arg Val Ile Gly Lys Gly His Phe Gly Val Val Tyr His Gly
1085 1090 1095

gaa tac ata gac cag gcc cag aat cga atc caa tgt gcc atc aag 3339
Glu Tyr Ile Asp Gln Ala Gln Asn Arg Ile Gln Cys Ala Ile Lys
1100 1105 1110

tca cta agt cgc atc aca gag atg cag cag gtg gag gcc ttc ctt 3384
Ser Leu Ser Arg Ile Thr Glu Met Gln Gln Val Glu Ala Phe Leu
1115 1120 1125

cga gag ggg ctg ctc atg cgt ggc ctg aac cac ccg aat gtg ctg 3429
Arg Glu Gly Leu Leu Met Arg Gly Leu Asn His Pro Asn Val Leu
1130 1135 1140

gct ctc att ggt atc atg ttg cca ccc gag ggc ctg ccc cat gtg 3474
Ala Leu Ile Gly Ile Met Leu Pro Pro Glu Gly Leu Pro His Val
1145 1150 1155

ctg ctg ccc tat atg tgc cac ggt gac ctg ctc cag ttc atc cgc 3519
Leu Leu Pro Tyr Met Cys His Gly Asp Leu Leu Gln Phe Ile Arg
1160 1165 1170

tca cct cag cgg aac ccc acc gtg aag gac ctc atc agc ttt ggc 3564
Ser Pro Gln Arg Asn Pro Thr Val Lys Asp Leu Ile Ser Phe Gly
1175 1180 1185

ctg cag gta gcc cat ggc atg gag tac ctc gca gag cag aag ttt 3609
Leu Gln Val Ala His Gly Met Glu Tyr Leu Ala Glu Gln Lys Phe
1190 1195 1200

gtg cac agg gac ctg gct gcg cga aac tgc atg ctg gac gag tca 3654
Val His Arg Asp Leu Ala Ala Arg Asn Cys Met Leu Asp Glu Ser
1205 1210 1215

ttc act gtc aaa gtg gct gac ttt ggt ttg gcc cgt gac atc ctg 3699
Phe Thr Val Lys Val Ala Asp Phe Gly Leu Ala Arg Asp Ile Leu
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gac aag gaa tac tat agt gtt caa cag cat cgc cac gct cgc cta 3744
Asp Lys Glu Tyr Tyr Ser Val Gln Gln His Arg His Ala Arg Leu
1235 1240 1245

cct gtg aag tgg atg gcg ctg gag agc ctg cag acc tat aga ttt 3789
Pro Val Lys Trp Met Ala Leu Glu Ser Leu Gln Thr Tyr Arg Phe
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acc acc aag tct gat gtg tgg tca ttt ggt gtg ctg ctg tgg gaa 3834
Thr Thr Lys Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu
1265 1270 1275

ctg ttg aca cgg ggt gcc cca cca tac ccc cac atc gac cct ttt 3879
Leu Leu Thr Arg Gly Ala Pro Pro Tyr Pro His Ile Asp Pro Phe
1280 1285 1290

gac ctc acc cac ttc ctg gcc cag ggt cgg cgc ctg ccc cag cct 3924
Asp Leu Thr His Phe Leu Ala Gln Gly Arg Arg Leu Pro Gln Pro
1295 1300 1305

gag tat tgc ccc aat tct ctg tac caa gtg atg cag caa tgc tgg 3969
Glu Tyr Cys Pro Asn Ser Leu Tyr Gln Val Met Gln Gln Cys Trp
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gag gcg gac cca gca gca cga ccc acc ttc gga gta cta gtg ggg 4014
Glu Ala Asp Pro Ala Ala Arg Pro Thr Phe Gly Val Leu Val Gly
1325 1330 1335

gaa gtg gag cag ata gtg tct gca ctg ctt ggg gac cat tat gtg 4059
Glu Val Glu Gln Ile Val Ser Ala Leu Leu Gly Asp His Tyr Val
1340 1345 1350

cag ctg cca gca acc tac atg aac ctg ggc ccc agc acc tca cat 4104
Gln Leu Pro Ala Thr Tyr Met Asn Leu Gly Pro Ser Thr Ser His
1355 1360 1365

gag atg aat gtg cat cca gaa cag cag cag tcc tca ccc atg cca 4149
Glu Met Asn Val His Pro Glu Gln Gln Gln Ser Ser Pro Met Pro
1370 1375 1380

ggg agt gca cac cga ccc cgg cca ctc tca gag cct cct cgg ccc 4194
Gly Ser Ala His Arg Pro Arg Pro Leu Ser Glu Pro Pro Arg Pro
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Thr

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<212> PRT
<213> Macaca fascicularis

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Pro Tyr Ala Ala Ser Arg Asp Phe Asn Val Lys Tyr Met Val Pro Ser
35 40 45

Phe Ser Ala Gly Gly Leu Val Gln Thr Met Val Thr Tyr Gln Gly Asp
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Lys Asn Glu Ser Ala Val Phe Val Ala Ile Arg Asn Arg Leu His Val
65 70 75 80

Leu Gly Pro Asp Leu Lys Ser Val Gln Ser Leu Ala Thr Gly Pro Ala
85 90 95

Gly Asp Pro Gly Cys Gln Thr Cys Ala Ala Cys Gly Pro Gly Pro His
100 105 110

Gly Pro Ser Gly Asp Thr Asp Thr Lys Val Leu Val Leu Glu Pro Ala
115 120 125

Leu Pro Ala Leu Val Ser Cys Gly Ser Ser Leu Gln Gly Arg Cys Phe
130 135 140

Leu His Asp Leu Asp Pro Gln Gly Thr Ala Val His Leu Ala Ala Pro
145 150 155 160

Ala Cys Leu Phe Ser Ala His His Asn Arg Pro Asp Asp Cys Pro Asp
165 170 175

Cys Val Ala Ser Pro Leu Gly Thr Arg Val Thr Val Val Glu Gln Gly
180 185 190

Gln Ala Ser Tyr Phe Tyr Val Ala Ser Ser Leu Asp Ala Ala Val Ala
195 200 205

Ala Ser Phe Ser Pro Arg Ser Val Ser Ile Arg Arg Leu Lys Ala Asp
210 215 220

Ala Ser Gly Phe Ala Pro Gly Phe Val Ala Leu Ser Val Leu Pro Lys
225 230 235 240

His Leu Val Ser Tyr Ser Ile Glu Tyr Val His Ser Phe His Thr Gly
245 250 255

Ala Phe Val Tyr Phe Leu Thr Val Gln Pro Ala Ser Val Thr Asp Ala
260 265 270

Pro Gly Ala Leu His Thr Arg Leu Ala Arg Leu Ser Ala Thr Glu Pro
275 280 285

Glu Leu Gly Asp Tyr Arg Glu Leu Val Leu Asp Cys Arg Phe Ala Pro
290 295 300

Lys Arg Arg Arg Arg Gly Ala Pro Glu Gly Gly Gln Pro Tyr Pro Val
305 310 315 320

Leu Arg Val Ala His Ser Ala Pro Val Gly Ala Gln Leu Ala Thr Glu
325 330 335

Leu Ser Ile Ala Glu Gly Gln Glu Val Leu Phe Gly Val Phe Val Ala
340 345 350

Gly Lys Asp Ser Gly Pro Gly Val Gly Pro Asn Ser Val Val Cys Ala
355 360 365

Phe Pro Ile Asp Leu Leu Asp Thr Leu Ile Asp Glu Gly Val Glu Arg
370 375 380

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

Phe Gln Ser Pro Ser Phe Cys Pro Asn Pro Pro Gly Leu Glu Ala Pro
405 410 415

Ser Pro Asn Thr Ser Cys Arg His Phe Pro Leu Leu Val Ser Ser Ser
420 425 430

Phe Ser Arg Val Asp Leu Phe Asn Gly Leu Leu Gly Thr Val Glu Val
435 440 445

Thr Ala Leu Tyr Val Thr Arg Leu Asp Asn Val Thr Val Ala His Met
450 455 460

Gly Thr Ala Asp Gly Arg Ile Leu Gln Val Glu Leu Ala Arg Ser Leu
465 470 475 480

Asn Tyr Leu Leu Tyr Val Ser Asn Phe Ser Leu Gly Asp Ser Gly Gln
485 490 495

Pro Val Gln Arg Asp Val Ser Arg Leu Gly Asp His Leu Phe Phe Ala
500 505 510

Ser Gly Asp Gln Val Phe Gln Val Pro Ile Gln Gly Pro Gly Cys Arg
515 520 525

His Phe Leu Thr Cys Gly Arg Cys Leu Arg Ala Gln Arg Phe Met Gly
530 535 540

Cys Gly Trp Cys Gly Asn Met Cys Gly Arg Gln Lys Glu Cys Pro Gly
545 550 555 560

Ser Trp Gln Gln Asp His Cys Pro Pro Lys Leu Thr Glu Phe His Pro
565 570 575

His Ser Gly Pro Leu Arg Gly Ser Thr Arg Leu Thr Leu Cys Gly Ser
580 585 590

Asn Phe Tyr Leu His Pro Ser Gly Leu Val Pro Glu Gly Thr His Gln
595 600 605

Ile Thr Val Gly Gln Ser Pro Cys Arg Pro Leu Pro Lys Asp Ser Ser
610 615 620

Lys Leu Arg Pro Val Pro Arg Lys Asp Phe Val Glu Glu Phe Glu Cys
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Glu Leu Glu Pro Leu Gly Thr Gln Ala Val Gly Pro Thr Asn Val Ser
645 650 655

Leu Thr Val Thr Asn Met Pro Pro Gly Lys His Phe Arg Val Asp Gly
660 665 670

Thr Ser Met Leu Arg Gly Phe Phe Phe Met Glu Pro Val Leu Ile Ala
675 680 685

Val Gln Pro Leu Phe Gly Pro Arg Ala Gly Gly Thr Cys Leu Thr Leu
690 695 700

Glu Gly Gln Ser Leu Ser Val Gly Thr Ser Arg Ala Val Leu Val Asn
705 710 715 720

Gly Thr Glu Cys Leu Leu Ala Arg Val Ser Glu Gly Gln Leu Leu Cys
725 730 735

Ala Thr Pro Pro Gly Ala Met Val Ala Ser Val Pro Leu Ser Leu Gln
740 745 750

Val Gly Gly Ala Gln Val Pro Gly Ser Trp Thr Phe His Tyr Arg Glu
755 760 765

Asp Pro Val Val Leu Ser Ile Ser Pro Asn Cys Gly Tyr Ser Asn Ser
770 775 780

His Ile Thr Ile Cys Gly Gln His Leu Thr Ser Ala Trp His Leu Val
785 790 795 800

Leu Ser Phe His Asp Gly Leu Arg Ala Val Glu Ser Arg Cys Glu Arg
805 810 815

Gln Leu Pro Glu Gln Gln Leu Cys Arg Leu Pro Glu Tyr Val Val Gln
820 825 830

Asp Pro Gln Gly Trp Val Ala Gly Asn Leu Ser Ala Trp Gly Asp Gly
835 840 845

Ala Ala Gly Phe Thr Leu Pro Gly Phe Arg Phe Leu Thr Pro Pro His
850 855 860

Pro Pro Ser Ala Asn Leu Ile Pro Leu Lys Pro Glu Glu His Ala Ile
865 870 875 880

Lys Phe Glu Tyr Ile Gly Leu Gly Ala Val Thr Asp Cys Val Gly Val
885 890 895

Asn Val Thr Val Gly Gly Glu Ser Cys Gln His Glu Phe Arg Gly Asp
900 905 910

Met Val Val Cys Pro Leu Pro Pro Ser Leu Gln Leu Gly Lys Asp Gly
915 920 925

Ala Pro Leu Gln Val Cys Val Asp Gly Glu Cys His Ile Leu Gly Arg
930 935 940

Val Val Trp Pro Gly Pro Asp Gly Val Pro Gln Ser Thr Leu Leu Gly
945 950 955 960

Ile Leu Leu Pro Leu Leu Leu Leu Val Ala Ala Leu Ala Thr Ala Leu
965 970 975

Val Phe Ser Tyr Trp Trp Gln Arg Lys Gln Leu Val Leu Pro Pro Asn
980 985 990

Leu Asp Asp Leu Ala Ser Leu Asp Gln Thr Thr Gly Ala Thr Pro Leu
995 1000 1005

Pro Ile Leu Tyr Ser Gly Ser Asp Tyr Arg Ser Gly Leu Ala Arg
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Pro Ala Thr Asp Gly Leu Asp Ser Thr Cys Val His Gly Ala Ser
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Val Lys Asp Val Leu Ile Pro His Glu Arg Val Val Ala His Ser
1070 1075 1080

Asp Arg Val Ile Gly Lys Gly His Phe Gly Val Val Tyr His Gly
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Glu Tyr Ile Asp Gln Ala Gln Asn Arg Ile Gln Cys Ala Ile Lys
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Ser Leu Ser Arg Ile Thr Glu Met Gln Gln Val Glu Ala Phe Leu
1115 1120 1125

Arg Glu Gly Leu Leu Met Arg Gly Leu Asn His Pro Asn Val Leu
1130 1135 1140

Ala Leu Ile Gly Ile Met Leu Pro Pro Glu Gly Leu Pro His Val
1145 1150 1155

Leu Leu Pro Tyr Met Cys His Gly Asp Leu Leu Gln Phe Ile Arg
1160 1165 1170

Ser Pro Gln Arg Asn Pro Thr Val Lys Asp Leu Ile Ser Phe Gly
1175 1180 1185

Leu Gln Val Ala His Gly Met Glu Tyr Leu Ala Glu Gln Lys Phe
1190 1195 1200

Val His Arg Asp Leu Ala Ala Arg Asn Cys Met Leu Asp Glu Ser
1205 1210 1215

Phe Thr Val Lys Val Ala Asp Phe Gly Leu Ala Arg Asp Ile Leu
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Asp Lys Glu Tyr Tyr Ser Val Gln Gln His Arg His Ala Arg Leu
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Pro Val Lys Trp Met Ala Leu Glu Ser Leu Gln Thr Tyr Arg Phe
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Thr Thr Lys Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu
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Leu Leu Thr Arg Gly Ala Pro Pro Tyr Pro His Ile Asp Pro Phe
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1295 1300 1305

Glu Tyr Cys Pro Asn Ser Leu Tyr Gln Val Met Gln Gln Cys Trp
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Glu Ala Asp Pro Ala Ala Arg Pro Thr Phe Gly Val Leu Val Gly
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Glu Val Glu Gln Ile Val Ser Ala Leu Leu Gly Asp His Tyr Val
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Gln Leu Pro Ala Thr Tyr Met Asn Leu Gly Pro Ser Thr Ser His
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Thr

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acctcgagtc gggcccccag ccaggcccac gcccaggtcc aggcccaggc cggtagggat 240

cctctagggt cccagctcgc ctcg atg gag ctc ctc ccg ccg ctg cct cag 291
Met Glu Leu Leu Pro Pro Leu Pro Gln
1 5

tcc ttc ctg ttg ctg ctg ctg ttg cct gcc aag ccc gcg gcg ggc gag 339
Ser Phe Leu Leu Leu Leu Leu Leu Pro Ala Lys Pro Ala Ala Gly Glu
10 15 20 25

gac tgg cag tgc ccg cgc acc ccc tac gcg gcc tct cgc gac ttt gac 387
Asp Trp Gln Cys Pro Arg Thr Pro Tyr Ala Ala Ser Arg Asp Phe Asp
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gtg aag tac gtg gtg ccc agc ttc tcc gcc gga ggc ctg gta cag gcc 435
Val Lys Tyr Val Val Pro Ser Phe Ser Ala Gly Gly Leu Val Gln Ala
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atg gtg acc tac gag ggc gac aga aat gag agt gct gtg ttt gta gcc 483
Met Val Thr Tyr Glu Gly Asp Arg Asn Glu Ser Ala Val Phe Val Ala
60 65 70

ata cgc aat cgc ctg cat gtg ctt ggg cct gac ctg aag tct gtc cag 531
Ile Arg Asn Arg Leu His Val Leu Gly Pro Asp Leu Lys Ser Val Gln
75 80 85

agc ctg gcc acg ggc cct gct gga gac cct ggc tgc cag acg tgt gca 579
Ser Leu Ala Thr Gly Pro Ala Gly Asp Pro Gly Cys Gln Thr Cys Ala
90 95 100 105

gcc tgt ggc cca gga ccc cac ggc cct ccc ggt gac aca gac aca aag 627
Ala Cys Gly Pro Gly Pro His Gly Pro Pro Gly Asp Thr Asp Thr Lys
110 115 120

gtg ctg gtg ctg gat ccc gcg ctg cct gcg ctg gtc agt tgt ggc tcc 675
Val Leu Val Leu Asp Pro Ala Leu Pro Ala Leu Val Ser Cys Gly Ser
125 130 135

agc ctg cag ggc cgc tgc ttc ctg cat gac cta gag ccc caa ggg aca 723
Ser Leu Gln Gly Arg Cys Phe Leu His Asp Leu Glu Pro Gln Gly Thr
140 145 150

gcc gtg cat ctg gca gcg cca gcc tgc ctc ttc tca gcc cac cat aac 771
Ala Val His Leu Ala Ala Pro Ala Cys Leu Phe Ser Ala His His Asn
155 160 165

cgg ccc gat gac tgc ccc gac tgt gtg gcc agc cca ttg ggc acc cgt 819
Arg Pro Asp Asp Cys Pro Asp Cys Val Ala Ser Pro Leu Gly Thr Arg
170 175 180 185

gta act gtg gtt gag caa ggc cag gcc tcc tat ttc tac gtg gca tcc 867
Val Thr Val Val Glu Gln Gly Gln Ala Ser Tyr Phe Tyr Val Ala Ser
190 195 200

tca ctg gac gca gcc gtg gct gcc agc ttc agc cca cgc tca gtg tct 915
Ser Leu Asp Ala Ala Val Ala Ala Ser Phe Ser Pro Arg Ser Val Ser
205 210 215

atc agg cgt ctc aag gct gac gcc tcg gga ttc gca ccg ggc ttt gtg 963
Ile Arg Arg Leu Lys Ala Asp Ala Ser Gly Phe Ala Pro Gly Phe Val
220 225 230

gcg ttg tca gtg ctg ccc aag cat ctt gtc tcc tac agt att gaa tac 1011
Ala Leu Ser Val Leu Pro Lys His Leu Val Ser Tyr Ser Ile Glu Tyr
235 240 245

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Val His Ser Phe His Thr Gly Ala Phe Val Tyr Phe Leu Thr Val Gln
250 255 260 265

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Pro Ala Ser Val Thr Asp Asp Pro Ser Ala Leu His Thr Arg Leu Ala
270 275 280

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Arg Leu Ser Ala Thr Glu Pro Glu Leu Gly Asp Tyr Arg Glu Leu Val
285 290 295

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Leu Asp Cys Arg Phe Ala Pro Lys Arg Arg Arg Arg Gly Ala Pro Glu
300 305 310

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Gly Gly Gln Pro Tyr Pro Val Leu Arg Val Ala His Ser Ala Pro Val
315 320 325

ggt gcc caa ctt gcc act gag ctg agc atc gcc gag ggc cag gaa gta 1299
Gly Ala Gln Leu Ala Thr Glu Leu Ser Ile Ala Glu Gly Gln Glu Val
330 335 340 345

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350 355 360

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Pro Asn Ser Val Val Cys Ala Phe Pro Ile Asp Leu Leu Asp Thr Leu
365 370 375

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395 400 405

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Pro Pro Gly Leu Glu Ala Leu Ser Pro Asn Thr Ser Cys Arg His Phe
410 415 420 425

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Pro Leu Leu Val Ser Ser Ser Phe Ser Arg Val Asp Leu Phe Asn Gly
430 435 440

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445 450 455

aac gtc aca gtg gca cac atg ggc aca atg gat ggg cgt atc ctg cag 1683
Asn Val Thr Val Ala His Met Gly Thr Met Asp Gly Arg Ile Leu Gln
460 465 470

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Val Glu Leu Val Arg Ser Leu Asn Tyr Leu Leu Tyr Val Ser Asn Phe
475 480 485

tca ctg ggt gac agt ggg cag ccc gtg cag cgg gat gtc agt cgt ctt 1779
Ser Leu Gly Asp Ser Gly Gln Pro Val Gln Arg Asp Val Ser Arg Leu
490 495 500 505

ggg gac cac cta ctc ttt gcc tct ggg gac cag gtt ttc cag gta cct 1827
Gly Asp His Leu Leu Phe Ala Ser Gly Asp Gln Val Phe Gln Val Pro
510 515 520

atc caa ggc cct ggc tgc cgc cac ttc ctg acc tgt ggg cgt tgc cta 1875
Ile Gln Gly Pro Gly Cys Arg His Phe Leu Thr Cys Gly Arg Cys Leu
525 530 535

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Arg Ala Trp His Phe Met Gly Cys Gly Trp Cys Gly Asn Met Cys Gly
540 545 550

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Gln Gln Lys Glu Cys Pro Gly Ser Trp Gln Gln Asp His Cys Pro Pro
555 560 565

aag ctt act gag ttc cac ccc cac agt gga cct cta agg ggc agt aca 2019
Lys Leu Thr Glu Phe His Pro His Ser Gly Pro Leu Arg Gly Ser Thr
570 575 580 585

agg ctg acc ctg tgt ggc tcc aac ttc tac ctt cac cct tct ggt ctg 2067
Arg Leu Thr Leu Cys Gly Ser Asn Phe Tyr Leu His Pro Ser Gly Leu
590 595 600

gtg cct gag gga acc cat cag gtc act gtg ggc caa agt ccc tgc cgg 2115
Val Pro Glu Gly Thr His Gln Val Thr Val Gly Gln Ser Pro Cys Arg
605 610 615

cca ctg ccc aag gac agc tca aaa ctc aga cca gtg ccc cgg aaa gac 2163
Pro Leu Pro Lys Asp Ser Ser Lys Leu Arg Pro Val Pro Arg Lys Asp
620 625 630

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Phe Val Glu Glu Phe Glu Cys Glu Leu Glu Pro Leu Gly Thr Gln Ala
635 640 645

gtg ggg cct acc aac gtc agc ctc acc gtg act aac atg cca ccg ggc 2259
Val Gly Pro Thr Asn Val Ser Leu Thr Val Thr Asn Met Pro Pro Gly
650 655 660 665

aag cac ttc cgg gta gac ggc acc tcc gtg ctg aga ggc ttc tct ttc 2307
Lys His Phe Arg Val Asp Gly Thr Ser Val Leu Arg Gly Phe Ser Phe
670 675 680

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Met Glu Pro Val Leu Ile Ala Val Gln Pro Leu Phe Gly Pro Arg Ala
685 690 695

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Gly Gly Thr Cys Leu Thr Leu Glu Gly Gln Ser Leu Ser Val Gly Thr
700 705 710

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Ser Arg Ala Val Leu Val Asn Gly Thr Glu Cys Leu Leu Ala Arg Val
715 720 725

agt gag ggg cag ctt tta tgt gcc aca ccc cct ggg gcc acg gtg gcc 2499
Ser Glu Gly Gln Leu Leu Cys Ala Thr Pro Pro Gly Ala Thr Val Ala
730 735 740 745

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Ser Val Pro Leu Ser Leu Gln Val Gly Gly Ala Gln Val Pro Gly Ser
750 755 760

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Trp Thr Phe Gln Tyr Arg Glu Asp Pro Val Val Leu Ser Ile Ser Pro
765 770 775

aac tgt ggc tac atc aac tcc cac atc acc atc tgt ggc cag cat cta 2643
Asn Cys Gly Tyr Ile Asn Ser His Ile Thr Ile Cys Gly Gln His Leu
780 785 790

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Thr Ser Ala Trp His Leu Val Leu Ser Phe His Asp Gly Leu Arg Ala
795 800 805

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Val Glu Ser Arg Cys Glu Arg Gln Leu Pro Glu Gln Gln Leu Cys Arg
810 815 820 825

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830 835 840

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Leu Ser Ala Arg Gly Asp Gly Ala Ala Gly Phe Thr Leu Pro Gly Phe
845 850 855

cgc ttc cta ccc cca ccc cat cca ccc agt gcc aac cta gtt cca ctg 2883
Arg Phe Leu Pro Pro Pro His Pro Pro Ser Ala Asn Leu Val Pro Leu
860 865 870

aag cct gag gag cat gcc att aag ttt gag tat att ggg ctg ggc gct 2931
Lys Pro Glu Glu His Ala Ile Lys Phe Glu Tyr Ile Gly Leu Gly Ala
875 880 885

gtg gct gac tgt gtg ggt atc aac gtg acc gtg ggt ggt gag agc tgc 2979
Val Ala Asp Cys Val Gly Ile Asn Val Thr Val Gly Gly Glu Ser Cys
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Gln His Glu Phe Arg Gly Asp Met Val Val Cys Pro Leu Pro Pro Ser
910 915 920

ctg cag ctt ggc cag gat ggt gcc cca ttg cag gtc tgc gta gat ggt 3075
Leu Gln Leu Gly Gln Asp Gly Ala Pro Leu Gln Val Cys Val Asp Gly
925 930 935

gaa tgt cat atc ctg ggt aga gtg gtg cgg cca ggg cca gat ggg gtc 3123
Glu Cys His Ile Leu Gly Arg Val Val Arg Pro Gly Pro Asp Gly Val
940 945 950

cca cag agc acg ctc ctt ggt atc ctg ctg cct ttg ctg ctg ctt gtg 3171
Pro Gln Ser Thr Leu Leu Gly Ile Leu Leu Pro Leu Leu Leu Leu Val
955 960 965

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Leu His Asp Leu Glu Pro Gln Gly Thr Ala Val His Leu Ala Ala Pro
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Cys Val Ala Ser Pro Leu Gly Thr Arg Val Thr Val Val Glu Gln Gly
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Gln Ala Ser Tyr Phe Tyr Val Ala Ser Ser Leu Asp Ala Ala Val Ala
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Ala Ser Phe Ser Pro Arg Ser Val Ser Ile Arg Arg Leu Lys Ala Asp
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Ala Ser Gly Phe Ala Pro Gly Phe Val Ala Leu Ser Val Leu Pro Lys
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His Leu Val Ser Tyr Ser Ile Glu Tyr Val His Ser Phe His Thr Gly
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Ala Phe Val Tyr Phe Leu Thr Val Gln Pro Ala Ser Val Thr Asp Asp
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Ser Pro Asn Thr Ser Cys Arg His Phe Pro Leu Leu Val Ser Ser Ser
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Phe Ser Arg Val Asp Leu Phe Asn Gly Leu Leu Gly Pro Val Gln Val
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Thr Ala Leu Tyr Val Thr Arg Leu Asp Asn Val Thr Val Ala His Met
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Pro Val Gln Arg Asp Val Ser Arg Leu Gly Asp His Leu Leu Phe Ala
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Ser Gly Asp Gln Val Phe Gln Val Pro Ile Gln Gly Pro Gly Cys Arg
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His Phe Leu Thr Cys Gly Arg Cys Leu Arg Ala Trp His Phe Met Gly
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Val Gln Pro Leu Phe Gly Pro Arg Ala Gly Gly Thr Cys Leu Thr Leu
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740 745 750

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755 760 765

Asp Pro Val Val Leu Ser Ile Ser Pro Asn Cys Gly Tyr Ile Asn Ser
770 775 780

His Ile Thr Ile Cys Gly Gln His Leu Thr Ser Ala Trp His Leu Val
785 790 795 800

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Pro Pro Ser Ala Asn Leu Val Pro Leu Lys Pro Glu Glu His Ala Ile
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Lys Phe Glu Tyr Ile Gly Leu Gly Ala Val Ala Asp Cys Val Gly Ile
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Met Val Val Cys Pro Leu Pro Pro Ser Leu Gln Leu Gly Gln Asp Gly
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Val Val Arg Pro Gly Pro Asp Gly Val Pro Gln Ser Thr Leu Leu Gly
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Ile Leu Leu Pro Leu Leu Leu Leu Val Ala Ala Leu Ala Thr Ala Leu
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Val Phe Ser Tyr Trp Trp Arg Arg Lys Gln Leu Val Leu Pro Pro Asn
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Lys Tyr Val Val Pro Ser Phe Ser Ala Gly Gly Arg Val Gln Ala Thr
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670 675 680

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Thr Phe His Tyr Lys Glu Asp Pro Ile Val Leu Asp Ile Ser Pro Lys
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Cys Gly Tyr Ser Gly Ser His Ile Met Ile His Gly Gln His Leu Thr
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880 885 890

gct gtg gca gac tgt gtg act gtg aac atg acc gtg ggt ggt gag gtc 2980
Ala Val Ala Asp Cys Val Thr Val Asn Met Thr Val Gly Gly Glu Val
895 900 905

tgc caa cat gag ctc cgg ggg gat gtg gtg atc tgc ccc ctg ccc cct 3028
Cys Gln His Glu Leu Arg Gly Asp Val Val Ile Cys Pro Leu Pro Pro
910 915 920

tcc ctg caa ctt ggc aag gat ggt gtc cca ttg cag gtc tgt gta gac 3076
Ser Leu Gln Leu Gly Lys Asp Gly Val Pro Leu Gln Val Cys Val Asp
925 930 935 940

ggt ggg tgt cac atc ctg agc caa gtg gtt cgc tca agc cca ggc agg 3124
Gly Gly Cys His Ile Leu Ser Gln Val Val Arg Ser Ser Pro Gly Arg
945 950 955

gcc tca cag agg ata ctc ctt att gct ctt ctg gtc ttg atc ctg ctt 3172
Ala Ser Gln Arg Ile Leu Leu Ile Ala Leu Leu Val Leu Ile Leu Leu
960 965 970

gtg gct gtg ctg gcc gtt gcc ctg atc ttt aac tcc cga aga cgg aaa 3220
Val Ala Val Leu Ala Val Ala Leu Ile Phe Asn Ser Arg Arg Arg Lys
975 980 985

aag cag cta ggt gct cac tcc ctc tcc cca aca aca ctc tct gac atc 3268
Lys Gln Leu Gly Ala His Ser Leu Ser Pro Thr Thr Leu Ser Asp Ile
990 995 1000

aac gat aca gct tcc ggg gct ccg aac cat gaa gaa tcg tca gag 3313
Asn Asp Thr Ala Ser Gly Ala Pro Asn His Glu Glu Ser Ser Glu
1005 1010 1015

agt agg gat ggg aca agt gtc cca ctg ctg cgg aca gag tct atc 3358
Ser Arg Asp Gly Thr Ser Val Pro Leu Leu Arg Thr Glu Ser Ile
1020 1025 1030

cgg ctc cag gat ctg gac agg atg ctc cta gct gag gtc aag gat 3403
Arg Leu Gln Asp Leu Asp Arg Met Leu Leu Ala Glu Val Lys Asp
1035 1040 1045

gta ctg att ccc cat gaa caa gtg gtc atc cat act gac caa gtc 3448
Val Leu Ile Pro His Glu Gln Val Val Ile His Thr Asp Gln Val
1050 1055 1060

att ggc aaa ggc cac ttt ggt gtt gtc tac cac gga gaa tat aca 3493
Ile Gly Lys Gly His Phe Gly Val Val Tyr His Gly Glu Tyr Thr
1065 1070 1075

gac gga gca cag aat cag acc cac tgt gcc atc aag tct ctg agt 3538
Asp Gly Ala Gln Asn Gln Thr His Cys Ala Ile Lys Ser Leu Ser
1080 1085 1090

cgc att aca gag gtg cag gag gtg gag gct ttc ctg cgg gag ggg 3583
Arg Ile Thr Glu Val Gln Glu Val Glu Ala Phe Leu Arg Glu Gly
1095 1100 1105

ctg ctc atg cgt ggc cta cat cac cca aac atc ctg gct ctc atc 3628
Leu Leu Met Arg Gly Leu His His Pro Asn Ile Leu Ala Leu Ile
1110 1115 1120

ggt atc atg ctg ccc ccg gag ggg ctt ccc cgg gtg ctg ttg ccc 3673
Gly Ile Met Leu Pro Pro Glu Gly Leu Pro Arg Val Leu Leu Pro
1125 1130 1135

tat atg cgc cac gga gac ctg ctt cgt ttc att cgc tcc cct cag 3718
Tyr Met Arg His Gly Asp Leu Leu Arg Phe Ile Arg Ser Pro Gln
1140 1145 1150

agg aac ccc act gtg aag gat ctt gtc agc ttt ggc ctg cag gta 3763
Arg Asn Pro Thr Val Lys Asp Leu Val Ser Phe Gly Leu Gln Val
1155 1160 1165

gcc tgt ggt atg gag tac ctg gca gag cag aag ttc gtg cac aga 3808
Ala Cys Gly Met Glu Tyr Leu Ala Glu Gln Lys Phe Val His Arg
1170 1175 1180

gac ctg gct gct agg aac tgc atg ctg gac gag tca ttc aca gtc 3853
Asp Leu Ala Ala Arg Asn Cys Met Leu Asp Glu Ser Phe Thr Val
1185 1190 1195

aag gtg gct gac ttt ggt ctg gca cgg ggc gtc cta gac aag gaa 3898
Lys Val Ala Asp Phe Gly Leu Ala Arg Gly Val Leu Asp Lys Glu
1200 1205 1210

tac tac agt gtt cgc cag cat cgc cat gct cgc ctg cca gtc aaa 3943
Tyr Tyr Ser Val Arg Gln His Arg His Ala Arg Leu Pro Val Lys
1215 1220 1225

tgg atg gca ctg gag agc ctg cag acc tac agg ttc acc acc aag 3988
Trp Met Ala Leu Glu Ser Leu Gln Thr Tyr Arg Phe Thr Thr Lys
1230 1235 1240

tcc gat gtg tgg tca ttc ggg gtg ctg ctc tgg gag cta cta aca 4033
Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu Leu Leu Thr
1245 1250 1255

cgg ggt gct cca ccc tac ccc cat atc gat ccc ttc gac ctc tct 4078
Arg Gly Ala Pro Pro Tyr Pro His Ile Asp Pro Phe Asp Leu Ser
1260 1265 1270

cac ttc ctg gct cag ggc cgc cgc ctg cct cag cct gag tac tgt 4123
His Phe Leu Ala Gln Gly Arg Arg Leu Pro Gln Pro Glu Tyr Cys
1275 1280 1285

cct gat tca ctg tat cac gtg atg ctt cga tgc tgg gag gct gac 4168
Pro Asp Ser Leu Tyr His Val Met Leu Arg Cys Trp Glu Ala Asp
1290 1295 1300

cca gcg gca cga ccc acc ttc aga gcc cta gtg ctg gaa gta aag 4213
Pro Ala Ala Arg Pro Thr Phe Arg Ala Leu Val Leu Glu Val Lys
1305 1310 1315

cag gta gtg gcc tca ctg ctt ggg gac cac tat gtg cag ctg aca 4258
Gln Val Val Ala Ser Leu Leu Gly Asp His Tyr Val Gln Leu Thr
1320 1325 1330

gca gct tat gtg aac gta ggc ccc aga gcg gtg gat gat ggg agt 4303
Ala Ala Tyr Val Asn Val Gly Pro Arg Ala Val Asp Asp Gly Ser
1335 1340 1345

gtg cct ccg gag cag gta cag ccc tcg cct cag cat tgc agg agc 4348
Val Pro Pro Glu Gln Val Gln Pro Ser Pro Gln His Cys Arg Ser
1350 1355 1360

acg tca aag ccc cgg cct ctc tca gag cca ccc ctg ccc act tga 4393
Thr Ser Lys Pro Arg Pro Leu Ser Glu Pro Pro Leu Pro Thr
1365 1370 1375

ccaaagccct gagtaggcca caggcactag atctgctaag tggccttgag caaattacaa 4453

gctgcctctg ggcctaggac aagcctcagc atggaaaacc tccactcttt agctttctgg 4513

ggccactgaa ggtgggaaac cgggcccatt tgagcccctc gttccagcat gagccagtga 4573

catttttgta gcatgtattt atgtaatgtc tgttttgtac ctgtttcgga atacagagga 4633

tccagcagtg atcacagaga tactacagta taaaataata taaataaata aatgaatgaa 4693

tattcgagca caaaaaaaaa aaaaaaa 4720

<210> 47
<211> 1378

<212> PRT
<213> Mus musculus

<400> 47

Met Gly Leu Pro Leu Pro Leu Leu Gln Ser Ser Leu Leu Leu Met Leu
1 5 10 15

Leu Leu Arg Leu Ser Ala Ala Ser Thr Asn Leu Asn Trp Gln Cys Pro
20 25 30

Arg Ile Pro Tyr Ala Ala Ser Arg Asp Phe Ser Val Lys Tyr Val Val
35 40 45

Pro Ser Phe Ser Ala Gly Gly Arg Val Gln Ala Thr Ala Ala Tyr Glu
50 55 60

Asp Ser Thr Asn Ser Ala Val Phe Val Ala Thr Arg Asn His Leu His
65 70 75 80

Val Leu Gly Pro Asp Leu Gln Phe Ile Glu Asn Leu Thr Thr Gly Pro
85 90 95

Ile Gly Asn Pro Gly Cys Gln Thr Cys Ala Ser Cys Gly Pro Gly Pro
100 105 110

His Gly Pro Pro Lys Asp Thr Asp Thr Leu Val Leu Val Met Glu Pro
115 120 125

Gly Leu Pro Ala Leu Val Ser Cys Gly Ser Thr Leu Gln Gly Arg Cys
130 135 140

Phe Leu His Glu Leu Glu Pro Arg Gly Lys Ala Leu His Leu Ala Ala
145 150 155 160

Pro Ala Cys Leu Phe Ser Ala Asn Asn Asn Lys Pro Glu Ala Cys Thr
165 170 175

Asp Cys Val Ala Ser Pro Leu Gly Thr Arg Val Thr Val Val Glu Gln
180 185 190

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

Ala Ala Ser Phe Ser Pro Arg Ser Val Ser Ile Arg Arg Leu Lys Ser
210 215 220

Asp Thr Ser Gly Phe Gln Pro Gly Phe Pro Ser Leu Ser Val Leu Pro
225 230 235 240

Lys Tyr Leu Ala Ser Tyr Leu Ile Lys Tyr Val Tyr Ser Phe His Ser
245 250 255

Gly Asp Phe Val Tyr Phe Leu Thr Val Gln Pro Ile Ser Val Thr Ser
260 265 270

Pro Pro Ser Ala Leu His Thr Arg Leu Val Arg Leu Asn Ala Val Glu
275 280 285

Pro Glu Ile Gly Asp Tyr Arg Glu Leu Val Leu Asp Cys His Phe Ala
290 295 300

Pro Lys Arg Arg Arg Arg Gly Ala Pro Glu Gly Thr Gln Pro Tyr Pro
305 310 315 320

Val Leu Gln Ala Ala His Ser Ala Pro Val Asp Ala Lys Leu Ala Val
325 330 335

Glu Leu Ser Ile Ser Glu Gly Gln Glu Val Leu Phe Gly Val Phe Val
340 345 350

Thr Val Lys Asp Gly Gly Ser Gly Met Gly Pro Asn Ser Val Val Cys
355 360 365

Ala Phe Pro Ile Tyr His Leu Asn Ile Leu Ile Glu Glu Gly Val Glu
370 375 380

Tyr Cys Cys His Ser Ser Asn Ser Ser Ser Leu Leu Ser Arg Gly Leu
385 390 395 400

Asp Phe Phe Gln Thr Pro Ser Phe Cys Pro Asn Pro Pro Gly Gly Glu
405 410 415

Ala Ser Gly Pro Ser Ser Arg Cys His Tyr Phe Pro Leu Met Val His
420 425 430

Ala Ser Phe Thr Arg Val Asp Leu Phe Asn Gly Leu Leu Gly Ser Val
435 440 445

Lys Val Thr Ala Leu His Val Thr Arg Leu Gly Asn Val Thr Val Ala
450 455 460

His Met Gly Thr Val Asp Gly Arg Val Leu Gln Val Glu Ile Ala Arg
465 470 475 480

Ser Leu Asn Tyr Leu Leu Tyr Val Ser Asn Phe Ser Leu Gly Ser Ser
485 490 495

Gly Gln Pro Val His Arg Asp Val Ser Arg Leu Gly Asn Asp Leu Leu
500 505 510

Phe Ala Ser Gly Asp Gln Val Phe Lys Val Pro Ile Gln Gly Pro Gly
515 520 525

Cys Arg His Phe Leu Thr Cys Trp Arg Cys Leu Arg Ala Gln Arg Phe
530 535 540

Met Gly Cys Gly Trp Cys Gly Asp Arg Cys Asp Arg Gln Lys Glu Cys
545 550 555 560

Pro Gly Ser Trp Gln Gln Asp His Cys Pro Pro Glu Ile Ser Glu Phe
565 570 575

Tyr Pro His Ser Gly Pro Leu Arg Gly Thr Thr Arg Leu Thr Leu Cys
580 585 590

Gly Ser Asn Phe Tyr Leu Arg Pro Asp Asp Val Val Pro Glu Gly Thr
595 600 605

His Gln Ile Thr Val Gly Gln Ser Pro Cys Arg Leu Leu Pro Lys Asp
610 615 620

Ser Ser Ser Pro Arg Pro Gly Ser Leu Lys Glu Phe Ile Gln Glu Leu
625 630 635 640

Glu Cys Glu Leu Glu Pro Leu Val Thr Gln Ala Val Gly Thr Thr Asn
645 650 655

Ile Ser Leu Val Ile Thr Asn Met Pro Ala Gly Lys His Phe Arg Val
660 665 670

Glu Gly Ile Ser Val Gln Glu Gly Phe Ser Phe Val Glu Pro Val Leu
675 680 685

Thr Ser Ile Lys Pro Asp Phe Gly Pro Arg Ala Gly Gly Thr Tyr Leu
690 695 700

Thr Leu Glu Gly Gln Ser Leu Ser Ile Ala Thr Ser Arg Ala Ala Leu
705 710 715 720

Val Asn Gly Thr Gln Cys Arg Leu Glu Gln Val Asn Glu Glu Gln Ile
725 730 735

Leu Cys Val Thr Pro Pro Gly Ala Gly Thr Ala Arg Val Pro Leu His
740 745 750

Leu Gln Ile Gly Gly Ala Glu Val Pro Gly Ser Trp Thr Phe His Tyr
755 760 765

Lys Glu Asp Pro Ile Val Leu Asp Ile Ser Pro Lys Cys Gly Tyr Ser
770 775 780

Gly Ser His Ile Met Ile His Gly Gln His Leu Thr Ser Ala Trp His
785 790 795 800

Phe Thr Leu Ser Phe His Asp Gly Gln Ser Thr Val Glu Ser Arg Cys
805 810 815

Ala Gly Gln Phe Val Glu Gln Gln Gln Arg Arg Cys Arg Leu Pro Glu
820 825 830

Tyr Val Val Arg Asn Pro Gln Gly Trp Ala Thr Gly Asn Leu Ser Val
835 840 845

Trp Gly Asp Gly Ala Ala Gly Phe Thr Leu Pro Gly Phe Arg Phe Leu
850 855 860

Pro Pro Pro Ser Pro Leu Arg Ala Gly Leu Val Glu Leu Lys Pro Glu
865 870 875 880

Glu His Ser Val Lys Val Glu Tyr Val Gly Leu Gly Ala Val Ala Asp
885 890 895

Cys Val Thr Val Asn Met Thr Val Gly Gly Glu Val Cys Gln His Glu
900 905 910

Leu Arg Gly Asp Val Val Ile Cys Pro Leu Pro Pro Ser Leu Gln Leu
915 920 925

Gly Lys Asp Gly Val Pro Leu Gln Val Cys Val Asp Gly Gly Cys His
930 935 940

Ile Leu Ser Gln Val Val Arg Ser Ser Pro Gly Arg Ala Ser Gln Arg
945 950 955 960

Ile Leu Leu Ile Ala Leu Leu Val Leu Ile Leu Leu Val Ala Val Leu
965 970 975

Ala Val Ala Leu Ile Phe Asn Ser Arg Arg Arg Lys Lys Gln Leu Gly
980 985 990

Ala His Ser Leu Ser Pro Thr Thr Leu Ser Asp Ile Asn Asp Thr Ala
995 1000 1005

Ser Gly Ala Pro Asn His Glu Glu Ser Ser Glu Ser Arg Asp Gly
1010 1015 1020

Thr Ser Val Pro Leu Leu Arg Thr Glu Ser Ile Arg Leu Gln Asp
1025 1030 1035

Leu Asp Arg Met Leu Leu Ala Glu Val Lys Asp Val Leu Ile Pro
1040 1045 1050

His Glu Gln Val Val Ile His Thr Asp Gln Val Ile Gly Lys Gly
1055 1060 1065

His Phe Gly Val Val Tyr His Gly Glu Tyr Thr Asp Gly Ala Gln
1070 1075 1080

Asn Gln Thr His Cys Ala Ile Lys Ser Leu Ser Arg Ile Thr Glu
1085 1090 1095

Val Gln Glu Val Glu Ala Phe Leu Arg Glu Gly Leu Leu Met Arg
1100 1105 1110

Gly Leu His His Pro Asn Ile Leu Ala Leu Ile Gly Ile Met Leu
1115 1120 1125

Pro Pro Glu Gly Leu Pro Arg Val Leu Leu Pro Tyr Met Arg His
1130 1135 1140

Gly Asp Leu Leu Arg Phe Ile Arg Ser Pro Gln Arg Asn Pro Thr
1145 1150 1155

Val Lys Asp Leu Val Ser Phe Gly Leu Gln Val Ala Cys Gly Met
1160 1165 1170

Glu Tyr Leu Ala Glu Gln Lys Phe Val His Arg Asp Leu Ala Ala
1175 1180 1185

Arg Asn Cys Met Leu Asp Glu Ser Phe Thr Val Lys Val Ala Asp
1190 1195 1200

Phe Gly Leu Ala Arg Gly Val Leu Asp Lys Glu Tyr Tyr Ser Val
1205 1210 1215

Arg Gln His Arg His Ala Arg Leu Pro Val Lys Trp Met Ala Leu
1220 1225 1230

Glu Ser Leu Gln Thr Tyr Arg Phe Thr Thr Lys Ser Asp Val Trp
1235 1240 1245

Ser Phe Gly Val Leu Leu Trp Glu Leu Leu Thr Arg Gly Ala Pro
1250 1255 1260

Pro Tyr Pro His Ile Asp Pro Phe Asp Leu Ser His Phe Leu Ala
1265 1270 1275

Gln Gly Arg Arg Leu Pro Gln Pro Glu Tyr Cys Pro Asp Ser Leu
1280 1285 1290

Tyr His Val Met Leu Arg Cys Trp Glu Ala Asp Pro Ala Ala Arg
1295 1300 1305

Pro Thr Phe Arg Ala Leu Val Leu Glu Val Lys Gln Val Val Ala
1310 1315 1320

Ser Leu Leu Gly Asp His Tyr Val Gln Leu Thr Ala Ala Tyr Val
1325 1330 1335

Asn Val Gly Pro Arg Ala Val Asp Asp Gly Ser Val Pro Pro Glu
1340 1345 1350

Gln Val Gln Pro Ser Pro Gln His Cys Arg Ser Thr Ser Lys Pro
1355 1360 1365

Arg Pro Leu Ser Glu Pro Pro Leu Pro Thr
1370 1375

<210> 48
<211> 1413
<212> DNA

<213> Artificial Sequence

<220>
<223> MOR07919 heavy chain

<220>
<221> CDS
<222> (1)..(1413)

<400> 48
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

gtc ctg tcc cag gtg caa ttg gtt cag agc ggc gcg gaa gtg aaa aaa 96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

ccg ggc gaa agc ctg aaa att agc tgc aaa ggt tcc gga tat tcc ttt 144
Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe
35 40 45

act aat tat tgg att tct tgg gtg cgc cag atg cct ggg aag ggt ctc 192
Thr Asn Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu
50 55 60

gag tgg atg ggc ttt atc tat ccg gat gat agc tat acc cgt tat tct 240
Glu Trp Met Gly Phe Ile Tyr Pro Asp Asp Ser Tyr Thr Arg Tyr Ser
65 70 75 80

ccg agc ttt cag ggc cag gtg acc att agc gcg gat aaa agc att agc 288
Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser
85 90 95

acc gcg tat ctt caa tgg agc agc ctg aaa gcg agc gat acg gcc atg 336
Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met
100 105 110

tat tat tgc gcg cgt ttt tct tat cgt cat tat ctt gat atg gat gat 384
Tyr Tyr Cys Ala Arg Phe Ser Tyr Arg His Tyr Leu Asp Met Asp Asp
115 120 125

cat tgg ggc caa ggc acc ctg gtg acg gtt agc tca gcc tcc acc aag 432
His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
130 135 140

ggt cca tcg gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg 480
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145 150 155 160

ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg 528
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
165 170 175

gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc 576
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
180 185 190

ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg 624

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
195 200 205

gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac 672
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
210 215 220

gtg aat cac aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc 720
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro
225 230 235 240

aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa 768
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
245 250 255

ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac 816
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
260 265 270

acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac 864
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
275 280 285

gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc 912
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
290 295 300

gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac 960
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305 310 315 320

agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg 1008
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
325 330 335

ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca 1056
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
340 345 350

gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa 1104
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
355 360 365

cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac 1152
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
370 375 380

cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc 1200
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385 390 395 400

gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc 1248
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
405 410 415

acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag 1296
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
420 425 430

ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc 1344

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
435 440 445

tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc 1392
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
450 455 460

tcc ctg tct ccg ggt aaa tga 1413
Ser Leu Ser Pro Gly Lys
465 470

<210> 49
<211> 470
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 49

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe
35 40 45

Thr Asn Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu
50 55 60

Glu Trp Met Gly Phe Ile Tyr Pro Asp Asp Ser Tyr Thr Arg Tyr Ser
65 70 75 80

Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser
85 90 95

Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met
100 105 110

Tyr Tyr Cys Ala Arg Phe Ser Tyr Arg His Tyr Leu Asp Met Asp Asp
115 120 125

His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
130 135 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145 150 155 160

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
165 170 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
180 185 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
195 200 205

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
210 215 220

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro
225 230 235 240

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
245 250 255

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
260 265 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
275 280 285

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
290 295 300

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305 310 315 320

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
325 330 335

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
340 345 350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
355 360 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
370 375 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385 390 395 400

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
405 410 415

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
420 425 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
435 440 445

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
450 455 460

Ser Leu Ser Pro Gly Lys
465 470

<210> 50
<211> 1401
<212> DNA
<213> Artificial Sequence

<220>
<223> MOR07692, MOR07923, MOR07924, MOR07925 and MOR07926 heavy chain

<220>
<221> CDS
<222> (1)..(1401)

<400> 50
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48
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1 5 10 15

gtc ctg tcc cag gtg caa ttg gtg gaa agc ggc ggc ggc ctg gtg caa 96
Val Leu Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

ccg ggc ggc agc ctg cgt ctg agc tgc gcg gcc tcc gga ttt acc ttt 144
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

aat tct tat tct atg tct tgg gtg cgc caa gcc cct ggg aag ggt ctc 192
Asn Ser Tyr Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

gag tgg gtg agc tat atc tct tct cgt tct agc act acc tat tat gcg 240
Glu Trp Val Ser Tyr Ile Ser Ser Arg Ser Ser Thr Thr Tyr Tyr Ala
65 70 75 80

gat agc gtg aaa ggc cgt ttt acc att tca cgt gat aat tcg aaa aac 288
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
85 90 95

acc ctg tat ctg caa atg aac agc ctg cgt gcg gaa gat acg gcc gtg 336
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
100 105 110

tat tat tgc gcg cgt ggt tat ttt cat ggt atg gat tat tgg ggc caa 384
Tyr Tyr Cys Ala Arg Gly Tyr Phe His Gly Met Asp Tyr Trp Gly Gln
115 120 125

ggc acc ctg gtg acg gtt agc tca gcc tcc acc aag ggt cca tcg gtc 432
Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
130 135 140

ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc 480
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
145 150 155 160

ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg 528
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
165 170 175

tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc 576
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
180 185 190

cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc 624
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
195 200 205

tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag 672
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
210 215 220

ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt gac 720
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
225 230 235 240

aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga 768
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
245 250 255

ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc 816
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
260 265 270

tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa 864
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
275 280 285

gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat 912
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
290 295 300

aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac cgg 960
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
305 310 315 320

gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag 1008
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
325 330 335

gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag 1056
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
340 345 350

aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac 1104
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
355 360 365

acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc ctg 1152
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
370 375 380

acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg 1200
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
385 390 395 400

gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg 1248
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
405 410 415

ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac 1296
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
420 425 430

aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat 1344
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
435 440 445

gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg 1392
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
450 455 460

ggt aaa tga 1401
Gly Lys
465

<210> 51
<211> 466
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 51

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Asn Ser Tyr Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu

50 55 60

Glu Trp Val Ser Tyr Ile Ser Ser Arg Ser Ser Thr Thr Tyr Tyr Ala
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
85 90 95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Gly Tyr Phe His Gly Met Asp Tyr Trp Gly Gln
115 120 125

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
130 135 140

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
145 150 155 160

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
165 170 175

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
180 185 190

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
195 200 205

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
210 215 220

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
225 230 235 240

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
245 250 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
260 265 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
275 280 285

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His

290 295 300

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
305 310 315 320

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
325 330 335

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
340 345 350

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
355 360 365

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
370 375 380

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
385 390 395 400

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
405 410 415

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
420 425 430

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
435 440 445

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
450 455 460

Gly Lys
465

<210> 52
<211> 702
<212> DNA
<213> Artificial Sequence

<220>
<223> MOR07919 light chain

<220>
<221> CDS
<222> (1)..(702)

<400> 52
atg gcc tgg gct ctg ctg ctc ctc acc ctc ctc act cag ggc aca gga 48
Met Ala Trp Ala Leu Leu Leu Leu Thr Leu Leu Thr Gln Gly Thr Gly
1 5 10 15

tcc tgg gct gat atc gaa ctg acc cag ccg cct tca gtg agc gtt gca 96
Ser Trp Ala Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala
20 25 30

cca ggt cag acc gcg cgt atc tcg tgt agc ggc gat tct ctt ggt tct 144
Pro Gly Gln Thr Ala Arg Ile Ser Cys Ser Gly Asp Ser Leu Gly Ser
35 40 45

aag tat gtt cat tgg tac cag cag aaa ccc ggg cag gcg cca gtt ctt 192
Lys Tyr Val His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu
50 55 60

gtg att tat cgt gat aat aag cgt ccc tca ggc atc ccg gaa cgc ttt 240
Val Ile Tyr Arg Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe
65 70 75 80

agc gga tcc aac agc ggc aac acc gcg acc ctg acc att agc ggc act 288
Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr
85 90 95

cag gcg gaa gac gaa gcg gat tat tat tgc cag tct tat gat gct act 336
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ala Thr
100 105 110

gag ttt act tat gtg ttt ggc ggc ggc acg aag tta acc gtc cta ggt 384
Glu Phe Thr Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
115 120 125

cag ccc aag gct gcc ccc tcg gtc act ctg ttc ccg ccc tcc tct gag 432
Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
130 135 140

gag ctt caa gcc aac aag gcc aca ctg gtg tgt ctc ata agt gac ttc 480
Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
145 150 155 160

tac ccg gga gcc gtg aca gtg gcc tgg aag gca gat agc agc ccc gtc 528
Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
165 170 175

aag gcg gga gtg gag acc acc aca ccc tcc aaa caa agc aac aac aag 576
Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
180 185 190

tac gcg gcc agc agc tat ctg agc ctg acg cct gag cag tgg aag tcc 624
Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
195 200 205

cac aga agc tac agc tgc cag gtc acg cat gaa ggg agc acc gtg gag 672
His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
210 215 220

aag aca gtg gcc cct aca gaa tgt tca tag 702
Lys Thr Val Ala Pro Thr Glu Cys Ser
225 230

<210> 53
<211> 233
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 53

Met Ala Trp Ala Leu Leu Leu Leu Thr Leu Leu Thr Gln Gly Thr Gly
1 5 10 15

Ser Trp Ala Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala
20 25 30

Pro Gly Gln Thr Ala Arg Ile Ser Cys Ser Gly Asp Ser Leu Gly Ser
35 40 45

Lys Tyr Val His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu
50 55 60

Val Ile Tyr Arg Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe
65 70 75 80

Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr
85 90 95

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ala Thr
100 105 110

Glu Phe Thr Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
115 120 125

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
130 135 140

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
145 150 155 160

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
165 170 175

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
180 185 190

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
195 200 205

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
210 215 220

Lys Thr Val Ala Pro Thr Glu Cys Ser
225 230

<210> 54
<211> 708
<212> DNA
<213> Artificial Sequence

<220>
<223> MOR07692 light chain

<220>
<221> CDS
<222> (1)..(708)

<400> 54
atg gtg ttg cag acc cag gtc ttc att tct ctg ttg ctc tgg atc tct 48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

ggt gcc tac ggg gat atc gtg ctg acc cag agc ccg gcg acc ctg agc 96
Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

ctg tct ccg ggc gaa cgt gcg acc ctg agc tgc aga gcg agc cag tct 144
Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

gtt tct ttt gat tat ctg ggt tgg tac cag cag aaa cca ggt caa gca 192
Val Ser Phe Asp Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

ccg cgt cta tta att tat ggt gct tct aat cgt gca act ggg gtc ccg 240
Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro
65 70 75 80

gcg cgt ttt agc ggc tct gga tcc ggc acg gat ttt acc ctg acc att 288
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

agc agc ctg gaa cct gaa gac ttt gcg act tat tat tgc cag cag tat 336
Ser Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr
100 105 110

tat aat atg cct tat acc ttt ggc cag ggt acg aaa gtt gaa att aaa 384
Tyr Asn Met Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
115 120 125

cgt acg gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag 432
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu

130 135 140

cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc 480
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa 528
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc 576
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag 624
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg 672
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

ccc gtc aca aag agc ttc aac agg gga gag tgt tag 708
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 55
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 55

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

Val Ser Phe Asp Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

Ser Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr
100 105 110

Tyr Asn Met Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 56
<211> 708
<212> DNA
<213> Artificial Sequence

<220>
<223> MOR07923 light chain

<220>
<221> CDS
<222> (1)..(708)

<400> 56
atg gtg ttg cag acc cag gtc ttc att tct ctg ttg ctc tgg atc tct 48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

ggt gcc tac ggg gat atc gtg ctg acc cag agc ccg gcg acc ctg agc 96
Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

ctg tct ccg ggc gaa cgt gcg acc ctg agc tgc aga gcg agc cag tct 144

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

gtt tct ttt gat tat ctg ggt tgg tac cag cag aaa cca ggt caa gca 192
Val Ser Phe Asp Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

ccg cgt cta tta att tat ggt gct tct aat cgt gca act ggg gtc ccg 240
Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro
65 70 75 80

gcg cgt ttt agc ggc tct gga tcc ggc acg gat ttt acc ctg acc att 288
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

agc agc ctg gaa cct gaa gac ttt gcg acc tat tat tgc ttt cag tat 336
Ser Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Tyr
100 105 110

ctt att gtt cct ttt acc ttt ggc cag ggt acg aaa gtt gaa att aaa 384
Leu Ile Val Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
115 120 125

cgt acg gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag 432
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc 480
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa 528
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc 576
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag 624
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg 672
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

ccc gtc aca aag agc ttc aac agg gga gag tgt tag 708
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 57
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 57

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

Val Ser Phe Asp Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

Ser Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Tyr
100 105 110

Leu Ile Val Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 58
<211> 708
<212> DNA
<213> Artificial Sequence

<220>
<223> MOR07924 light chain

<220>
<221> CDS
<222> (1)..(708)

<400> 58
atg gtg ttg cag acc cag gtc ttc att tct ctg ttg ctc tgg atc tct 48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

ggt gcc tac ggg gat atc gtg ctg acc cag agc ccg gcg acc ctg agc 96
Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

ctg tct ccg ggc gaa cgt gcg acc ctg agc tgc aga gcg agc cag tct 144
Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

gtt tct ttt gat tat ctg ggt tgg tac cag cag aaa cca ggt caa gca 192
Val Ser Phe Asp Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

ccg cgt cta tta att tat ggt gct tct aat cgt gca act ggg gtc ccg 240
Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro
65 70 75 80

gcg cgt ttt agc ggc tct gga tcc ggc acg gat ttt acc ctg acc att 288
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

agc agc ctg gaa cct gaa gac ttt gcg acc tat tat tgc cag cag tat 336
Ser Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr
100 105 110

aat att aat cct ttt acc ttt ggc cag ggt acg aaa gtt gaa att aaa 384
Asn Ile Asn Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
115 120 125

cgt acg gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag 432
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc 480
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa 528
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc 576
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag 624
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg 672
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

ccc gtc aca aag agc ttc aac agg gga gag tgt tag 708
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 59
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 59

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

Val Ser Phe Asp Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

Ser Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr
100 105 110

Asn Ile Asn Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu

130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 60
<211> 708
<212> DNA
<213> Artificial Sequence

<220>
<223> MOR07925 light chain

<220>
<221> CDS
<222> (1)..(708)

<400> 60
atg gtg ttg cag acc cag gtc ttc att tct ctg ttg ctc tgg atc tct 48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

ggt gcc tac ggg gat atc gtg ctg acc cag agc ccg gcg acc ctg agc 96
Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

ctg tct ccg ggc gaa cgt gcg acc ctg agc tgc aga gcg agc cag tct 144
Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

gtt tct ttt gat tat ctg ggt tgg tac cag cag aaa cca ggt caa gca 192
Val Ser Phe Asp Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

ccg cgt cta tta att tat ggt gct tct aat cgt gca act ggg gtc ccg 240
Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro
65 70 75 80

gcg cgt ttt agc ggc tct gga tcc ggc acg gat ttt acc ctg acc att 288
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

agc agc ctg gaa cct gaa gac ttt gcg acc tat tat tgc ctt cag tat 336
Ser Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Tyr
100 105 110

ttt aat cct cct cat acc ttt ggc cag ggt acg aaa gtt gaa att aaa 384
Phe Asn Pro Pro His Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
115 120 125

cgt acg gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag 432
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc 480
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa 528
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc 576
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag 624
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg 672
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

ccc gtc aca aag agc ttc aac agg gga gag tgt tag 708
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 61
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 61

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

Val Ser Phe Asp Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

Ser Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Tyr
100 105 110

Phe Asn Pro Pro His Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 62
<211> 708
<212> DNA
<213> Artificial Sequence

<220>
<223> MOR07926 light chain

<220>
<221> CDS
<222> (1)..(708)

<400> 62
atg gtg ttg cag acc cag gtc ttc att tct ctg ttg ctc tgg atc tct 48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

ggt gcc tac ggg gat atc gtg ctg acc cag agc ccg gcg acc ctg agc 96
Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

ctg tct ccg ggc gaa cgt gcg acc ctg agc tgc aga gcg agc cag tct 144
Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

gtt tct ttt gat tat ctg ggt tgg tac cag cag aaa cca ggt caa gca 192
Val Ser Phe Asp Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

ccg cgt cta tta att tat ggt gct tct aat cgt gca act ggg gtc ccg 240
Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro
65 70 75 80

gcg cgt ttt agc ggc tct gga tcc ggc acg gat ttt acc ctg acc att 288
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

agc agc ctg gaa cct gaa gac ttt gcg acc tat tat tgc ttt cag gct 336
Ser Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Ala
100 105 110

ctt att atg cct ttt acc ttt ggc cag ggt acg aaa gtt gaa att aaa 384
Leu Ile Met Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
115 120 125

cgt acg gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag 432
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc 480
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa 528
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc 576
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag 624
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg 672
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser

210 215 220

ccc gtc aca aag agc ttc aac agg gga gag tgt tag 708
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 63
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 63

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

Val Ser Phe Asp Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

Ser Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Ala
100 105 110

Leu Ile Met Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 64
<211> 1551
<212> DNA
<213> Artificial Sequence

<220>
<223> MOR7919 heavy chain

<220>
<221> CDS
<222> (45)..(1457)

<400> 64
taatacgact cactataggg agacccaagc tggctagcgc cacc atg aaa cac ctg 56
Met Lys His Leu
1

tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg gtc ctg tcc cag 104
Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln
5 10 15 20

gtg caa ttg gtt cag agc ggc gcg gaa gtg aaa aaa ccg ggc gaa agc 152
Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser
25 30 35

ctg aaa att agc tgc aaa ggt tcc gga tat tcc ttt act aat tat tgg 200
Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Asn Tyr Trp
40 45 50

att tct tgg gtg cgc cag atg cct ggg aag ggt ctc gag tgg atg ggc 248
Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
55 60 65

ttt atc tat ccg gat gat agc tat acc cgt tat tct ccg agc ttt cag 296
Phe Ile Tyr Pro Asp Asp Ser Tyr Thr Arg Tyr Ser Pro Ser Phe Gln
70 75 80

ggc cag gtg acc att agc gcg gat aaa agc att agc acc gcg tat ctt 344
Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
85 90 95 100

caa tgg agc agc ctg aaa gcg agc gat acg gcc atg tat tat tgc gcg 392

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
105 110 115

cgt ttt tct tat cgt cat tat ctt gat atg gat gat cat tgg ggc caa 440
Arg Phe Ser Tyr Arg His Tyr Leu Asp Met Asp Asp His Trp Gly Gln
120 125 130

ggc acc ctg gtg acg gtt agc tca gcc tcc acc aag ggt cca tcg gtc 488
Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
135 140 145

ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc 536
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
150 155 160

ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg 584
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
165 170 175 180

tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc 632
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
185 190 195

cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc 680
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
200 205 210

tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag 728
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
215 220 225

ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt gac 776
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
230 235 240

aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga 824
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
245 250 255 260

ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc 872
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
265 270 275

tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa 920
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
280 285 290

gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat 968
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
295 300 305

aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac cgg 1016
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
310 315 320

gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag 1064
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
325 330 335 340

gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag 1112

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
345 350 355

aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac 1160
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
360 365 370

acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc ctg 1208
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
375 380 385

acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg 1256
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
390 395 400

gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg 1304
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
405 410 415 420

ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac 1352
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
425 430 435

aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat 1400
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
440 445 450

gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg 1448
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
455 460 465

ggt aaa tga gggcccgttt aaacgggtgg catccctgtg acccctcccc 1497
Gly Lys
470

agtgcctctc ctggccctgg aagttgccac tccagtgccc accagccttg tcct 1551

<210> 65
<211> 470
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 65

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe
35 40 45

Thr Asn Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu
50 55 60

Glu Trp Met Gly Phe Ile Tyr Pro Asp Asp Ser Tyr Thr Arg Tyr Ser
65 70 75 80

Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser
85 90 95

Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met
100 105 110

Tyr Tyr Cys Ala Arg Phe Ser Tyr Arg His Tyr Leu Asp Met Asp Asp
115 120 125

His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
130 135 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145 150 155 160

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
165 170 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
180 185 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
195 200 205

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
210 215 220

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro
225 230 235 240

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
245 250 255

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
260 265 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
275 280 285

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
290 295 300

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305 310 315 320

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
325 330 335

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
340 345 350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
355 360 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
370 375 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385 390 395 400

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
405 410 415

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
420 425 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
435 440 445

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
450 455 460

Ser Leu Ser Pro Gly Lys
465 470

<210> 66
<211> 1539
<212> DNA
<213> Artificial Sequence

<220>
<223> MOR7692, MOR7923, MOR7924, MOR7925 and MOR7926 heavy chain

<220>
<221> CDS
<222> (45)..(1445)

<400> 66
taatacgact cactataggg agacccaagc tggctagcgc cacc atg aaa cac ctg 56
Met Lys His Leu
1

tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg gtc ctg tcc cag 104
Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln
5 10 15 20

gtg caa ttg gtg gaa agc ggc ggc ggc ctg gtg caa ccg ggc ggc agc 152
Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
25 30 35

ctg cgt ctg agc tgc gcg gcc tcc gga ttt acc ttt aat tct tat tct 200
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Ser Tyr Ser
40 45 50

atg tct tgg gtg cgc caa gcc cct ggg aag ggt ctc gag tgg gtg agc 248
Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
55 60 65

tat atc tct tct cgt tct agc act acc tat tat gcg gat agc gtg aaa 296
Tyr Ile Ser Ser Arg Ser Ser Thr Thr Tyr Tyr Ala Asp Ser Val Lys
70 75 80

ggc cgt ttt acc att tca cgt gat aat tcg aaa aac acc ctg tat ctg 344
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
85 90 95 100

caa atg aac agc ctg cgt gcg gaa gat acg gcc gtg tat tat tgc gcg 392
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
105 110 115

cgt ggt tat ttt cat ggt atg gat tat tgg ggc caa ggc acc ctg gtg 440
Arg Gly Tyr Phe His Gly Met Asp Tyr Trp Gly Gln Gly Thr Leu Val
120 125 130

acg gtt agc tca gcc tcc acc aag ggt cca tcg gtc ttc ccc ctg gca 488
Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
135 140 145

ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg 536
Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
150 155 160

gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc 584
Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
165 170 175 180

gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca 632
Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
185 190 195

gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg 680
Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
200 205 210

ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac acc 728
Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr

215 220 225

aag gtg gac aag aga gtt gag ccc aaa tct tgt gac aaa act cac aca 776
Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
230 235 240

tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc 824
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
245 250 255 260

ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct 872
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
265 270 275

gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc 920
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
280 285 290

aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca 968
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
295 300 305

aag ccg cgg gag gag cag tac aac agc acg tac cgg gtg gtc agc gtc 1016
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
310 315 320

ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc 1064
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
325 330 335 340

aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc 1112
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
345 350 355

aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca 1160
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
360 365 370

tcc cgg gag gag atg acc aag aac cag gtc agc ctg acc tgc ctg gtc 1208
Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
375 380 385

aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg 1256
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
390 395 400

cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac 1304
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
405 410 415 420

ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg 1352
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
425 430 435

cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac 1400
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
440 445 450

aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tga 1445
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

455 460 465

gggcccgttt aaacgggtgg catccctgtg acccctcccc agtgcctctc ctggccctgg 1505

aagttgccac tccagtgccc accagccttg tcct 1539

<210> 67
<211> 466
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 67

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Asn Ser Tyr Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ser Tyr Ile Ser Ser Arg Ser Ser Thr Thr Tyr Tyr Ala
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
85 90 95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Gly Tyr Phe His Gly Met Asp Tyr Trp Gly Gln
115 120 125

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
130 135 140

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
145 150 155 160

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
165 170 175

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
180 185 190

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
195 200 205

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
210 215 220

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
225 230 235 240

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
245 250 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
260 265 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
275 280 285

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
290 295 300

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
305 310 315 320

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
325 330 335

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
340 345 350

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
355 360 365

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
370 375 380

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
385 390 395 400

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
405 410 415

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
420 425 430

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
435 440 445

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
450 455 460

Gly Lys
465

<210> 68
<211> 840
<212> DNA
<213> Artificial Sequence

<220>
<223> MOR07919 lambda light chain

<220>
<221> CDS
<222> (45)..(746)

<400> 68
taatacgact cactataggg agacccaagc tggctagcgc cacc atg gcc tgg gct 56
Met Ala Trp Ala
1

ctg ctg ctc ctc acc ctc ctc act cag ggc aca gga tcc tgg gct gat 104
Leu Leu Leu Leu Thr Leu Leu Thr Gln Gly Thr Gly Ser Trp Ala Asp
5 10 15 20

atc gaa ctg acc cag ccg cct tca gtg agc gtt gca cca ggt cag acc 152
Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln Thr
25 30 35

gcg cgt atc tcg tgt agc ggc gat tct ctt ggt tct aag tat gtt cat 200
Ala Arg Ile Ser Cys Ser Gly Asp Ser Leu Gly Ser Lys Tyr Val His
40 45 50

tgg tac cag cag aaa ccc ggg cag gcg cca gtt ctt gtg att tat cgt 248
Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Arg
55 60 65

gat aat aag cgt ccc tca ggc atc ccg gaa cgc ttt agc gga tcc aac 296
Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn
70 75 80

agc ggc aac acc gcg acc ctg acc att agc ggc act cag gcg gaa gac 344
Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu Asp
85 90 95 100

gaa gcg gat tat tat tgc cag tct tat gat gct act gag ttt act tat 392

Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ala Thr Glu Phe Thr Tyr
105 110 115

gtg ttt ggc ggc ggc acg aag tta acc gtc cta ggt cag ccc aag gct 440
Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala
120 125 130

gcc ccc tcg gtc act ctg ttc ccg ccc tcc tct gag gag ctt caa gcc 488
Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala
135 140 145

aac aag gcc aca ctg gtg tgt ctc ata agt gac ttc tac ccg gga gcc 536
Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala
150 155 160

gtg aca gtg gcc tgg aag gca gat agc agc ccc gtc aag gcg gga gtg 584
Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val
165 170 175 180

gag acc acc aca ccc tcc aaa caa agc aac aac aag tac gcg gcc agc 632
Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser
185 190 195

agc tat ctg agc ctg acg cct gag cag tgg aag tcc cac aga agc tac 680
Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
200 205 210

agc tgc cag gtc acg cat gaa ggg agc acc gtg gag aag aca gtg gcc 728
Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala
215 220 225

cct aca gaa tgt tca tag gggcccgttt aaacgggtgg catccctgtg 776
Pro Thr Glu Cys Ser
230

acccctcccc agtgcctctc ctggccctgg aagttgccac tccagtgccc accagccttg 836

tcct 840

<210> 69
<211> 233
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 69

Met Ala Trp Ala Leu Leu Leu Leu Thr Leu Leu Thr Gln Gly Thr Gly
1 5 10 15

Ser Trp Ala Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala
20 25 30

Pro Gly Gln Thr Ala Arg Ile Ser Cys Ser Gly Asp Ser Leu Gly Ser
35 40 45

Lys Tyr Val His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu
50 55 60

Val Ile Tyr Arg Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe
65 70 75 80

Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr
85 90 95

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ala Thr
100 105 110

Glu Phe Thr Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
115 120 125

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
130 135 140

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
145 150 155 160

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
165 170 175

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
180 185 190

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
195 200 205

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
210 215 220

Lys Thr Val Ala Pro Thr Glu Cys Ser
225 230

<210> 70
<211> 846
<212> DNA
<213> Artificial Sequence

<220>
<223> MOR07692 kappa light chain

<220>

<221> CDS
<222> (45)..(752)

<400> 70
taatacgact cactataggg agacccaagc tggctagcgc cacc atg gtg ttg cag 56
Met Val Leu Gln
1

acc cag gtc ttc att tct ctg ttg ctc tgg atc tct ggt gcc tac ggg 104
Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly
5 10 15 20

gat atc gtg ctg acc cag agc ccg gcg acc ctg agc ctg tct ccg ggc 152
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
25 30 35

gaa cgt gcg acc ctg agc tgc aga gcg agc cag tct gtt tct ttt gat 200
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Phe Asp
40 45 50

tat ctg ggt tgg tac cag cag aaa cca ggt caa gca ccg cgt cta tta 248
Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
55 60 65

att tat ggt gct tct aat cgt gca act ggg gtc ccg gcg cgt ttt agc 296
Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
70 75 80

ggc tct gga tcc ggc acg gat ttt acc ctg acc att agc agc ctg gaa 344
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
85 90 95 100

cct gaa gac ttt gcg act tat tat tgc cag cag tat tat aat atg cct 392
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Asn Met Pro
105 110 115

tat acc ttt ggc cag ggt acg aaa gtt gaa att aaa cgt acg gtg gct 440
Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
120 125 130

gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct 488
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
135 140 145

gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag 536
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
150 155 160

gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc 584
Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
165 170 175 180

cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc 632
Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
185 190 195

agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc 680
Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
200 205 210

tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag 728
Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
215 220 225

agc ttc aac agg gga gag tgt tag gggcccgttt aaacgggtgg catccctgtg 782
Ser Phe Asn Arg Gly Glu Cys
230 235

acccctcccc agtgcctctc ctggccctgg aagttgccac tccagtgccc accagccttg 842

tcct 846

<210> 71
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 71

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

Val Ser Phe Asp Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

Ser Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr
100 105 110

Tyr Asn Met Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe

145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 72
<211> 846
<212> DNA
<213> Artificial Sequence

<220>
<223> MOR07923 kappa light chain

<220>
<221> CDS
<222> (45)..(752)

<400> 72
taatacgact cactataggg agacccaagc tggctagcgc cacc atg gtg ttg cag 56
Met Val Leu Gln
1

acc cag gtc ttc att tct ctg ttg ctc tgg atc tct ggt gcc tac ggg 104
Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly
5 10 15 20

gat atc gtg ctg acc cag agc ccg gcg acc ctg agc ctg tct ccg ggc 152
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
25 30 35

gaa cgt gcg acc ctg agc tgc aga gcg agc cag tct gtt tct ttt gat 200
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Phe Asp
40 45 50

tat ctg ggt tgg tac cag cag aaa cca ggt caa gca ccg cgt cta tta 248
Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
55 60 65

att tat ggt gct tct aat cgt gca act ggg gtc ccg gcg cgt ttt agc 296
Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
70 75 80

ggc tct gga tcc ggc acg gat ttt acc ctg acc att agc agc ctg gaa 344
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
85 90 95 100

cct gaa gac ttt gcg acc tat tat tgc ttt cag tat ctt att gtt cct 392
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Tyr Leu Ile Val Pro
105 110 115

ttt acc ttt ggc cag ggt acg aaa gtt gaa att aaa cgt acg gtg gct 440
Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
120 125 130

gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct 488
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
135 140 145

gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag 536
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
150 155 160

gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc 584
Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
165 170 175 180

cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc 632
Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
185 190 195

agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc 680
Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
200 205 210

tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag 728
Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
215 220 225

agc ttc aac agg gga gag tgt tag gggcccgttt aaacgggtgg catccctgtg 782
Ser Phe Asn Arg Gly Glu Cys
230 235

acccctcccc agtgcctctc ctggccctgg aagttgccac tccagtgccc accagccttg 842

tcct 846

<210> 73
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 73

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

Val Ser Phe Asp Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

Ser Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Tyr
100 105 110

Leu Ile Val Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 74
<211> 846
<212> DNA
<213> Artificial Sequence

<220>
<223> MOR07924 kappa light chain

<220>
<221> CDS
<222> (45)..(752)

<400> 74
taatacgact cactataggg agacccaagc tggctagcgc cacc atg gtg ttg cag 56
Met Val Leu Gln
1

acc cag gtc ttc att tct ctg ttg ctc tgg atc tct ggt gcc tac ggg 104
Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly
5 10 15 20

gat atc gtg ctg acc cag agc ccg gcg acc ctg agc ctg tct ccg ggc 152
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
25 30 35

gaa cgt gcg acc ctg agc tgc aga gcg agc cag tct gtt tct ttt gat 200
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Phe Asp
40 45 50

tat ctg ggt tgg tac cag cag aaa cca ggt caa gca ccg cgt cta tta 248
Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
55 60 65

att tat ggt gct tct aat cgt gca act ggg gtc ccg gcg cgt ttt agc 296
Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
70 75 80

ggc tct gga tcc ggc acg gat ttt acc ctg acc att agc agc ctg gaa 344
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
85 90 95 100

cct gaa gac ttt gcg acc tat tat tgc cag cag tat aat att aat cct 392
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Asn Pro
105 110 115

ttt acc ttt ggc cag ggt acg aaa gtt gaa att aaa cgt acg gtg gct 440
Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
120 125 130

gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct 488
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
135 140 145

gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag 536
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
150 155 160

gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc 584
Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
165 170 175 180

cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc 632
Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu

185 190 195

agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc 680
Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
200 205 210

tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag 728
Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
215 220 225

agc ttc aac agg gga gag tgt tag gggcccgttt aaacgggtgg catccctgtg 782
Ser Phe Asn Arg Gly Glu Cys
230 235

acccctcccc agtgcctctc ctggccctgg aagttgccac tccagtgccc accagccttg 842

tcct 846

<210> 75
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 75

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

Val Ser Phe Asp Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

Ser Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr
100 105 110

Asn Ile Asn Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 76
<211> 846
<212> DNA
<213> Artificial Sequence

<220>
<223> MOR07925 kappa light chain

<220>
<221> CDS
<222> (45)..(752)

<400> 76
taatacgact cactataggg agacccaagc tggctagcgc cacc atg gtg ttg cag 56
Met Val Leu Gln
1

acc cag gtc ttc att tct ctg ttg ctc tgg atc tct ggt gcc tac ggg 104
Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly
5 10 15 20

gat atc gtg ctg acc cag agc ccg gcg acc ctg agc ctg tct ccg ggc 152
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
25 30 35

gaa cgt gcg acc ctg agc tgc aga gcg agc cag tct gtt tct ttt gat 200
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Phe Asp
40 45 50

tat ctg ggt tgg tac cag cag aaa cca ggt caa gca ccg cgt cta tta 248

Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
55 60 65

att tat ggt gct tct aat cgt gca act ggg gtc ccg gcg cgt ttt agc 296
Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
70 75 80

ggc tct gga tcc ggc acg gat ttt acc ctg acc att agc agc ctg gaa 344
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
85 90 95 100

cct gaa gac ttt gcg acc tat tat tgc ctt cag tat ttt aat cct cct 392
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Tyr Phe Asn Pro Pro
105 110 115

cat acc ttt ggc cag ggt acg aaa gtt gaa att aaa cgt acg gtg gct 440
His Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
120 125 130

gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct 488
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
135 140 145

gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag 536
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
150 155 160

gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc 584
Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
165 170 175 180

cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc 632
Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
185 190 195

agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc 680
Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
200 205 210

tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag 728
Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
215 220 225

agc ttc aac agg gga gag tgt tag gggcccgttt aaacgggtgg catccctgtg 782
Ser Phe Asn Arg Gly Glu Cys
230 235

acccctcccc agtgcctctc ctggccctgg aagttgccac tccagtgccc accagccttg 842

tcct 846

<210> 77
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 77

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

Val Ser Phe Asp Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

Ser Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Tyr
100 105 110

Phe Asn Pro Pro His Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 78
<211> 846
<212> DNA
<213> Artificial Sequence

<220>
<223> MOR07926 kappa light chain

<220>
<221> CDS
<222> (45)..(752)

<400> 78
taatacgact cactataggg agacccaagc tggctagcgc cacc atg gtg ttg cag 56
Met Val Leu Gln
1

acc cag gtc ttc att tct ctg ttg ctc tgg atc tct ggt gcc tac ggg 104
Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly
5 10 15 20

gat atc gtg ctg acc cag agc ccg gcg acc ctg agc ctg tct ccg ggc 152
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
25 30 35

gaa cgt gcg acc ctg agc tgc aga gcg agc cag tct gtt tct ttt gat 200
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Phe Asp
40 45 50

tat ctg ggt tgg tac cag cag aaa cca ggt caa gca ccg cgt cta tta 248
Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
55 60 65

att tat ggt gct tct aat cgt gca act ggg gtc ccg gcg cgt ttt agc 296
Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
70 75 80

ggc tct gga tcc ggc acg gat ttt acc ctg acc att agc agc ctg gaa 344
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
85 90 95 100

cct gaa gac ttt gcg acc tat tat tgc ttt cag gct ctt att atg cct 392
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Ala Leu Ile Met Pro
105 110 115

ttt acc ttt ggc cag ggt acg aaa gtt gaa att aaa cgt acg gtg gct 440
Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
120 125 130

gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct 488
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
135 140 145

gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag 536
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
150 155 160

gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc 584
Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
165 170 175 180

cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc 632
Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
185 190 195

agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc 680
Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
200 205 210

tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag 728
Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
215 220 225

agc ttc aac agg gga gag tgt tag gggcccgttt aaacgggtgg catccctgtg 782
Ser Phe Asn Arg Gly Glu Cys
230 235

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tcct 846

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1 5 10 15

Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

Val Ser Phe Asp Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

Ser Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Ala

100 105 110

Leu Ile Met Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

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1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60

Xaa Xaa Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100 105 110

Xaa Xaa Xaa Xaa Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 81
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<400> 81

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu

1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60

Xaa Xaa Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100 105 110

Xaa Xaa Xaa Xaa Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

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<222> (90)..(98)
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<400> 82

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95

Xaa Xaa Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 83
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<223> Xaa can be any naturally occurring amino acid

<400> 83

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1 5 10 15

Thr Ala Arg Ile Ser Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Xaa Val Ile Xaa
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95

Xaa Xaa Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
100 105 110

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<110> DAIICHI SANKYO COMPANY, LIMITED

<120> ANTI-MST1R ANTIBODIES AND USES THEREOF

<130> DSPCT-FP1004

<150> US 61/151,411
<151> 2009-02-10

<160> 83

<170> PatentIn version 3.5

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Gly Tyr Phe His Gly Met Asp Tyr
1 5

<210> 2
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<400> 2

Tyr Ile Ser Ser Arg Ser Ser Thr Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

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1 5 10

<210> 5
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<400> 5

Phe Ile Tyr Pro Asp Asp Ser Tyr Thr Arg Tyr Ser Pro Ser Phe Gln
1 5 10 15

Gly

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Gln Gln Tyr Tyr Asn Met Pro Tyr Thr
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Gln Ser Tyr Asp Ala Thr Glu Phe Thr Tyr Val
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Arg Ala Ser Gln Ser Val Ser Phe Asp Tyr Leu Gly
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Ser Gly Asp Ser Leu Gly Ser Lys Tyr Val His
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Arg Asp Asn Lys Arg Pro Ser
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Glu Asp Trp Gln Cys Pro Arg Thr Pro Tyr Ala Ala Ser Arg Asp Phe
1 5 10 15

Asp Val Lys Tyr Val Val Pro Ser Phe Ser Ala Gly Gly Leu Val Gln
20 25 30

Ala Met Val Thr Tyr Glu Gly Asp Arg Asn Glu Ser Ala Val Phe Val
35 40 45

Ala Ile Arg Asn Arg Leu His Val Leu Gly Pro Asp Leu Lys Ser Val
50 55 60

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

Ala Ala Cys Gly Pro Gly Pro His Gly Pro Pro Gly Asp Thr Asp Thr
85 90 95

Lys Val Leu Val Leu Asp Pro Ala Leu Pro Ala Leu Val Ser Cys Gly
100 105 110

Ser Ser Leu Gln Gly Arg Cys Phe Leu His Asp Leu Glu Pro Gln Gly
115 120 125

Thr Ala Val His Leu Ala Ala Pro Ala Cys Leu Phe Ser Ala His His
130 135 140

Asn Arg Pro Asp Asp Cys Pro Asp Cys Val Ala Ser Pro Leu Gly Thr
145 150 155 160

Arg Val Thr Val Val Glu Gln Gly Gln Ala Ser Tyr Phe Tyr Val Ala
165 170 175

Ser Ser Leu Asp Ala Ala Val Ala Gly Ser Phe Ser Pro Arg Ser Val
180 185 190

Ser Ile Arg Arg Leu Lys Ala Asp Ala Ser Gly Phe Ala Pro Gly Phe
195 200 205

Val Ala Leu Ser Val Leu Pro Lys His Leu Val Ser Tyr Ser Ile Glu
210 215 220

Tyr Val His Ser Phe His Thr Gly Ala Phe Val Tyr Phe Leu Thr Val
225 230 235 240

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

Ala Arg Leu Ser Ala Thr Glu Pro Glu Leu Gly Asp Tyr Arg Glu Leu
260 265 270

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Val Leu Asp Cys Arg Phe Ala Pro Lys Arg Arg Arg Arg Gly Ala Pro
        275                 280                 285

Glu Gly Gly Gln Pro Tyr Pro Val Leu Gln Val Ala His Ser Ala Pro
    290                 295                 300

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

Val Leu Phe Gly Val Phe Val Thr Gly Lys Asp Gly Gly Pro Gly Val
                325                 330                 335

Gly Pro Asn Ser Val Val Cys Ala Phe Pro Ile Asp Leu Leu Asp Thr
            340                 345                 350

Leu Ile Asp Glu Gly Val Glu Arg Cys Cys Glu Ser Pro Val His Pro
        355                 360                 365

Gly Leu Arg Arg Gly Leu Asp Phe Phe Gln Ser Pro Ser Phe Cys Pro
    370                 375                 380

Asn Pro Pro Gly Leu Glu Ala Leu Ser Pro Asn Thr Ser Cys Arg His
385                 390                 395                 400

Phe Pro Leu Leu Val Ser Ser Ser Phe Ser Arg Val Asp Leu Phe Asn
                405                 410                 415

Gly Leu Leu Gly Pro Val Gln Val Thr Ala Leu Tyr Val Thr Arg Leu
            420                 425                 430

Asp Asn Val Thr Val Ala His Met Gly Thr Met Asp Gly Arg Ile Leu
        435                 440                 445

Gln Val Glu Leu Val Arg Ser Leu Asn Tyr Leu Leu Tyr Val Ser Asn
    450                 455                 460

Phe Ser Leu Gly Asp Ser Gly Gln Pro Val Gln Arg Asp Val Ser Arg
465                 470                 475                 480

Leu Gly Asp His Leu Leu Phe Ala Ser Gly Asp Gln Val Phe Gln Val
                485                 490                 495

Pro Ile Arg Gly Pro Gly Cys Arg His Phe Leu Thr Cys Gly Arg Cys
            500                 505                 510

Leu Arg Ala Trp His Phe Met Gly Cys Gly Trp Cys Gly Asn Met Cys
        515                 520                 525

Gly Gln Gln Lys Glu Cys Pro Gly Ser Trp Gln Gln Asp His Cys Pro
    530                 535                 540
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Pro Lys Leu
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<212> DNA
<213> Homo sapiens

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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

agc ctg cgt ctg agc tgc gcg gcc tcc gga ttt acc ttt aat tct tat 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Ser Tyr
20 25 30

tct atg tct tgg gtg cgc caa gcc cct ggg aag ggt ctc gag tgg gtg 144
Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

agc tat atc tct tct cgt tct agc act acc tat tat gcg gat agc gtg 192
Ser Tyr Ile Ser Ser Arg Ser Ser Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

aaa ggc cgt ttt acc att tca cgt gat aat tcg aaa aac acc ctg tat 240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

ctg caa atg aac agc ctg cgt gcg gaa gat acg gcc gtg tat tat tgc 288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

gcg cgt ggt tat ttt cat ggt atg gat tat tgg ggc caa ggc acc ctg 336
Ala Arg Gly Tyr Phe His Gly Met Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

gtg acg gtt agc tca 351
Val Thr Val Ser Ser
115

<210> 19
<211> 117
<212> PRT
<213> Homo sapiens

<400> 19

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Ser Tyr
20 25 30

Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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Ser Tyr Ile Ser Ser Arg Ser Ser Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Tyr Phe His Gly Met Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110

Val Thr Val Ser Ser
        115
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<210> 20
<211> 363
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> (1)..(363)

<400> 20

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cag gtg caa ttg gtt cag agc ggc gcg gaa gtg aaa aaa ccg ggc gaa          48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1               5                   10                  15

agc ctg aaa att agc tgc aaa ggt tcc gga tat tcc ttt act aat tat          96
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Asn Tyr
            20                  25                  30

tgg att tct tgg gtg cgc cag atg cct ggg aag ggt ctc gag tgg atg         144
Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
        35                  40                  45

ggc ttt atc tat ccg gat gat agc tat acc cgt tat tct ccg agc ttt         192
Gly Phe Ile Tyr Pro Asp Asp Ser Tyr Thr Arg Tyr Ser Pro Ser Phe
    50                  55                  60

cag ggc cag gtg acc att agc gcg gat aaa agc att agc acc gcg tat         240
Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

ctt caa tgg agc agc ctg aaa gcg agc gat acg gcc atg tat tat tgc         288
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95

gcg cgt ttt tct tat cgt cat tat ctt gat atg gat gat cat tgg ggc         336
Ala Arg Phe Ser Tyr Arg His Tyr Leu Asp Met Asp Asp His Trp Gly
            100                 105                 110

caa ggc acc ctg gtg acg gtt agc tca                                    363
Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<210> 21
<211> 121
<212> PRT

<213> Homo sapiens

<400> 21

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1               5                   10                  15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Asn Tyr
            20                  25                  30

Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
        35                  40                  45

Gly Phe Ile Tyr Pro Asp Asp Ser Tyr Thr Arg Tyr Ser Pro Ser Phe
    50                  55                  60

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

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95

Ala Arg Phe Ser Tyr Arg His Tyr Leu Asp Met Asp Asp His Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<210> 22
<211> 330
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(330)

<400> 22

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gat atc gtg ctg acc cag agc ccg gcg acc ctg agc ctg tct ccg ggc          48
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15

gaa cgt gcg acc ctg agc tgc aga gcg agc cag tct gtt tct ttt gat          96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Phe Asp
            20                  25                  30

tat ctg ggt tgg tac cag cag aaa cca ggt caa gca ccg cgt cta tta         144
Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45

att tat ggt gct tct aat cgt gca act ggg gtc ccg gcg cgt ttt agc         192
Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
    50                  55                  60

ggc tct gga tcc ggc acg gat ttt acc ctg acc att agc agc ctg gaa         240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65                  70                  75                  80

cct gaa gac ttt gcg act tat tat tgc cag cag tat tat aat atg cct         288
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Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Asn Met Pro
85 90 95

tat acc ttt ggc cag ggt acg aaa gtt gaa att aaa cgt acg 330
Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 23
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<212> PRT
<213> Homo sapiens

<400> 23

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Phe Asp
20 25 30

Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Asn Met Pro
85 90 95

Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 24
<211> 330
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(330)

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

acc gcg cgt atc tcg tgt agc ggc gat tct ctt ggt tct aag tat gtt 96
Thr Ala Arg Ile Ser Cys Ser Gly Asp Ser Leu Gly Ser Lys Tyr Val
20 25 30

cat tgg tac cag cag aaa ccc ggg cag gcg cca gtt ctt gtg att tat 144
His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

cgt gat aat aag cgt ccc tca ggc atc ccg gaa cgc ttt agc gga tcc 192
Arg Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser

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    50                  55                  60

aac agc ggc aac acc gcg acc ctg acc att agc ggc act cag gcg gaa        240
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
65                  70                  75                  80

gac gaa gcg gat tat tat tgc cag tct tat gat gct act gag ttt act        288
Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ala Thr Glu Phe Thr
                85                  90                  95

tat gtg ttt ggc ggc ggc acg aag tta acc gtt ctt ggc cag                330
Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
            100                 105                 110


<210>  25
<211>  110
<212>  PRT
<213>  Homo sapiens

<400>  25

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


Thr Ala Arg Ile Ser Cys Ser Gly Asp Ser Leu Gly Ser Lys Tyr Val
            20                  25                  30


His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
        35                  40                  45


Arg Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60


Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
65                  70                  75                  80


Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ala Thr Glu Phe Thr
                85                  90                  95


Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
            100                 105                 110


<210>  26
<211>  330
<212>  DNA
<213>  Homo sapiens


<220>
<221>  CDS
<222>  (1)..(330)

<400>  26
gat atc gtg ctg acc cag agc ccg gcg acc ctg agc ctg tct ccg ggc         48
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15

gaa cgt gcg acc ctg agc tgc aga gcg agc cag tct gtt tct ttt gat         96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Phe Asp
            20                  25                  30
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tat ctg ggt tgg tac cag cag aaa cca ggt caa gca ccg cgt cta tta        144
Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45

att tat ggt gct tct aat cgt gca act ggg gtc ccg gcg cgt ttt agc        192
Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
    50                  55                  60

ggc tct gga tcc ggc acg gat ttt acc ctg acc att agc agc ctg gaa        240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65                  70                  75                  80

cct gaa gac ttt gcg acc tat tat tgc ttt cag tat ctt att gtt cct        288
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Tyr Leu Ile Val Pro
                85                  90                  95

ttt acc ttt ggc cag ggt acg aaa gtt gaa att aaa cgt acg                330
Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
            100                 105                 110


<210>  27
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<400>  27

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Phe Asp
            20                  25                  30

Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45

Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65                  70                  75                  80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Tyr Leu Ile Val Pro
                85                  90                  95

Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
            100                 105                 110


<210>  28
<211>  330
<212>  DNA
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<220>
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<222>  (1)..(330)

<400>  28
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gat atc gtg ctg acc cag agc ccg gcg acc ctg agc ctg tct ccg ggc          48
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15

gaa cgt gcg acc ctg agc tgc aga gcg agc cag tct gtt tct ttt gat          96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Phe Asp
            20                  25                  30

tat ctg ggt tgg tac cag cag aaa cca ggt caa gca ccg cgt cta tta         144
Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45

att tat ggt gct tct aat cgt gca act ggg gtc ccg gcg cgt ttt agc         192
Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
    50                  55                  60

ggc tct gga tcc ggc acg gat ttt acc ctg acc att agc agc ctg gaa         240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65                  70                  75                  80

cct gaa gac ttt gcg acc tat tat tgc cag cag tat aat att aat cct         288
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Asn Pro
                85                  90                  95

ttt acc ttt ggc cag ggt acg aaa gtt gaa att aaa cgt acg                 330
Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
            100                 105                 110
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<210> 29
<211> 110
<212> PRT
<213> Homo sapiens

<400> 29

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Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Phe Asp
            20                  25                  30

Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45

Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65                  70                  75                  80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Asn Pro
                85                  90                  95

Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
            100                 105                 110
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<210> 30
<211> 330
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(330)

<400> 30
gat atc gtg ctg acc cag agc ccg gcg acc ctg agc ctg tct ccg ggc 48
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

gaa cgt gcg acc ctg agc tgc aga gcg agc cag tct gtt tct ttt gat 96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Phe Asp
20 25 30

tat ctg ggt tgg tac cag cag aaa cca ggt caa gca ccg cgt cta tta 144
Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

att tat ggt gct tct aat cgt gca act ggg gtc ccg gcg cgt ttt agc 192
Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

ggc tct gga tcc ggc acg gat ttt acc ctg acc att agc agc ctg gaa 240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

cct gaa gac ttt gcg acc tat tat tgc ctt cag tat ttt aat cct cct 288
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Tyr Phe Asn Pro Pro
85 90 95

cat acc ttt ggc cag ggt acg aaa gtt gaa att aaa cgt acg 330
His Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 31
<211> 110
<212> PRT
<213> Homo sapiens

<400> 31

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Phe Asp
20 25 30

Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Tyr Phe Asn Pro Pro
85 90 95

His Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr

100 105 110

<210> 32
<211> 330
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(330)

<400> 32

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gat atc gtg ctg acc cag agc ccg gcg acc ctg agc ctg tct ccg ggc          48
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1               5                  10                  15

gaa cgt gcg acc ctg agc tgc aga gcg agc cag tct gtt tct ttt gat          96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Phe Asp
            20                  25                  30

tat ctg ggt tgg tac cag cag aaa cca ggt caa gca ccg cgt cta tta         144
Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45

att tat ggt gct tct aat cgt gca act ggg gtc ccg gcg cgt ttt agc         192
Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
    50                  55                  60

ggc tct gga tcc ggc acg gat ttt acc ctg acc att agc agc ctg gaa         240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65                  70                  75                  80

cct gaa gac ttt gcg acc tat tat tgc ttt cag gct ctt att atg cct         288
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Ala Leu Ile Met Pro
                85                  90                  95

ttt acc ttt ggc cag ggt acg aaa gtt gaa att aaa cgt acg                 330
Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
            100                 105                 110
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<210> 33
<211> 110
<212> PRT
<213> Homo sapiens

<400> 33

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Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1               5                  10                  15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Phe Asp
            20                  25                  30

Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45

Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65                  70                  75                  80
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Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Ala Leu Ile Met Pro
85 90 95

Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 34
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR forward primer

<400> 34
ttggcccagt ccagacctcg agtc 24

<210> 35
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR reverse primer

<400> 35
actctgtgga gtgagggacc taatg 25

<210> 36
<211> 4200
<212> DNA
<213> Macaca fascicularis

<220>
<221> CDS
<222> (1)..(4200)

<400> 36
atg gag ctc ctc cct ccg ctg cct cag tcc ttc tta ctg ctg ctg ctg 48
Met Glu Leu Leu Pro Pro Leu Pro Gln Ser Phe Leu Leu Leu Leu Leu
1 5 10 15

ttg cct gcc aag ccc gcg gcg gcc aag gaa tgg cag tgc ccg cgc acc 96
Leu Pro Ala Lys Pro Ala Ala Ala Lys Glu Trp Gln Cys Pro Arg Thr
20 25 30

ccc tac gcg gcc tct cga gac ttt aac gtg aag tac atg gtg ccc agc 144
Pro Tyr Ala Ala Ser Arg Asp Phe Asn Val Lys Tyr Met Val Pro Ser
35 40 45

ttc tcc gcc gga ggc ctg gtg cag acc atg gtg acc tac cag ggc gac 192
Phe Ser Ala Gly Gly Leu Val Gln Thr Met Val Thr Tyr Gln Gly Asp
50 55 60

aaa aat gag agt gct gtg ttt gta gcc ata cgc aat cgc ctg cac gtg 240
Lys Asn Glu Ser Ala Val Phe Val Ala Ile Arg Asn Arg Leu His Val
65 70 75 80

ctt ggg cct gac ctg aag tct gtc cag agc ctg gcc acg ggc cct gct 288
Leu Gly Pro Asp Leu Lys Ser Val Gln Ser Leu Ala Thr Gly Pro Ala
85 90 95

```
ggg gac cct ggc tgc cag acg tgt gca gcc tgt ggc cca ggc ccc cac          336
Gly Asp Pro Gly Cys Gln Thr Cys Ala Ala Cys Gly Pro Gly Pro His
            100                 105                 110

ggc cct tcc ggt gac aca gac aca aag gtg ctg gtg ctg gag ccc gcg          384
Gly Pro Ser Gly Asp Thr Asp Thr Lys Val Leu Val Leu Glu Pro Ala
        115                 120                 125

ctg cct gcc ctg gtc agt tgt ggc tcc agc ctg cag ggc cgc tgc ttc          432
Leu Pro Ala Leu Val Ser Cys Gly Ser Ser Leu Gln Gly Arg Cys Phe
    130                 135                 140

ctg cat gac cta gat ccc caa ggg aca gcc gtg cat ctg gca gcg cca          480
Leu His Asp Leu Asp Pro Gln Gly Thr Ala Val His Leu Ala Ala Pro
145                 150                 155                 160

gcc tgc ctc ttc tca gcc cac cat aac cgg ccc gat gac tgc ccc gac          528
Ala Cys Leu Phe Ser Ala His His Asn Arg Pro Asp Asp Cys Pro Asp
                165                 170                 175

tgt gtg gcc agc cca ttg ggc acc cgt gtg act gtg gtt gag caa ggc          576
Cys Val Ala Ser Pro Leu Gly Thr Arg Val Thr Val Val Glu Gln Gly
            180                 185                 190

cag gcc tcc tat ttc tac gtg gca tcc tca ctg gac gca gcc gtg gct          624
Gln Ala Ser Tyr Phe Tyr Val Ala Ser Ser Leu Asp Ala Ala Val Ala
        195                 200                 205

gcc agc ttc agc cca cgc tca gtg tct atc agg cgt ctc aag gcc gac          672
Ala Ser Phe Ser Pro Arg Ser Val Ser Ile Arg Arg Leu Lys Ala Asp
    210                 215                 220

gcc tcg gga ttt gca ccg ggc ttt gtg gca ttg tca gtg ctg ccc aag          720
Ala Ser Gly Phe Ala Pro Gly Phe Val Ala Leu Ser Val Leu Pro Lys
225                 230                 235                 240

cat ctt gtc tcc tac agt att gaa tat gtg cac agc ttc cat acg gga          768
His Leu Val Ser Tyr Ser Ile Glu Tyr Val His Ser Phe His Thr Gly
                245                 250                 255

gcc ttc gtc tac ttc ctg act gta cag ccg gcc agc gtg act gat gct          816
Ala Phe Val Tyr Phe Leu Thr Val Gln Pro Ala Ser Val Thr Asp Ala
            260                 265                 270

cct ggt gcc ctg cac aca cgc ctg gca cga ctt agc gcc act gag cca          864
Pro Gly Ala Leu His Thr Arg Leu Ala Arg Leu Ser Ala Thr Glu Pro
        275                 280                 285

gag ttg ggt gac tat cgg gag ctg gtc ctc gac tgc aga ttt gct cca          912
Glu Leu Gly Asp Tyr Arg Glu Leu Val Leu Asp Cys Arg Phe Ala Pro
    290                 295                 300

aaa cgc agg cgc cgg ggg gcc cca gag ggc gga cag ccc tac cct gtg          960
Lys Arg Arg Arg Arg Gly Ala Pro Glu Gly Gly Gln Pro Tyr Pro Val
305                 310                 315                 320

ctg cgg gtg gcc cac tct gct cca gtg ggt gct caa ctt gcc act gag         1008
Leu Arg Val Ala His Ser Ala Pro Val Gly Ala Gln Leu Ala Thr Glu
                325                 330                 335

ctg agc att gct gag ggc cag gaa gtg cta ttt ggg gtc ttt gtg gct         1056
Leu Ser Ile Ala Glu Gly Gln Glu Val Leu Phe Gly Val Phe Val Ala
            340                 345                 350

ggc aag gat agt ggc cct ggc gtg ggc ccc aac tct gtc gtc tgt gcc         1104
Gly Lys Asp Ser Gly Pro Gly Val Gly Pro Asn Ser Val Val Cys Ala
        355                 360                 365
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ttc ccc att gac ctg ctg gac aca tta att gat gaa ggt gtg gag cgc        1152
Phe Pro Ile Asp Leu Leu Asp Thr Leu Ile Asp Glu Gly Val Glu Arg
    370                 375                 380

tgt tgt gaa tcc cca gtc cat cca ggc ctc cgg cga ggc ctc gac ttc        1200
Cys Cys Glu Ser Pro Val His Pro Gly Leu Arg Arg Gly Leu Asp Phe
385                 390                 395                 400

ttc cag tca ccc agt ttt tgc ccc aac ccg cct ggc ctg gag gcc ccc        1248
Phe Gln Ser Pro Ser Phe Cys Pro Asn Pro Pro Gly Leu Glu Ala Pro
                405                 410                 415

agc ccc aac acc agc tgc cgc cac ttc cct ttg ctg gtc agt agc agc        1296
Ser Pro Asn Thr Ser Cys Arg His Phe Pro Leu Leu Val Ser Ser Ser
            420                 425                 430

ttc tca cgt gtg gac cta ttc aat ggg ctg ttg gga aca gta gag gtc        1344
Phe Ser Arg Val Asp Leu Phe Asn Gly Leu Leu Gly Thr Val Glu Val
        435                 440                 445

act gca ctg tat gtg aca cgc ctt gac aac gtc aca gtg gca cac atg        1392
Thr Ala Leu Tyr Val Thr Arg Leu Asp Asn Val Thr Val Ala His Met
    450                 455                 460

ggc aca gcg gat ggg cgt atc ctg cag gtg gag ctg gcc agg tca ctc        1440
Gly Thr Ala Asp Gly Arg Ile Leu Gln Val Glu Leu Ala Arg Ser Leu
465                 470                 475                 480

aac tac ttg ctg tat gtg tcc aac ttc tca ctg ggt gac agt ggg cag        1488
Asn Tyr Leu Leu Tyr Val Ser Asn Phe Ser Leu Gly Asp Ser Gly Gln
                485                 490                 495

ccc gtg cag cgg gat gtc agt cgc ctt ggg gac cac cta ttc ttc gcc        1536
Pro Val Gln Arg Asp Val Ser Arg Leu Gly Asp His Leu Phe Phe Ala
            500                 505                 510

tct ggg gac cag gtt ttc cag gta cct atc caa ggc cct ggc tgc cgc        1584
Ser Gly Asp Gln Val Phe Gln Val Pro Ile Gln Gly Pro Gly Cys Arg
        515                 520                 525

cac ttc ctc acc tgt ggg cgt tgc cta agg gca cag cgt ttc atg ggc        1632
His Phe Leu Thr Cys Gly Arg Cys Leu Arg Ala Gln Arg Phe Met Gly
    530                 535                 540

tgt ggc tgg tgt ggg aac atg tgt ggc cgg cag aag gag tgt cct ggc        1680
Cys Gly Trp Cys Gly Asn Met Cys Gly Arg Gln Lys Glu Cys Pro Gly
545                 550                 555                 560

tcc tgg caa cag gac cac tgt ccg cct aag ctt act gag ttc cac ccc        1728
Ser Trp Gln Gln Asp His Cys Pro Pro Lys Leu Thr Glu Phe His Pro
                565                 570                 575

cac agt gga cct tta agg ggc agt aca agg ctg acc ctg tgt ggc tcc        1776
His Ser Gly Pro Leu Arg Gly Ser Thr Arg Leu Thr Leu Cys Gly Ser
            580                 585                 590

aac ttc tac ctg cac cct tct ggt ctg gtg cct gag gga acc cat cag        1824
Asn Phe Tyr Leu His Pro Ser Gly Leu Val Pro Glu Gly Thr His Gln
        595                 600                 605

atc acg gtg ggc caa agt ccc tgc cgg cca ctg ccc aag gac agc tca        1872
Ile Thr Val Gly Gln Ser Pro Cys Arg Pro Leu Pro Lys Asp Ser Ser
    610                 615                 620

aaa ctc aga cca gtg ccc cgg aaa gac ttt gta gag gag ttt gag tgt        1920
Lys Leu Arg Pro Val Pro Arg Lys Asp Phe Val Glu Glu Phe Glu Cys
625                 630                 635                 640
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gaa ctg gag ccc ttg ggc acc caa gca gtg ggg cct acc aac gtc agc        1968
Glu Leu Glu Pro Leu Gly Thr Gln Ala Val Gly Pro Thr Asn Val Ser
                645                 650                 655

ctc acc gtg act aac atg cca ccg ggc aag cac ttc cgg gta gac ggc        2016
Leu Thr Val Thr Asn Met Pro Pro Gly Lys His Phe Arg Val Asp Gly
            660                 665                 670

acc tcc atg ctg aga ggc ttc ttt ttc atg gag cca gtg ctg ata gca        2064
Thr Ser Met Leu Arg Gly Phe Phe Phe Met Glu Pro Val Leu Ile Ala
        675                 680                 685

gtg caa ccc ctc ttt ggc cca cgg gca gga ggc acc tgt ctc act ctt        2112
Val Gln Pro Leu Phe Gly Pro Arg Ala Gly Gly Thr Cys Leu Thr Leu
    690                 695                 700

gaa ggc cag agt ctg tct gta ggc acc agc cgg gct gtg ctg gtc aat        2160
Glu Gly Gln Ser Leu Ser Val Gly Thr Ser Arg Ala Val Leu Val Asn
705                 710                 715                 720

ggg act gag tgt ctg cta gca cgg gtc agt gag ggg cag ctt tta tgt        2208
Gly Thr Glu Cys Leu Leu Ala Arg Val Ser Glu Gly Gln Leu Leu Cys
                725                 730                 735

gcc aca ccc cct ggg gcc atg gtg gcc agt gtc ccc ctt agc ctg cag        2256
Ala Thr Pro Pro Gly Ala Met Val Ala Ser Val Pro Leu Ser Leu Gln
            740                 745                 750

gtg ggg ggt gcc cag gta cct ggt tcc tgg acc ttc cac tac aga gaa        2304
Val Gly Gly Ala Gln Val Pro Gly Ser Trp Thr Phe His Tyr Arg Glu
        755                 760                 765

gac cct gtc gtg cta agc atc agc ccc aac tgt ggc tac agc aac tcc        2352
Asp Pro Val Val Leu Ser Ile Ser Pro Asn Cys Gly Tyr Ser Asn Ser
    770                 775                 780

cac atc acc atc tgt ggc cag cat cta act tca gca tgg cac tta gtg        2400
His Ile Thr Ile Cys Gly Gln His Leu Thr Ser Ala Trp His Leu Val
785                 790                 795                 800

ctg tca ttc cat gac ggg ctt agg gca gtg gag agc agg tgt gag agg        2448
Leu Ser Phe His Asp Gly Leu Arg Ala Val Glu Ser Arg Cys Glu Arg
                805                 810                 815

cag ctt cca gag cag cag ttg tgc cgc ctg cct gaa tat gtg gtc caa        2496
Gln Leu Pro Glu Gln Gln Leu Cys Arg Leu Pro Glu Tyr Val Val Gln
            820                 825                 830

gac ccc cag gga tgg gtg gca gga aat ctg agt gcc tgg ggg gat gga        2544
Asp Pro Gln Gly Trp Val Ala Gly Asn Leu Ser Ala Trp Gly Asp Gly
        835                 840                 845

gct gct ggc ttt aca ctg cct ggc ttt cgc ttc cta acc cca ccc cat        2592
Ala Ala Gly Phe Thr Leu Pro Gly Phe Arg Phe Leu Thr Pro Pro His
    850                 855                 860

cca ccc agt gcc aac cta att cca ctg aag cct gag gag cat gcc att        2640
Pro Pro Ser Ala Asn Leu Ile Pro Leu Lys Pro Glu Glu His Ala Ile
865                 870                 875                 880

aag ttt gag tat att ggg ctg ggt gct gtg act gac tgc gtg ggt gtc        2688
Lys Phe Glu Tyr Ile Gly Leu Gly Ala Val Thr Asp Cys Val Gly Val
                885                 890                 895

aac gtg acc gtg ggt ggt gag agc tgc cag cac gag ttc cgg ggg gac        2736
Asn Val Thr Val Gly Gly Glu Ser Cys Gln His Glu Phe Arg Gly Asp
            900                 905                 910
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atg gtt gtc tgc ccc ctg ccc cca tcc ctg cag ctt ggc aag gat ggt       2784
Met Val Val Cys Pro Leu Pro Pro Ser Leu Gln Leu Gly Lys Asp Gly
        915                 920                 925

gcc cca ctg cag gtc tgc gtg gat ggt gaa tgt cac atc ctg ggt aga       2832
Ala Pro Leu Gln Val Cys Val Asp Gly Glu Cys His Ile Leu Gly Arg
    930                 935                 940

gtg gtg tgg cca ggg cca gat ggg gtc cca cag agc acg ctc ctt ggt       2880
Val Val Trp Pro Gly Pro Asp Gly Val Pro Gln Ser Thr Leu Leu Gly
945                 950                 955                 960

atc ctg ctg cct ttg ctg ctg ctt gtg gcc gca ttg gcc act gca ctg       2928
Ile Leu Leu Pro Leu Leu Leu Leu Val Ala Ala Leu Ala Thr Ala Leu
                965                 970                 975

gtc ttc agc tac tgg tgg cag agg aag cag cta gtt ctt cct ccc aac       2976
Val Phe Ser Tyr Trp Trp Gln Arg Lys Gln Leu Val Leu Pro Pro Asn
            980                 985                 990

ctg gat gac ctg gca tcc ctg gac  cag act act gga gcc  aca ccc ctg     3024
Leu Asp Asp Leu Ala Ser Leu Asp  Gln Thr Thr Gly Ala  Thr Pro Leu
        995                 1000                1005

cct att  ctc tac tcg ggc tct  gac tac aga agt ggc  ctt gca cgc        3069
Pro Ile  Leu Tyr Ser Gly Ser  Asp Tyr Arg Ser Gly  Leu Ala Arg
    1010                1015                1020

cct gcc  act gat ggt cta gat  tcc act tgt gtc cat  gga gca tcc        3114
Pro Ala  Thr Asp Gly Leu Asp  Ser Thr Cys Val His  Gly Ala Ser
    1025                1030                1035

ttc tcc  aat agt gaa gat gaa  tcc tgt gtt cca ctg  ctg cgg aaa        3159
Phe Ser  Asn Ser Glu Asp Glu  Ser Cys Val Pro Leu  Leu Arg Lys
    1040                1045                1050

gag tcc  atc cag cta agg gac  ctg gac tct gcg ctg  ttg gct gag        3204
Glu Ser  Ile Gln Leu Arg Asp  Leu Asp Ser Ala Leu  Leu Ala Glu
    1055                1060                1065

gtc aag  gat gtg ctg att ccc  cat gag cgg gtg gtc  gcc cac agt        3249
Val Lys  Asp Val Leu Ile Pro  His Glu Arg Val Val  Ala His Ser
    1070                1075                1080

gac cga  gtc att ggc aaa ggc  cac ttt gga gtt gtc  tac cat gga        3294
Asp Arg  Val Ile Gly Lys Gly  His Phe Gly Val Val  Tyr His Gly
    1085                1090                1095

gaa tac  ata gac cag gcc cag  aat cga atc caa tgt  gcc atc aag        3339
Glu Tyr  Ile Asp Gln Ala Gln  Asn Arg Ile Gln Cys  Ala Ile Lys
    1100                1105                1110

tca cta  agt cgc atc aca gag  atg cag cag gtg gag  gcc ttc ctt        3384
Ser Leu  Ser Arg Ile Thr Glu  Met Gln Gln Val Glu  Ala Phe Leu
    1115                1120                1125

cga gag  ggg ctg ctc atg cgt  ggc ctg aac cac ccg  aat gtg ctg        3429
Arg Glu  Gly Leu Leu Met Arg  Gly Leu Asn His Pro  Asn Val Leu
    1130                1135                1140

gct ctc  att ggt atc atg ttg  cca ccc gag ggc ctg  ccc cat gtg        3474
Ala Leu  Ile Gly Ile Met Leu  Pro Pro Glu Gly Leu  Pro His Val
    1145                1150                1155

ctg ctg  ccc tat atg tgc cac  ggt gac ctg ctc cag  ttc atc cgc        3519
Leu Leu  Pro Tyr Met Cys His  Gly Asp Leu Leu Gln  Phe Ile Arg
    1160                1165                1170
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tca cct  cag cgg aac ccc acc  gtg aag gac ctc atc  agc ttt ggc        3564
Ser Pro  Gln Arg Asn Pro Thr  Val Lys Asp Leu Ile  Ser Phe Gly
    1175                 1180                 1185

ctg cag  gta gcc cat ggc atg  gag tac ctc gca gag  cag aag ttt        3609
Leu Gln  Val Ala His Gly Met  Glu Tyr Leu Ala Glu  Gln Lys Phe
    1190                 1195                 1200

gtg cac  agg gac ctg gct gcg  cga aac tgc atg ctg  gac gag tca        3654
Val His  Arg Asp Leu Ala Ala  Arg Asn Cys Met Leu  Asp Glu Ser
    1205                 1210                 1215

ttc act  gtc aaa gtg gct gac  ttt ggt ttg gcc cgt  gac atc ctg        3699
Phe Thr  Val Lys Val Ala Asp  Phe Gly Leu Ala Arg  Asp Ile Leu
    1220                 1225                 1230

gac aag  gaa tac tat agt gtt  caa cag cat cgc cac  gct cgc cta        3744
Asp Lys  Glu Tyr Tyr Ser Val  Gln Gln His Arg His  Ala Arg Leu
    1235                 1240                 1245

cct gtg  aag tgg atg gcg ctg  gag agc ctg cag acc  tat aga ttt        3789
Pro Val  Lys Trp Met Ala Leu  Glu Ser Leu Gln Thr  Tyr Arg Phe
    1250                 1255                 1260

acc acc  aag tct gat gtg tgg  tca ttt ggt gtg ctg  ctg tgg gaa        3834
Thr Thr  Lys Ser Asp Val Trp  Ser Phe Gly Val Leu  Leu Trp Glu
    1265                 1270                 1275

ctg ttg  aca cgg ggt gcc cca  cca tac ccc cac atc  gac cct ttt        3879
Leu Leu  Thr Arg Gly Ala Pro  Pro Tyr Pro His Ile  Asp Pro Phe
    1280                 1285                 1290

gac ctc  acc cac ttc ctg gcc  cag ggt cgg cgc ctg  ccc cag cct        3924
Asp Leu  Thr His Phe Leu Ala  Gln Gly Arg Arg Leu  Pro Gln Pro
    1295                 1300                 1305

gag tat  tgc ccc aat tct ctg  tac caa gtg atg cag  caa tgc tgg        3969
Glu Tyr  Cys Pro Asn Ser Leu  Tyr Gln Val Met Gln  Gln Cys Trp
    1310                 1315                 1320

gag gcg  gac cca gca gca cga  ccc acc ttc gga gta  cta gtg ggg        4014
Glu Ala  Asp Pro Ala Ala Arg  Pro Thr Phe Gly Val  Leu Val Gly
    1325                 1330                 1335

gaa gtg  gag cag ata gtg tct  gca ctg ctt ggg gac  cat tat gtg        4059
Glu Val  Glu Gln Ile Val Ser  Ala Leu Leu Gly Asp  His Tyr Val
    1340                 1345                 1350

cag ctg  cca gca acc tac atg  aac ctg ggc ccc agc  acc tca cat        4104
Gln Leu  Pro Ala Thr Tyr Met  Asn Leu Gly Pro Ser  Thr Ser His
    1355                 1360                 1365

gag atg  aat gtg cat cca gaa  cag cag cag tcc tca  ccc atg cca        4149
Glu Met  Asn Val His Pro Glu  Gln Gln Gln Ser Ser  Pro Met Pro
    1370                 1375                 1380

ggg agt  gca cac cga ccc cgg  cca ctc tca gag cct  cct cgg ccc        4194
Gly Ser  Ala His Arg Pro Arg  Pro Leu Ser Glu Pro  Pro Arg Pro
    1385                 1390                 1395

act tga                                                             4200
Thr
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<210> 37
<211> 1399

<212> PRT
<213> Macaca fascicularis

<400> 37

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Met Glu Leu Leu Pro Pro Leu Pro Gln Ser Phe Leu Leu Leu Leu Leu
1               5                  10                  15

Leu Pro Ala Lys Pro Ala Ala Ala Lys Glu Trp Gln Cys Pro Arg Thr
            20                  25                  30

Pro Tyr Ala Ala Ser Arg Asp Phe Asn Val Lys Tyr Met Val Pro Ser
        35                  40                  45

Phe Ser Ala Gly Gly Leu Val Gln Thr Met Val Thr Tyr Gln Gly Asp
    50                  55                  60

Lys Asn Glu Ser Ala Val Phe Val Ala Ile Arg Asn Arg Leu His Val
65                  70                  75                  80

Leu Gly Pro Asp Leu Lys Ser Val Gln Ser Leu Ala Thr Gly Pro Ala
                85                  90                  95

Gly Asp Pro Gly Cys Gln Thr Cys Ala Ala Cys Gly Pro Gly Pro His
            100                 105                 110

Gly Pro Ser Gly Asp Thr Asp Thr Lys Val Leu Val Leu Glu Pro Ala
        115                 120                 125

Leu Pro Ala Leu Val Ser Cys Gly Ser Ser Leu Gln Gly Arg Cys Phe
    130                 135                 140

Leu His Asp Leu Asp Pro Gln Gly Thr Ala Val His Leu Ala Ala Pro
145                 150                 155                 160

Ala Cys Leu Phe Ser Ala His His Asn Arg Pro Asp Asp Cys Pro Asp
                165                 170                 175

Cys Val Ala Ser Pro Leu Gly Thr Arg Val Thr Val Val Glu Gln Gly
            180                 185                 190

Gln Ala Ser Tyr Phe Tyr Val Ala Ser Ser Leu Asp Ala Ala Val Ala
        195                 200                 205

Ala Ser Phe Ser Pro Arg Ser Val Ser Ile Arg Arg Leu Lys Ala Asp
    210                 215                 220

Ala Ser Gly Phe Ala Pro Gly Phe Val Ala Leu Ser Val Leu Pro Lys
225                 230                 235                 240

His Leu Val Ser Tyr Ser Ile Glu Tyr Val His Ser Phe His Thr Gly
                245                 250                 255
```

Ala Phe Val Tyr Phe Leu Thr Val Gln Pro Ala Ser Val Thr Asp Ala
260 265 270

Pro Gly Ala Leu His Thr Arg Leu Ala Arg Leu Ser Ala Thr Glu Pro
275 280 285

Glu Leu Gly Asp Tyr Arg Glu Leu Val Leu Asp Cys Arg Phe Ala Pro
290 295 300

Lys Arg Arg Arg Arg Gly Ala Pro Glu Gly Gly Gln Pro Tyr Pro Val
305 310 315 320

Leu Arg Val Ala His Ser Ala Pro Val Gly Ala Gln Leu Ala Thr Glu
325 330 335

Leu Ser Ile Ala Glu Gly Gln Glu Val Leu Phe Gly Val Phe Val Ala
340 345 350

Gly Lys Asp Ser Gly Pro Gly Val Gly Pro Asn Ser Val Val Cys Ala
355 360 365

Phe Pro Ile Asp Leu Leu Asp Thr Leu Ile Asp Glu Gly Val Glu Arg
370 375 380

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

Phe Gln Ser Pro Ser Phe Cys Pro Asn Pro Pro Gly Leu Glu Ala Pro
405 410 415

Ser Pro Asn Thr Ser Cys Arg His Phe Pro Leu Leu Val Ser Ser Ser
420 425 430

Phe Ser Arg Val Asp Leu Phe Asn Gly Leu Leu Gly Thr Val Glu Val
435 440 445

Thr Ala Leu Tyr Val Thr Arg Leu Asp Asn Val Thr Val Ala His Met
450 455 460

Gly Thr Ala Asp Gly Arg Ile Leu Gln Val Glu Leu Ala Arg Ser Leu
465 470 475 480

Asn Tyr Leu Leu Tyr Val Ser Asn Phe Ser Leu Gly Asp Ser Gly Gln
485 490 495

Pro Val Gln Arg Asp Val Ser Arg Leu Gly Asp His Leu Phe Phe Ala
500 505 510

Ser Gly Asp Gln Val Phe Gln Val Pro Ile Gln Gly Pro Gly Cys Arg
515 520 525

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His Phe Leu Thr Cys Gly Arg Cys Leu Arg Ala Gln Arg Phe Met Gly
    530                 535                 540

Cys Gly Trp Cys Gly Asn Met Cys Gly Arg Gln Lys Glu Cys Pro Gly
545                 550                 555                 560

Ser Trp Gln Gln Asp His Cys Pro Pro Lys Leu Thr Glu Phe His Pro
                565                 570                 575

His Ser Gly Pro Leu Arg Gly Ser Thr Arg Leu Thr Leu Cys Gly Ser
            580                 585                 590

Asn Phe Tyr Leu His Pro Ser Gly Leu Val Pro Glu Gly Thr His Gln
        595                 600                 605

Ile Thr Val Gly Gln Ser Pro Cys Arg Pro Leu Pro Lys Asp Ser Ser
    610                 615                 620

Lys Leu Arg Pro Val Pro Arg Lys Asp Phe Val Glu Glu Phe Glu Cys
625                 630                 635                 640

Glu Leu Glu Pro Leu Gly Thr Gln Ala Val Gly Pro Thr Asn Val Ser
                645                 650                 655

Leu Thr Val Thr Asn Met Pro Pro Gly Lys His Phe Arg Val Asp Gly
            660                 665                 670

Thr Ser Met Leu Arg Gly Phe Phe Phe Met Glu Pro Val Leu Ile Ala
        675                 680                 685

Val Gln Pro Leu Phe Gly Pro Arg Ala Gly Gly Thr Cys Leu Thr Leu
    690                 695                 700

Glu Gly Gln Ser Leu Ser Val Gly Thr Ser Arg Ala Val Leu Val Asn
705                 710                 715                 720

Gly Thr Glu Cys Leu Leu Ala Arg Val Ser Glu Gly Gln Leu Leu Cys
                725                 730                 735

Ala Thr Pro Pro Gly Ala Met Val Ala Ser Val Pro Leu Ser Leu Gln
            740                 745                 750

Val Gly Gly Ala Gln Val Pro Gly Ser Trp Thr Phe His Tyr Arg Glu
        755                 760                 765

Asp Pro Val Val Leu Ser Ile Ser Pro Asn Cys Gly Tyr Ser Asn Ser
    770                 775                 780

His Ile Thr Ile Cys Gly Gln His Leu Thr Ser Ala Trp His Leu Val
785                 790                 795                 800
```

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Leu Ser Phe His Asp Gly Leu Arg Ala Val Glu Ser Arg Cys Glu Arg
                805                 810                 815

Gln Leu Pro Glu Gln Gln Leu Cys Arg Leu Pro Glu Tyr Val Val Gln
            820                 825                 830

Asp Pro Gln Gly Trp Val Ala Gly Asn Leu Ser Ala Trp Gly Asp Gly
        835                 840                 845

Ala Ala Gly Phe Thr Leu Pro Gly Phe Arg Phe Leu Thr Pro Pro His
    850                 855                 860

Pro Pro Ser Ala Asn Leu Ile Pro Leu Lys Pro Glu Glu His Ala Ile
865                 870                 875                 880

Lys Phe Glu Tyr Ile Gly Leu Gly Ala Val Thr Asp Cys Val Gly Val
                885                 890                 895

Asn Val Thr Val Gly Gly Glu Ser Cys Gln His Glu Phe Arg Gly Asp
            900                 905                 910

Met Val Val Cys Pro Leu Pro Pro Ser Leu Gln Leu Gly Lys Asp Gly
        915                 920                 925

Ala Pro Leu Gln Val Cys Val Asp Gly Glu Cys His Ile Leu Gly Arg
    930                 935                 940

Val Val Trp Pro Gly Pro Asp Gly Val Pro Gln Ser Thr Leu Leu Gly
945                 950                 955                 960

Ile Leu Leu Pro Leu Leu Leu Leu Val Ala Ala Leu Ala Thr Ala Leu
                965                 970                 975

Val Phe Ser Tyr Trp Trp Gln Arg Lys Gln Leu Val Leu Pro Pro Asn
            980                 985                 990

Leu Asp Asp Leu Ala Ser Leu Asp  Gln Thr Thr Gly Ala  Thr Pro Leu
        995                 1000                1005

Pro Ile  Leu Tyr Ser Gly Ser  Asp Tyr Arg Ser Gly  Leu Ala Arg
    1010                1015                1020

Pro Ala  Thr Asp Gly Leu Asp  Ser Thr Cys Val His  Gly Ala Ser
    1025                1030                1035

Phe Ser  Asn Ser Glu Asp Glu  Ser Cys Val Pro Leu  Leu Arg Lys
    1040                1045                1050

Glu Ser  Ile Gln Leu Arg Asp  Leu Asp Ser Ala Leu  Leu Ala Glu
    1055                1060                1065
```

```
Val Lys  Asp Val Leu Ile Pro  His Glu Arg Val Val  Ala His Ser
    1070                 1075                 1080

Asp Arg  Val Ile Gly Lys Gly  His Phe Gly Val Val  Tyr His Gly
    1085                 1090                 1095

Glu Tyr  Ile Asp Gln Ala Gln  Asn Arg Ile Gln Cys  Ala Ile Lys
    1100                 1105                 1110

Ser Leu  Ser Arg Ile Thr Glu  Met Gln Gln Val Glu  Ala Phe Leu
    1115                 1120                 1125

Arg Glu  Gly Leu Leu Met Arg  Gly Leu Asn His Pro  Asn Val Leu
    1130                 1135                 1140

Ala Leu  Ile Gly Ile Met Leu  Pro Pro Glu Gly Leu  Pro His Val
    1145                 1150                 1155

Leu Leu  Pro Tyr Met Cys His  Gly Asp Leu Leu Gln  Phe Ile Arg
    1160                 1165                 1170

Ser Pro  Gln Arg Asn Pro Thr  Val Lys Asp Leu Ile  Ser Phe Gly
    1175                 1180                 1185

Leu Gln  Val Ala His Gly Met  Glu Tyr Leu Ala Glu  Gln Lys Phe
    1190                 1195                 1200

Val His  Arg Asp Leu Ala Ala  Arg Asn Cys Met Leu  Asp Glu Ser
    1205                 1210                 1215

Phe Thr  Val Lys Val Ala Asp  Phe Gly Leu Ala Arg  Asp Ile Leu
    1220                 1225                 1230

Asp Lys  Glu Tyr Tyr Ser Val  Gln Gln His Arg His  Ala Arg Leu
    1235                 1240                 1245

Pro Val  Lys Trp Met Ala Leu  Glu Ser Leu Gln Thr  Tyr Arg Phe
    1250                 1255                 1260

Thr Thr  Lys Ser Asp Val Trp  Ser Phe Gly Val Leu  Leu Trp Glu
    1265                 1270                 1275

Leu Leu  Thr Arg Gly Ala Pro  Pro Tyr Pro His Ile  Asp Pro Phe
    1280                 1285                 1290

Asp Leu  Thr His Phe Leu Ala  Gln Gly Arg Arg Leu  Pro Gln Pro
    1295                 1300                 1305

Glu Tyr  Cys Pro Asn Ser Leu  Tyr Gln Val Met Gln  Gln Cys Trp
    1310                 1315                 1320
```

Glu Ala Asp Pro Ala Ala Arg Pro Thr Phe Gly Val Leu Val Gly
1325 1330 1335

Glu Val Glu Gln Ile Val Ser Ala Leu Leu Gly Asp His Tyr Val
1340 1345 1350

Gln Leu Pro Ala Thr Tyr Met Asn Leu Gly Pro Ser Thr Ser His
1355 1360 1365

Glu Met Asn Val His Pro Glu Gln Gln Gln Ser Ser Pro Met Pro
1370 1375 1380

Gly Ser Ala His Arg Pro Arg Pro Leu Ser Glu Pro Pro Arg Pro
1385 1390 1395

Thr

<210> 38
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR forward primer for human MST1R

<400> 38
gaggactggc agtgcccgcg cac 23

<210> 39
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR reverse primer for human MST1R

<400> 39
tcaagtgggc cgaggaggct ctg 23

<210> 40
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR forward primer for cynomolgus monkey MST1R

<400> 40
aaggaatggc agtgcccgcg cacc 24

<210> 41
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR forward primer for mouse MST1R

<400> 41
tcaagtgggc cgaggaggct ctgag 25

<210> 42
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR forward primer for mouse MST1R

<400> 42
tccaccaacc tgaactggca gtg 23

<210> 43
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR reverse primer for mouse MST1R

<400> 43
tcaagtgggc aggggtggct ctg 23

<210> 44
<211> 4785
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
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gggcgggggt ccgctatctt ggggctgtcg ggaccgctgc ttaaatttgg cccagtccag 180

acctcgagtc gggcccccag ccaggcccac gcccaggtcc aggcccaggc cggtagggat 240

cctctagggt cccagctcgc ctcg atg gag ctc ctc ccg ccg ctg cct cag 291
Met Glu Leu Leu Pro Pro Leu Pro Gln
1 5

tcc ttc ctg ttg ctg ctg ctg ttg cct gcc aag ccc gcg gcg ggc gag 339
Ser Phe Leu Leu Leu Leu Leu Leu Pro Ala Lys Pro Ala Ala Gly Glu
10 15 20 25

gac tgg cag tgc ccg cgc acc ccc tac gcg gcc tct cgc gac ttt gac 387
Asp Trp Gln Cys Pro Arg Thr Pro Tyr Ala Ala Ser Arg Asp Phe Asp
30 35 40

gtg aag tac gtg gtg ccc agc ttc tcc gcc gga ggc ctg gta cag gcc 435
Val Lys Tyr Val Val Pro Ser Phe Ser Ala Gly Gly Leu Val Gln Ala
45 50 55

atg gtg acc tac gag ggc gac aga aat gag agt gct gtg ttt gta gcc 483
Met Val Thr Tyr Glu Gly Asp Arg Asn Glu Ser Ala Val Phe Val Ala
60 65 70

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ata cgc aat cgc ctg cat gtg ctt ggg cct gac ctg aag tct gtc cag          531
Ile Arg Asn Arg Leu His Val Leu Gly Pro Asp Leu Lys Ser Val Gln
    75                  80                  85

agc ctg gcc acg ggc cct gct gga gac cct ggc tgc cag acg tgt gca          579
Ser Leu Ala Thr Gly Pro Ala Gly Asp Pro Gly Cys Gln Thr Cys Ala
90                  95                  100                 105

gcc tgt ggc cca gga ccc cac ggc cct ccc ggt gac aca gac aca aag          627
Ala Cys Gly Pro Gly Pro His Gly Pro Pro Gly Asp Thr Asp Thr Lys
                110                 115                 120

gtg ctg gtg ctg gat ccc gcg ctg cct gcg ctg gtc agt tgt ggc tcc          675
Val Leu Val Leu Asp Pro Ala Leu Pro Ala Leu Val Ser Cys Gly Ser
            125                 130                 135

agc ctg cag ggc cgc tgc ttc ctg cat gac cta gag ccc caa ggg aca          723
Ser Leu Gln Gly Arg Cys Phe Leu His Asp Leu Glu Pro Gln Gly Thr
        140                 145                 150

gcc gtg cat ctg gca gcg cca gcc tgc ctc ttc tca gcc cac cat aac          771
Ala Val His Leu Ala Ala Pro Ala Cys Leu Phe Ser Ala His His Asn
    155                 160                 165

cgg ccc gat gac tgc ccc gac tgt gtg gcc agc cca ttg ggc acc cgt          819
Arg Pro Asp Asp Cys Pro Asp Cys Val Ala Ser Pro Leu Gly Thr Arg
170                 175                 180                 185

gta act gtg gtt gag caa ggc cag gcc tcc tat ttc tac gtg gca tcc          867
Val Thr Val Val Glu Gln Gly Gln Ala Ser Tyr Phe Tyr Val Ala Ser
                190                 195                 200

tca ctg gac gca gcc gtg gct gcc agc ttc agc cca cgc tca gtg tct          915
Ser Leu Asp Ala Ala Val Ala Ala Ser Phe Ser Pro Arg Ser Val Ser
            205                 210                 215

atc agg cgt ctc aag gct gac gcc tcg gga ttc gca ccg ggc ttt gtg          963
Ile Arg Arg Leu Lys Ala Asp Ala Ser Gly Phe Ala Pro Gly Phe Val
        220                 225                 230

gcg ttg tca gtg ctg ccc aag cat ctt gtc tcc tac agt att gaa tac         1011
Ala Leu Ser Val Leu Pro Lys His Leu Val Ser Tyr Ser Ile Glu Tyr
    235                 240                 245

gtg cac agc ttc cac acg gga gcc ttc gta tac ttc ctg act gta cag         1059
Val His Ser Phe His Thr Gly Ala Phe Val Tyr Phe Leu Thr Val Gln
250                 255                 260                 265

ccg gcc agc gtg aca gat gat cct agt gcc ctg cac aca cgc ctg gca         1107
Pro Ala Ser Val Thr Asp Asp Pro Ser Ala Leu His Thr Arg Leu Ala
                270                 275                 280

cgg ctt agc gcc act gag cca gag ttg ggt gac tat cgg gag ctg gtc         1155
Arg Leu Ser Ala Thr Glu Pro Glu Leu Gly Asp Tyr Arg Glu Leu Val
            285                 290                 295

ctc gac tgc aga ttt gct cca aaa cgc agg cgc cgg ggg gcc cca gaa         1203
Leu Asp Cys Arg Phe Ala Pro Lys Arg Arg Arg Arg Gly Ala Pro Glu
        300                 305                 310

ggc gga cag ccc tac cct gtg ctg cgg gtg gcc cac tcc gct cca gtg         1251
Gly Gly Gln Pro Tyr Pro Val Leu Arg Val Ala His Ser Ala Pro Val
    315                 320                 325

ggt gcc caa ctt gcc act gag ctg agc atc gcc gag ggc cag gaa gta         1299
Gly Ala Gln Leu Ala Thr Glu Leu Ser Ile Ala Glu Gly Gln Glu Val
330                 335                 340                 345
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cta ttt ggg gtc ttt gtg act ggc aag gat ggt ggt cct ggc gtg ggc        1347
Leu Phe Gly Val Phe Val Thr Gly Lys Asp Gly Gly Pro Gly Val Gly
                350                 355                 360

ccc aac tct gtc gtc tgt gcc ttc ccc att gac ctg ctg gac aca cta        1395
Pro Asn Ser Val Val Cys Ala Phe Pro Ile Asp Leu Leu Asp Thr Leu
            365                 370                 375

att gat gag ggt gtg gag cgc tgt tgt gaa tcc cca gtc cat cca ggc        1443
Ile Asp Glu Gly Val Glu Arg Cys Cys Glu Ser Pro Val His Pro Gly
        380                 385                 390

ctc cgg cga ggc ctc gac ttc ttc cag tcg ccc agt ttt tgc ccc aac        1491
Leu Arg Arg Gly Leu Asp Phe Phe Gln Ser Pro Ser Phe Cys Pro Asn
    395                 400                 405

ccg cct ggc ctg gaa gcc ctc agc ccc aac acc agc tgc cgc cac ttc        1539
Pro Pro Gly Leu Glu Ala Leu Ser Pro Asn Thr Ser Cys Arg His Phe
410                 415                 420                 425

cct ctg ctg gtc agt agc agc ttc tca cgt gtg gac cta ttc aat ggg        1587
Pro Leu Leu Val Ser Ser Ser Phe Ser Arg Val Asp Leu Phe Asn Gly
                430                 435                 440

ctg ttg gga cca gta cag gtc act gca ttg tat gtg aca cgc ctt gac        1635
Leu Leu Gly Pro Val Gln Val Thr Ala Leu Tyr Val Thr Arg Leu Asp
            445                 450                 455

aac gtc aca gtg gca cac atg ggc aca atg gat ggg cgt atc ctg cag        1683
Asn Val Thr Val Ala His Met Gly Thr Met Asp Gly Arg Ile Leu Gln
        460                 465                 470

gtg gag ctg gtc agg tca cta aac tac ttg ctg tat gtg tcc aac ttc        1731
Val Glu Leu Val Arg Ser Leu Asn Tyr Leu Leu Tyr Val Ser Asn Phe
    475                 480                 485

tca ctg ggt gac agt ggg cag ccc gtg cag cgg gat gtc agt cgt ctt        1779
Ser Leu Gly Asp Ser Gly Gln Pro Val Gln Arg Asp Val Ser Arg Leu
490                 495                 500                 505

ggg gac cac cta ctc ttt gcc tct ggg gac cag gtt ttc cag gta cct        1827
Gly Asp His Leu Leu Phe Ala Ser Gly Asp Gln Val Phe Gln Val Pro
                510                 515                 520

atc caa ggc cct ggc tgc cgc cac ttc ctg acc tgt ggg cgt tgc cta        1875
Ile Gln Gly Pro Gly Cys Arg His Phe Leu Thr Cys Gly Arg Cys Leu
            525                 530                 535

agg gca tgg cat ttc atg ggc tgt ggc tgg tgt ggg aac atg tgc ggc        1923
Arg Ala Trp His Phe Met Gly Cys Gly Trp Cys Gly Asn Met Cys Gly
        540                 545                 550

cag cag aag gag tgt cct ggc tcc tgg caa cag gac cac tgc cca cct        1971
Gln Gln Lys Glu Cys Pro Gly Ser Trp Gln Gln Asp His Cys Pro Pro
    555                 560                 565

aag ctt act gag ttc cac ccc cac agt gga cct cta agg ggc agt aca        2019
Lys Leu Thr Glu Phe His Pro His Ser Gly Pro Leu Arg Gly Ser Thr
570                 575                 580                 585

agg ctg acc ctg tgt ggc tcc aac ttc tac ctt cac cct tct ggt ctg        2067
Arg Leu Thr Leu Cys Gly Ser Asn Phe Tyr Leu His Pro Ser Gly Leu
                590                 595                 600

gtg cct gag gga acc cat cag gtc act gtg ggc caa agt ccc tgc cgg        2115
Val Pro Glu Gly Thr His Gln Val Thr Val Gly Gln Ser Pro Cys Arg
            605                 610                 615
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cca ctg ccc aag gac agc tca aaa ctc aga cca gtg ccc cgg aaa gac      2163
Pro Leu Pro Lys Asp Ser Ser Lys Leu Arg Pro Val Pro Arg Lys Asp
        620                 625                 630

ttt gta gag gag ttt gag tgt gaa ctg gag ccc ttg ggc acc cag gca      2211
Phe Val Glu Glu Phe Glu Cys Glu Leu Glu Pro Leu Gly Thr Gln Ala
    635                 640                 645

gtg ggg cct acc aac gtc agc ctc acc gtg act aac atg cca ccg ggc      2259
Val Gly Pro Thr Asn Val Ser Leu Thr Val Thr Asn Met Pro Pro Gly
650                 655                 660                 665

aag cac ttc cgg gta gac ggc acc tcc gtg ctg aga ggc ttc tct ttc      2307
Lys His Phe Arg Val Asp Gly Thr Ser Val Leu Arg Gly Phe Ser Phe
                670                 675                 680

atg gag cca gtg ctg ata gca gtg caa ccc ctc ttt ggc cca cgg gca      2355
Met Glu Pro Val Leu Ile Ala Val Gln Pro Leu Phe Gly Pro Arg Ala
            685                 690                 695

gga ggc acc tgt ctc act ctt gaa ggc cag agt ctg tct gta ggc acc      2403
Gly Gly Thr Cys Leu Thr Leu Glu Gly Gln Ser Leu Ser Val Gly Thr
        700                 705                 710

agc cgg gct gtg ctg gtc aat ggg act gag tgt ctg cta gca cgg gtc      2451
Ser Arg Ala Val Leu Val Asn Gly Thr Glu Cys Leu Leu Ala Arg Val
    715                 720                 725

agt gag ggg cag ctt tta tgt gcc aca ccc cct ggg gcc acg gtg gcc      2499
Ser Glu Gly Gln Leu Leu Cys Ala Thr Pro Pro Gly Ala Thr Val Ala
730                 735                 740                 745

agt gtc ccc ctt agc ctg cag gtg ggg ggt gcc cag gta cct ggt tcc      2547
Ser Val Pro Leu Ser Leu Gln Val Gly Gly Ala Gln Val Pro Gly Ser
                750                 755                 760

tgg acc ttc cag tac aga gaa gac cct gtc gtg cta agc atc agc ccc      2595
Trp Thr Phe Gln Tyr Arg Glu Asp Pro Val Val Leu Ser Ile Ser Pro
            765                 770                 775

aac tgt ggc tac atc aac tcc cac atc acc atc tgt ggc cag cat cta      2643
Asn Cys Gly Tyr Ile Asn Ser His Ile Thr Ile Cys Gly Gln His Leu
        780                 785                 790

act tca gca tgg cac tta gtg ctg tca ttc cat gac ggg ctt agg gca      2691
Thr Ser Ala Trp His Leu Val Leu Ser Phe His Asp Gly Leu Arg Ala
    795                 800                 805

gtg gaa agc agg tgt gag agg cag ctt cca gag cag cag ctg tgc cgc      2739
Val Glu Ser Arg Cys Glu Arg Gln Leu Pro Glu Gln Gln Leu Cys Arg
810                 815                 820                 825

ctt cct gaa tat gtg gtc cga gac ccc cag gga tgg gtg gca ggg aat      2787
Leu Pro Glu Tyr Val Val Arg Asp Pro Gln Gly Trp Val Ala Gly Asn
                830                 835                 840

ctg agt gcc cga ggg gat gga gct gct ggc ttt aca ctg cct ggc ttt      2835
Leu Ser Ala Arg Gly Asp Gly Ala Ala Gly Phe Thr Leu Pro Gly Phe
            845                 850                 855

cgc ttc cta ccc cca ccc cat cca ccc agt gcc aac cta gtt cca ctg      2883
Arg Phe Leu Pro Pro Pro His Pro Pro Ser Ala Asn Leu Val Pro Leu
        860                 865                 870

aag cct gag gag cat gcc att aag ttt gag tat att ggg ctg ggc gct      2931
Lys Pro Glu Glu His Ala Ile Lys Phe Glu Tyr Ile Gly Leu Gly Ala
    875                 880                 885
```

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gtg gct gac tgt gtg ggt atc aac gtg acc gtg ggt ggt gag agc tgc        2979
Val Ala Asp Cys Val Gly Ile Asn Val Thr Val Gly Gly Glu Ser Cys
890                 895                 900                 905

cag cac gag ttc cgg ggg gac atg gtt gtc tgc ccc ctg ccc cca tcc        3027
Gln His Glu Phe Arg Gly Asp Met Val Val Cys Pro Leu Pro Pro Ser
                910                 915                 920

ctg cag ctt ggc cag gat ggt gcc cca ttg cag gtc tgc gta gat ggt        3075
Leu Gln Leu Gly Gln Asp Gly Ala Pro Leu Gln Val Cys Val Asp Gly
            925                 930                 935

gaa tgt cat atc ctg ggt aga gtg gtg cgg cca ggg cca gat ggg gtc        3123
Glu Cys His Ile Leu Gly Arg Val Val Arg Pro Gly Pro Asp Gly Val
        940                 945                 950

cca cag agc acg ctc ctt ggt atc ctg ctg cct ttg ctg ctg ctt gtg        3171
Pro Gln Ser Thr Leu Leu Gly Ile Leu Leu Pro Leu Leu Leu Leu Val
    955                 960                 965

gct gca ctg gcg act gca ctg gtc ttc agc tac tgg tgg cgg agg aag        3219
Ala Ala Leu Ala Thr Ala Leu Val Phe Ser Tyr Trp Trp Arg Arg Lys
970                 975                 980                 985

cag cta gtt ctt cct ccc aac ctg aat gac ctg gca tcc ctg gac  cag        3267
Gln Leu Val Leu Pro Pro Asn Leu Asn Asp Leu Ala Ser Leu Asp  Gln
                990                 995                1000

act gct gga gcc  aca ccc ctg cct att  ctg tac tcg ggc tct  gac        3312
Thr Ala Gly Ala  Thr Pro Leu Pro Ile  Leu Tyr Ser Gly Ser  Asp
            1005                1010                1015

tac aga agt ggc  ctt gca ctc cct gcc  att gat ggt ctg gat  tcc        3357
Tyr Arg Ser Gly  Leu Ala Leu Pro Ala  Ile Asp Gly Leu Asp  Ser
            1020                1025                1030

acc act tgt gtc  cat gga gca tcc ttc  tcc gat agt gaa gat  gaa        3402
Thr Thr Cys Val  His Gly Ala Ser Phe  Ser Asp Ser Glu Asp  Glu
            1035                1040                1045

tcc tgt gtg cca  ctg ctg cgg aaa gag  tcc atc cag cta agg  gac        3447
Ser Cys Val Pro  Leu Leu Arg Lys Glu  Ser Ile Gln Leu Arg  Asp
            1050                1055                1060

ctg gac tct gcg  ctc ttg gct gag gtc  aag gat gtg ctg att  ccc        3492
Leu Asp Ser Ala  Leu Leu Ala Glu Val  Lys Asp Val Leu Ile  Pro
            1065                1070                1075

cat gag cgg gtg  gtc acc cac agt gac  cga gtc att ggc aaa  ggc        3537
His Glu Arg Val  Val Thr His Ser Asp  Arg Val Ile Gly Lys  Gly
            1080                1085                1090

cac ttt gga gtt  gtc tac cac gga gaa  tac ata gac cag gcc  cag        3582
His Phe Gly Val  Val Tyr His Gly Glu  Tyr Ile Asp Gln Ala  Gln
            1095                1100                1105

aat cga atc caa  tgt gcc atc aag tca  cta agt cgc atc aca  gag        3627
Asn Arg Ile Gln  Cys Ala Ile Lys Ser  Leu Ser Arg Ile Thr  Glu
            1110                1115                1120

atg cag cag gtg  gag gcc ttc ctg cga  gag ggg ctg ctc atg  cgt        3672
Met Gln Gln Val  Glu Ala Phe Leu Arg  Glu Gly Leu Leu Met  Arg
            1125                1130                1135

ggc ctg aac cac  ccg aat gtg ctg gct  ctc att ggt atc atg  ttg        3717
Gly Leu Asn His  Pro Asn Val Leu Ala  Leu Ile Gly Ile Met  Leu
            1140                1145                1150
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cca cct gag ggc  ctg ccc cat gtg ctg  ctg ccc tat atg tgc  cac          3762
Pro Pro Glu Gly  Leu Pro His Val Leu  Leu Pro Tyr Met Cys  His
            1155                 1160                 1165

ggt gac ctg ctc  cag ttc atc cgc tca  cct cag cgg aac ccc  acc          3807
Gly Asp Leu Leu  Gln Phe Ile Arg Ser  Pro Gln Arg Asn Pro  Thr
            1170                 1175                 1180

gtg aag gac ctc  atc agc ttt ggc ctg  cag gta gcc cgc ggc  atg          3852
Val Lys Asp Leu  Ile Ser Phe Gly Leu  Gln Val Ala Arg Gly  Met
            1185                 1190                 1195

gag tac ctg gca  gag cag aag ttt gtg  cac agg gac ctg gct  gcg          3897
Glu Tyr Leu Ala  Glu Gln Lys Phe Val  His Arg Asp Leu Ala  Ala
            1200                 1205                 1210

cgg aac tgc atg  ctg gac gag tca ttc  aca gtc aag gtg gct  gac          3942
Arg Asn Cys Met  Leu Asp Glu Ser Phe  Thr Val Lys Val Ala  Asp
            1215                 1220                 1225

ttt ggt ttg gcc  cgc gac atc ctg gac  agg gag tac tat agt  gtt          3987
Phe Gly Leu Ala  Arg Asp Ile Leu Asp  Arg Glu Tyr Tyr Ser  Val
            1230                 1235                 1240

caa cag cat cgc  cac gct cgc cta cct  gtg aag tgg atg gcg  ctg          4032
Gln Gln His Arg  His Ala Arg Leu Pro  Val Lys Trp Met Ala  Leu
            1245                 1250                 1255

gag agc ctg cag  acc tat aga ttt acc  acc aag tct gat gtg  tgg          4077
Glu Ser Leu Gln  Thr Tyr Arg Phe Thr  Thr Lys Ser Asp Val  Trp
            1260                 1265                 1270

tca ttt ggt gtg  ctg ctg tgg gaa ctg  ctg aca cgg ggt gcc  cca          4122
Ser Phe Gly Val  Leu Leu Trp Glu Leu  Leu Thr Arg Gly Ala  Pro
            1275                 1280                 1285

cca tac cgc cac  att gac cct ttt gac  ctt acc cac ttc ctg  gcc          4167
Pro Tyr Arg His  Ile Asp Pro Phe Asp  Leu Thr His Phe Leu  Ala
            1290                 1295                 1300

cag ggt cgg cgc  ctg ccc cag cct gag  tat tgc cct gat tct  ctg          4212
Gln Gly Arg Arg  Leu Pro Gln Pro Glu  Tyr Cys Pro Asp Ser  Leu
            1305                 1310                 1315

tac caa gtg atg  cag caa tgc tgg gag  gca gac cca gca gtg  cga          4257
Tyr Gln Val Met  Gln Gln Cys Trp Glu  Ala Asp Pro Ala Val  Arg
            1320                 1325                 1330

ccc acc ttc aga  gta cta gtg ggg gag  gtg gag cag ata gtg  tct          4302
Pro Thr Phe Arg  Val Leu Val Gly Glu  Val Glu Gln Ile Val  Ser
            1335                 1340                 1345

gca ctg ctt ggg  gac cat tat gtg cag  ctg cca gca acc tac  atg          4347
Ala Leu Leu Gly  Asp His Tyr Val Gln  Leu Pro Ala Thr Tyr  Met
            1350                 1355                 1360

aac ttg ggc ccc  agc acc tcg cat gag  atg aat gtg cgt cca  gaa          4392
Asn Leu Gly Pro  Ser Thr Ser His Glu  Met Asn Val Arg Pro  Glu
            1365                 1370                 1375

cag ccg cag ttc  tca ccc atg cca ggg  aat gta cgc cgg ccc  cgg          4437
Gln Pro Gln Phe  Ser Pro Met Pro Gly  Asn Val Arg Arg Pro  Arg
            1380                 1385                 1390

cca ctc tca gag  cct cct cgg ccc act  tga cttagttctt gggctggacc        4487
Pro Leu Ser Glu  Pro Pro Arg Pro Thr
            1395                 1400
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tgcttagctg ccttgagcta accccaagct gcctctgggc catgccaggc cagagggcag 4547

tggccctcca ccttgttcct gccctttaac tttcagaggc aataggtaaa tggggcccat 4607

taggtccctc actccacaga gtgagccagt gagggcagtc ctgcaacatg tatttatgga 4667

gtgcctgctg tggaccctgt cttctgggca cagtggactc agcagtgacc acaccaacac 4727

tgacccttga accaataaag gaacaaatga ctattaaagc acaaaaaaaa aaaaaaaa 4785

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Met Glu Leu Leu Pro Pro Leu Pro Gln Ser Phe Leu Leu Leu Leu Leu
1 5 10 15

Leu Pro Ala Lys Pro Ala Ala Gly Glu Asp Trp Gln Cys Pro Arg Thr
20 25 30

Pro Tyr Ala Ala Ser Arg Asp Phe Asp Val Lys Tyr Val Val Pro Ser
35 40 45

Phe Ser Ala Gly Gly Leu Val Gln Ala Met Val Thr Tyr Glu Gly Asp
50 55 60

Arg Asn Glu Ser Ala Val Phe Val Ala Ile Arg Asn Arg Leu His Val
65 70 75 80

Leu Gly Pro Asp Leu Lys Ser Val Gln Ser Leu Ala Thr Gly Pro Ala
85 90 95

Gly Asp Pro Gly Cys Gln Thr Cys Ala Ala Cys Gly Pro Gly Pro His
100 105 110

Gly Pro Pro Gly Asp Thr Asp Thr Lys Val Leu Val Leu Asp Pro Ala
115 120 125

Leu Pro Ala Leu Val Ser Cys Gly Ser Ser Leu Gln Gly Arg Cys Phe
130 135 140

Leu His Asp Leu Glu Pro Gln Gly Thr Ala Val His Leu Ala Ala Pro
145 150 155 160

Ala Cys Leu Phe Ser Ala His His Asn Arg Pro Asp Asp Cys Pro Asp
165 170 175

Cys Val Ala Ser Pro Leu Gly Thr Arg Val Thr Val Val Glu Gln Gly
180 185 190

Gln Ala Ser Tyr Phe Tyr Val Ala Ser Ser Leu Asp Ala Ala Val Ala
195 200 205

```
Ala Ser Phe Ser Pro Arg Ser Val Ser Ile Arg Arg Leu Lys Ala Asp
    210                 215                 220

Ala Ser Gly Phe Ala Pro Gly Phe Val Ala Leu Ser Val Leu Pro Lys
225                 230                 235                 240

His Leu Val Ser Tyr Ser Ile Glu Tyr Val His Ser Phe His Thr Gly
                245                 250                 255

Ala Phe Val Tyr Phe Leu Thr Val Gln Pro Ala Ser Val Thr Asp Asp
            260                 265                 270

Pro Ser Ala Leu His Thr Arg Leu Ala Arg Leu Ser Ala Thr Glu Pro
        275                 280                 285

Glu Leu Gly Asp Tyr Arg Glu Leu Val Leu Asp Cys Arg Phe Ala Pro
    290                 295                 300

Lys Arg Arg Arg Arg Gly Ala Pro Glu Gly Gly Gln Pro Tyr Pro Val
305                 310                 315                 320

Leu Arg Val Ala His Ser Ala Pro Val Gly Ala Gln Leu Ala Thr Glu
                325                 330                 335

Leu Ser Ile Ala Glu Gly Gln Glu Val Leu Phe Gly Val Phe Val Thr
            340                 345                 350

Gly Lys Asp Gly Gly Pro Gly Val Gly Pro Asn Ser Val Val Cys Ala
        355                 360                 365

Phe Pro Ile Asp Leu Leu Asp Thr Leu Ile Asp Glu Gly Val Glu Arg
    370                 375                 380

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

Phe Gln Ser Pro Ser Phe Cys Pro Asn Pro Pro Gly Leu Glu Ala Leu
                405                 410                 415

Ser Pro Asn Thr Ser Cys Arg His Phe Pro Leu Leu Val Ser Ser Ser
            420                 425                 430

Phe Ser Arg Val Asp Leu Phe Asn Gly Leu Leu Gly Pro Val Gln Val
        435                 440                 445

Thr Ala Leu Tyr Val Thr Arg Leu Asp Asn Val Thr Val Ala His Met
    450                 455                 460

Gly Thr Met Asp Gly Arg Ile Leu Gln Val Glu Leu Val Arg Ser Leu
465                 470                 475                 480
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Asn Tyr Leu Leu Tyr Val Ser Asn Phe Ser Leu Gly Asp Ser Gly Gln
485 490 495

Pro Val Gln Arg Asp Val Ser Arg Leu Gly Asp His Leu Leu Phe Ala
500 505 510

Ser Gly Asp Gln Val Phe Gln Val Pro Ile Gln Gly Pro Gly Cys Arg
515 520 525

His Phe Leu Thr Cys Gly Arg Cys Leu Arg Ala Trp His Phe Met Gly
530 535 540

Cys Gly Trp Cys Gly Asn Met Cys Gly Gln Gln Lys Glu Cys Pro Gly
545 550 555 560

Ser Trp Gln Gln Asp His Cys Pro Pro Lys Leu Thr Glu Phe His Pro
565 570 575

His Ser Gly Pro Leu Arg Gly Ser Thr Arg Leu Thr Leu Cys Gly Ser
580 585 590

Asn Phe Tyr Leu His Pro Ser Gly Leu Val Pro Glu Gly Thr His Gln
595 600 605

Val Thr Val Gly Gln Ser Pro Cys Arg Pro Leu Pro Lys Asp Ser Ser
610 615 620

Lys Leu Arg Pro Val Pro Arg Lys Asp Phe Val Glu Glu Phe Glu Cys
625 630 635 640

Glu Leu Glu Pro Leu Gly Thr Gln Ala Val Gly Pro Thr Asn Val Ser
645 650 655

Leu Thr Val Thr Asn Met Pro Pro Gly Lys His Phe Arg Val Asp Gly
660 665 670

Thr Ser Val Leu Arg Gly Phe Ser Phe Met Glu Pro Val Leu Ile Ala
675 680 685

Val Gln Pro Leu Phe Gly Pro Arg Ala Gly Gly Thr Cys Leu Thr Leu
690 695 700

Glu Gly Gln Ser Leu Ser Val Gly Thr Ser Arg Ala Val Leu Val Asn
705 710 715 720

Gly Thr Glu Cys Leu Leu Ala Arg Val Ser Glu Gly Gln Leu Leu Cys
725 730 735

Ala Thr Pro Pro Gly Ala Thr Val Ala Ser Val Pro Leu Ser Leu Gln
740 745 750

Val Gly Gly Ala Gln Val Pro Gly Ser Trp Thr Phe Gln Tyr Arg Glu
755 760 765

Asp Pro Val Val Leu Ser Ile Ser Pro Asn Cys Gly Tyr Ile Asn Ser
770 775 780

His Ile Thr Ile Cys Gly Gln His Leu Thr Ser Ala Trp His Leu Val
785 790 795 800

Leu Ser Phe His Asp Gly Leu Arg Ala Val Glu Ser Arg Cys Glu Arg
805 810 815

Gln Leu Pro Glu Gln Gln Leu Cys Arg Leu Pro Glu Tyr Val Val Arg
820 825 830

Asp Pro Gln Gly Trp Val Ala Gly Asn Leu Ser Ala Arg Gly Asp Gly
835 840 845

Ala Ala Gly Phe Thr Leu Pro Gly Phe Arg Phe Leu Pro Pro Pro His
850 855 860

Pro Pro Ser Ala Asn Leu Val Pro Leu Lys Pro Glu Glu His Ala Ile
865 870 875 880

Lys Phe Glu Tyr Ile Gly Leu Gly Ala Val Ala Asp Cys Val Gly Ile
885 890 895

Asn Val Thr Val Gly Gly Glu Ser Cys Gln His Glu Phe Arg Gly Asp
900 905 910

Met Val Val Cys Pro Leu Pro Pro Ser Leu Gln Leu Gly Gln Asp Gly
915 920 925

Ala Pro Leu Gln Val Cys Val Asp Gly Glu Cys His Ile Leu Gly Arg
930 935 940

Val Val Arg Pro Gly Pro Asp Gly Val Pro Gln Ser Thr Leu Leu Gly
945 950 955 960

Ile Leu Leu Pro Leu Leu Leu Leu Val Ala Ala Leu Ala Thr Ala Leu
965 970 975

Val Phe Ser Tyr Trp Trp Arg Arg Lys Gln Leu Val Leu Pro Pro Asn
980 985 990

Leu Asn Asp Leu Ala Ser Leu Asp Gln Thr Ala Gly Ala Thr Pro Leu
995 1000 1005

Pro Ile Leu Tyr Ser Gly Ser Asp Tyr Arg Ser Gly Leu Ala Leu
1010 1015 1020

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Pro Ala  Ile Asp Gly Leu Asp  Ser Thr Thr Cys Val  His Gly Ala
    1025                 1030                 1035

Ser Phe  Ser Asp Ser Glu Asp  Glu Ser Cys Val Pro  Leu Leu Arg
    1040                 1045                 1050

Lys Glu  Ser Ile Gln Leu Arg  Asp Leu Asp Ser Ala  Leu Leu Ala
    1055                 1060                 1065

Glu Val  Lys Asp Val Leu Ile  Pro His Glu Arg Val  Val Thr His
    1070                 1075                 1080

Ser Asp  Arg Val Ile Gly Lys  Gly His Phe Gly Val  Val Tyr His
    1085                 1090                 1095

Gly Glu  Tyr Ile Asp Gln Ala  Gln Asn Arg Ile Gln  Cys Ala Ile
    1100                 1105                 1110

Lys Ser  Leu Ser Arg Ile Thr  Glu Met Gln Gln Val  Glu Ala Phe
    1115                 1120                 1125

Leu Arg  Glu Gly Leu Leu Met  Arg Gly Leu Asn His  Pro Asn Val
    1130                 1135                 1140

Leu Ala  Leu Ile Gly Ile Met  Leu Pro Pro Glu Gly  Leu Pro His
    1145                 1150                 1155

Val Leu  Leu Pro Tyr Met Cys  His Gly Asp Leu Leu  Gln Phe Ile
    1160                 1165                 1170

Arg Ser  Pro Gln Arg Asn Pro  Thr Val Lys Asp Leu  Ile Ser Phe
    1175                 1180                 1185

Gly Leu  Gln Val Ala Arg Gly  Met Glu Tyr Leu Ala  Glu Gln Lys
    1190                 1195                 1200

Phe Val  His Arg Asp Leu Ala  Ala Arg Asn Cys Met  Leu Asp Glu
    1205                 1210                 1215

Ser Phe  Thr Val Lys Val Ala  Asp Phe Gly Leu Ala  Arg Asp Ile
    1220                 1225                 1230

Leu Asp  Arg Glu Tyr Tyr Ser  Val Gln Gln His Arg  His Ala Arg
    1235                 1240                 1245

Leu Pro  Val Lys Trp Met Ala  Leu Glu Ser Leu Gln  Thr Tyr Arg
    1250                 1255                 1260

Phe Thr  Thr Lys Ser Asp Val  Trp Ser Phe Gly Val  Leu Leu Trp
    1265                 1270                 1275
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Glu Leu  Leu Thr Arg Gly Ala  Pro Pro Tyr Arg His  Ile Asp Pro
    1280                  1285                  1290

Phe Asp  Leu Thr His Phe Leu  Ala Gln Gly Arg Arg  Leu Pro Gln
    1295                  1300                  1305

Pro Glu  Tyr Cys Pro Asp Ser  Leu Tyr Gln Val Met  Gln Gln Cys
    1310                  1315                  1320

Trp Glu  Ala Asp Pro Ala Val  Arg Pro Thr Phe Arg  Val Leu Val
    1325                  1330                  1335

Gly Glu  Val Glu Gln Ile Val  Ser Ala Leu Leu Gly  Asp His Tyr
    1340                  1345                  1350

Val Gln  Leu Pro Ala Thr Tyr  Met Asn Leu Gly Pro  Ser Thr Ser
    1355                  1360                  1365

His Glu  Met Asn Val Arg Pro  Glu Gln Pro Gln Phe  Ser Pro Met
    1370                  1375                  1380

Pro Gly  Asn Val Arg Arg Pro  Arg Pro Leu Ser Glu  Pro Pro Arg
    1385                  1390                  1395

Pro Thr
    1400
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ttgccaggga ccagggcagg ggggcagctg cccaggagct ttcagtaccg ctgcgtaaag       180

ctggtctcag ctcggaccct gagtctggtt cgatcaagtc ctggaccttc tgggattccc       240

aaggggcccc agctca atg ggg ctg cct ctg ccg ctg ctt caa tcc tct ctt       292
                  Met Gly Leu Pro Leu Pro Leu Leu Gln Ser Ser Leu
                  1               5                  10

ctg cta atg ctt ctt ttg cgg ctg tcg gcg gcg tcc acc aac ctg aac       340
Leu Leu Met Leu Leu Leu Arg Leu Ser Ala Ala Ser Thr Asn Leu Asn
        15                  20                  25

tgg cag tgc cca cga ata ccc tac gca gcc tcc cga gac ttc agt gtc       388
Trp Gln Cys Pro Arg Ile Pro Tyr Ala Ala Ser Arg Asp Phe Ser Val
    30                  35                  40
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aag tac gtg gtc ccc agc ttc tcc gcg ggg ggc cgg gta cag gcc acc          436
Lys Tyr Val Val Pro Ser Phe Ser Ala Gly Gly Arg Val Gln Ala Thr
45                  50                  55                  60

gca gcc tac gag gac agt aca aat agt gcg gtg ttt gtg gcc aca cgc          484
Ala Ala Tyr Glu Asp Ser Thr Asn Ser Ala Val Phe Val Ala Thr Arg
                65                  70                  75

aat cac ctg cac gtg ctt ggg cct gac ctg cag ttc ata gag aac ctg          532
Asn His Leu His Val Leu Gly Pro Asp Leu Gln Phe Ile Glu Asn Leu
            80                  85                  90

acc act ggc cct atc ggg aac cct ggc tgc cag act tgt gcg agc tgt          580
Thr Thr Gly Pro Ile Gly Asn Pro Gly Cys Gln Thr Cys Ala Ser Cys
        95                  100                 105

ggt cca ggc cct cat gga cca cca aag gac aca gac aca ctg gtg cta          628
Gly Pro Gly Pro His Gly Pro Pro Lys Asp Thr Asp Thr Leu Val Leu
    110                 115                 120

gtg atg gag cca ggt ttg cca gcc ctg gtc agc tgt ggc tca acc cta          676
Val Met Glu Pro Gly Leu Pro Ala Leu Val Ser Cys Gly Ser Thr Leu
125                 130                 135                 140

cag ggc cgc tgc ttc ctg cat gag ctg gag cct cgg ggg aaa gcc ctg          724
Gln Gly Arg Cys Phe Leu His Glu Leu Glu Pro Arg Gly Lys Ala Leu
                145                 150                 155

cac tta gca gct cca gcc tgc cta ttc tca gca aac aat aac aag cct          772
His Leu Ala Ala Pro Ala Cys Leu Phe Ser Ala Asn Asn Asn Lys Pro
            160                 165                 170

gag gcc tgc acg gac tgt gtg gct agc ccc ctg ggc act cgt gtg act          820
Glu Ala Cys Thr Asp Cys Val Ala Ser Pro Leu Gly Thr Arg Val Thr
        175                 180                 185

gtg gtg gag cag ggg cat gct tcc tac ttc tat gtg gca tct tcg cta          868
Val Val Glu Gln Gly His Ala Ser Tyr Phe Tyr Val Ala Ser Ser Leu
    190                 195                 200

gac cca gag ttg gcc gct agc ttt agc ccc cgc tcg gtg tcc atc cgt          916
Asp Pro Glu Leu Ala Ala Ser Phe Ser Pro Arg Ser Val Ser Ile Arg
205                 210                 215                 220

cgt cta aag tct gat act tct gga ttc caa cca ggt ttt ccg tcg ctg          964
Arg Leu Lys Ser Asp Thr Ser Gly Phe Gln Pro Gly Phe Pro Ser Leu
                225                 230                 235

tcg gtg ctg ccc aaa tat ttg gcc tcc tac ctc atc aaa tat gtg tac         1012
Ser Val Leu Pro Lys Tyr Leu Ala Ser Tyr Leu Ile Lys Tyr Val Tyr
            240                 245                 250

agc ttc cac tcg ggg gat ttt gtc tac ttt ctg act gtc cag ccc atc         1060
Ser Phe His Ser Gly Asp Phe Val Tyr Phe Leu Thr Val Gln Pro Ile
        255                 260                 265

agt gtc aca agc cct ccc agt gcc ttg cat aca cgt ctg gtc cgg ctc         1108
Ser Val Thr Ser Pro Pro Ser Ala Leu His Thr Arg Leu Val Arg Leu
    270                 275                 280

aat gct gta gag cca gag att ggt gac tac cgg gag ctg gtc ttg gac         1156
Asn Ala Val Glu Pro Glu Ile Gly Asp Tyr Arg Glu Leu Val Leu Asp
285                 290                 295                 300

tgt cat ttt gca cct aaa cgc cgg cgc cgt gga gcc ccg gag ggc aca         1204
Cys His Phe Ala Pro Lys Arg Arg Arg Arg Gly Ala Pro Glu Gly Thr
                305                 310                 315
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cag ccc tac cca gtg ctt cag gca gcc cac tct gct cca gtg gat gcc        1252
Gln Pro Tyr Pro Val Leu Gln Ala Ala His Ser Ala Pro Val Asp Ala
            320                 325                 330

aaa ctg gct gtg gaa ctg agc att tca gag ggc cag gaa gtg ctt ttt        1300
Lys Leu Ala Val Glu Leu Ser Ile Ser Glu Gly Gln Glu Val Leu Phe
        335                 340                 345

ggg gtc ttt gtg acc gtc aag gat ggt ggc tct ggc atg ggt ccc aac        1348
Gly Val Phe Val Thr Val Lys Asp Gly Gly Ser Gly Met Gly Pro Asn
    350                 355                 360

tct gtt gta tgt gcc ttc ccc att tac cac ctg aac atc ctg att gaa        1396
Ser Val Val Cys Ala Phe Pro Ile Tyr His Leu Asn Ile Leu Ile Glu
365                 370                 375                 380

gag ggt gtc gaa tat tgc tgt cac tct tca aat tct tct tcc ctg ttg        1444
Glu Gly Val Glu Tyr Cys Cys His Ser Ser Asn Ser Ser Ser Leu Leu
                385                 390                 395

tcg aga ggc ctt gac ttc ttc cag acg ccc agt ttt tgt cct aat ccg        1492
Ser Arg Gly Leu Asp Phe Phe Gln Thr Pro Ser Phe Cys Pro Asn Pro
            400                 405                 410

cct ggt gga gag gcc tcc ggc ccc agc tcc cgt tgc cac tac ttc cct        1540
Pro Gly Gly Glu Ala Ser Gly Pro Ser Ser Arg Cys His Tyr Phe Pro
        415                 420                 425

ttg atg gtc cac gct agc ttc acc cgt gtg gac ctc ttc aat gga ctg        1588
Leu Met Val His Ala Ser Phe Thr Arg Val Asp Leu Phe Asn Gly Leu
    430                 435                 440

tta gga tca gtg aag gtc acc gca ctg cat gtg aca cgt ctt ggc aat        1636
Leu Gly Ser Val Lys Val Thr Ala Leu His Val Thr Arg Leu Gly Asn
445                 450                 455                 460

gtt aca gtg gcc cac atg ggc act gtg gat ggg cgt gtc cta cag gtg        1684
Val Thr Val Ala His Met Gly Thr Val Asp Gly Arg Val Leu Gln Val
                465                 470                 475

gag ata gcc agg tca ctc aac tac ctg ctg tat gtg tcc aac ttc tcc        1732
Glu Ile Ala Arg Ser Leu Asn Tyr Leu Leu Tyr Val Ser Asn Phe Ser
            480                 485                 490

ctg ggc agc agt gga cag cct gtt cat cgg gat gtc agc cgc ctc ggg        1780
Leu Gly Ser Ser Gly Gln Pro Val His Arg Asp Val Ser Arg Leu Gly
        495                 500                 505

aat gac cta ctc ttt gcc tct ggg gac cag gtc ttc aag gtg ccc atc        1828
Asn Asp Leu Leu Phe Ala Ser Gly Asp Gln Val Phe Lys Val Pro Ile
    510                 515                 520

cag ggc cct ggc tgt cgt cat ttt ctc acc tgt tgg cgt tgc ctg aga        1876
Gln Gly Pro Gly Cys Arg His Phe Leu Thr Cys Trp Arg Cys Leu Arg
525                 530                 535                 540

gca cag cgc ttc atg gga tgt ggc tgg tgt ggg gac cgg tgt gac cgg        1924
Ala Gln Arg Phe Met Gly Cys Gly Trp Cys Gly Asp Arg Cys Asp Arg
                545                 550                 555

cag aag gag tgt cct ggc tcc tgg caa cag gac cac tgt ccg cct gag        1972
Gln Lys Glu Cys Pro Gly Ser Trp Gln Gln Asp His Cys Pro Pro Glu
            560                 565                 570

atc agt gag ttc tat cct cac agc ggg cct cta agg ggc act acg agg        2020
Ile Ser Glu Phe Tyr Pro His Ser Gly Pro Leu Arg Gly Thr Thr Arg
        575                 580                 585
```

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ctc acc ctt tgt ggc tcc aac ttc tac ctg cga cct gat gat gtc gta      2068
Leu Thr Leu Cys Gly Ser Asn Phe Tyr Leu Arg Pro Asp Asp Val Val
    590                 595                 600

cct gag gga aca cac cag atc acc gtg ggc caa agt ccc tgc cga ctg      2116
Pro Glu Gly Thr His Gln Ile Thr Val Gly Gln Ser Pro Cys Arg Leu
605                 610                 615                 620

ctg cct aag gac tct tca agc cct agg cca ggg tcc ctc aag gaa ttc      2164
Leu Pro Lys Asp Ser Ser Ser Pro Arg Pro Gly Ser Leu Lys Glu Phe
                625                 630                 635

ata cag gaa ctt gaa tgt gag ctg gag ccc ctg gtc acc cag gca gtg      2212
Ile Gln Glu Leu Glu Cys Glu Leu Glu Pro Leu Val Thr Gln Ala Val
            640                 645                 650

ggg act aca aac atc agc ctt gtc atc acc aac atg cca gca ggc aag      2260
Gly Thr Thr Asn Ile Ser Leu Val Ile Thr Asn Met Pro Ala Gly Lys
        655                 660                 665

cac ttc cga gtg gaa ggc atc tct gta cag gaa ggc ttc tct ttc gtg      2308
His Phe Arg Val Glu Gly Ile Ser Val Gln Glu Gly Phe Ser Phe Val
    670                 675                 680

gag cca gtg ctg aca tca ata aaa cct gac ttt ggc ccg cgg gct ggg      2356
Glu Pro Val Leu Thr Ser Ile Lys Pro Asp Phe Gly Pro Arg Ala Gly
685                 690                 695                 700

ggt act tat ctc acc ctc gaa ggc cag agc ctg tct att gcc acc agc      2404
Gly Thr Tyr Leu Thr Leu Glu Gly Gln Ser Leu Ser Ile Ala Thr Ser
                705                 710                 715

cga gct gcg ctg gtc aat gga acc cag tgc cgg ctg gaa cag gtc aat      2452
Arg Ala Ala Leu Val Asn Gly Thr Gln Cys Arg Leu Glu Gln Val Asn
            720                 725                 730

gag gag cag atc tta tgt gtc acg cct cct gga gct ggc acg gcc agg      2500
Glu Glu Gln Ile Leu Cys Val Thr Pro Pro Gly Ala Gly Thr Ala Arg
        735                 740                 745

gtc ccc ctt cat ctg cag ata ggg ggt gct gag gtg cct ggc tcc tgg      2548
Val Pro Leu His Leu Gln Ile Gly Gly Ala Glu Val Pro Gly Ser Trp
    750                 755                 760

acc ttt cac tac aag gaa gac cct att gtg ttg gac atc agt ccc aag      2596
Thr Phe His Tyr Lys Glu Asp Pro Ile Val Leu Asp Ile Ser Pro Lys
765                 770                 775                 780

tgt ggc tac agt ggc tcc cac atc atg atc cat ggc cag cat ctg act      2644
Cys Gly Tyr Ser Gly Ser His Ile Met Ile His Gly Gln His Leu Thr
                785                 790                 795

tca gca tgg cac ttc acg cta tca ttc cat gat gga caa agt aca gtg      2692
Ser Ala Trp His Phe Thr Leu Ser Phe His Asp Gly Gln Ser Thr Val
            800                 805                 810

gag agc agg tgt gcg ggg cag ttt gtg gaa caa cag cag cgt cga tgt      2740
Glu Ser Arg Cys Ala Gly Gln Phe Val Glu Gln Gln Gln Arg Arg Cys
        815                 820                 825

cgc ctg cct gaa tat gtg gtc cga aac cct cag ggg tgg gca aca ggg      2788
Arg Leu Pro Glu Tyr Val Val Arg Asn Pro Gln Gly Trp Ala Thr Gly
    830                 835                 840

aat ctg agc gtc tgg ggt gat gga gca gct ggc ttc aca ctg cct ggt      2836
Asn Leu Ser Val Trp Gly Asp Gly Ala Ala Gly Phe Thr Leu Pro Gly
845                 850                 855                 860
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ttt cgc ttc ctg ccc cca ccc agt cca ctc aga gct ggc ctg gtt gag        2884
Phe Arg Phe Leu Pro Pro Pro Ser Pro Leu Arg Ala Gly Leu Val Glu
                865                 870                 875

ttg aaa cct gaa gaa cat tca gtt aaa gtt gag tat gtc ggg ctg ggc        2932
Leu Lys Pro Glu Glu His Ser Val Lys Val Glu Tyr Val Gly Leu Gly
            880                 885                 890

gct gtg gca gac tgt gtg act gtg aac atg acc gtg ggt ggt gag gtc        2980
Ala Val Ala Asp Cys Val Thr Val Asn Met Thr Val Gly Gly Glu Val
        895                 900                 905

tgc caa cat gag ctc cgg ggg gat gtg gtg atc tgc ccc ctg ccc cct        3028
Cys Gln His Glu Leu Arg Gly Asp Val Val Ile Cys Pro Leu Pro Pro
    910                 915                 920

tcc ctg caa ctt ggc aag gat ggt gtc cca ttg cag gtc tgt gta gac        3076
Ser Leu Gln Leu Gly Lys Asp Gly Val Pro Leu Gln Val Cys Val Asp
925                 930                 935                 940

ggt ggg tgt cac atc ctg agc caa gtg gtt cgc tca agc cca ggc agg        3124
Gly Gly Cys His Ile Leu Ser Gln Val Val Arg Ser Ser Pro Gly Arg
                945                 950                 955

gcc tca cag agg ata ctc ctt att gct ctt ctg gtc ttg atc ctg ctt        3172
Ala Ser Gln Arg Ile Leu Leu Ile Ala Leu Leu Val Leu Ile Leu Leu
            960                 965                 970

gtg gct gtg ctg gcc gtt gcc ctg atc ttt aac tcc cga aga cgg aaa        3220
Val Ala Val Leu Ala Val Ala Leu Ile Phe Asn Ser Arg Arg Arg Lys
        975                 980                 985

aag cag cta ggt gct cac tcc ctc tcc cca aca aca  ctc tct gac atc        3268
Lys Gln Leu Gly Ala His Ser Leu Ser Pro Thr Thr  Leu Ser Asp Ile
    990                 995                 1000

aac  gat aca gct tcc ggg  gct ccg aac cat gaa  gaa tcg tca gag          3313
Asn  Asp Thr Ala Ser Gly  Ala Pro Asn His Glu  Glu Ser Ser Glu
1005                1010                1015

agt  agg gat ggg aca agt  gtc cca ctg ctg cgg  aca gag tct atc          3358
Ser  Arg Asp Gly Thr Ser  Val Pro Leu Leu Arg  Thr Glu Ser Ile
1020                1025                1030

cgg  ctc cag gat ctg gac  agg atg ctc cta gct  gag gtc aag gat          3403
Arg  Leu Gln Asp Leu Asp  Arg Met Leu Leu Ala  Glu Val Lys Asp
1035                1040                1045

gta  ctg att ccc cat gaa  caa gtg gtc atc cat  act gac caa gtc          3448
Val  Leu Ile Pro His Glu  Gln Val Val Ile His  Thr Asp Gln Val
1050                1055                1060

att  ggc aaa ggc cac ttt  ggt gtt gtc tac cac  gga gaa tat aca          3493
Ile  Gly Lys Gly His Phe  Gly Val Val Tyr His  Gly Glu Tyr Thr
1065                1070                1075

gac  gga gca cag aat cag  acc cac tgt gcc atc  aag tct ctg agt          3538
Asp  Gly Ala Gln Asn Gln  Thr His Cys Ala Ile  Lys Ser Leu Ser
1080                1085                1090

cgc  att aca gag gtg cag  gag gtg gag gct ttc  ctg cgg gag ggg          3583
Arg  Ile Thr Glu Val Gln  Glu Val Glu Ala Phe  Leu Arg Glu Gly
1095                1100                1105

ctg  ctc atg cgt ggc cta  cat cac cca aac atc  ctg gct ctc atc          3628
Leu  Leu Met Arg Gly Leu  His His Pro Asn Ile  Leu Ala Leu Ile
1110                1115                1120
```

```
ggt  atc atg ctg ccc ccg  gag ggg ctt ccc cgg  gtg ctg ttg ccc        3673
Gly  Ile Met Leu Pro Pro  Glu Gly Leu Pro Arg  Val Leu Leu Pro
1125                 1130                 1135

tat  atg cgc cac gga gac  ctg ctt cgt ttc att  cgc tcc cct cag        3718
Tyr  Met Arg His Gly Asp  Leu Leu Arg Phe Ile  Arg Ser Pro Gln
1140                 1145                 1150

agg  aac ccc act gtg aag  gat ctt gtc agc ttt  ggc ctg cag gta        3763
Arg  Asn Pro Thr Val Lys  Asp Leu Val Ser Phe  Gly Leu Gln Val
1155                 1160                 1165

gcc  tgt ggt atg gag tac  ctg gca gag cag aag  ttc gtg cac aga        3808
Ala  Cys Gly Met Glu Tyr  Leu Ala Glu Gln Lys  Phe Val His Arg
1170                 1175                 1180

gac  ctg gct gct agg aac  tgc atg ctg gac gag  tca ttc aca gtc        3853
Asp  Leu Ala Ala Arg Asn  Cys Met Leu Asp Glu  Ser Phe Thr Val
1185                 1190                 1195

aag  gtg gct gac ttt ggt  ctg gca cgg ggc gtc  cta gac aag gaa        3898
Lys  Val Ala Asp Phe Gly  Leu Ala Arg Gly Val  Leu Asp Lys Glu
1200                 1205                 1210

tac  tac agt gtt cgc cag  cat cgc cat gct cgc  ctg cca gtc aaa        3943
Tyr  Tyr Ser Val Arg Gln  His Arg His Ala Arg  Leu Pro Val Lys
1215                 1220                 1225

tgg  atg gca ctg gag agc  ctg cag acc tac agg  ttc acc acc aag        3988
Trp  Met Ala Leu Glu Ser  Leu Gln Thr Tyr Arg  Phe Thr Thr Lys
1230                 1235                 1240

tcc  gat gtg tgg tca ttc  ggg gtg ctg ctc tgg  gag cta cta aca        4033
Ser  Asp Val Trp Ser Phe  Gly Val Leu Leu Trp  Glu Leu Leu Thr
1245                 1250                 1255

cgg  ggt gct cca ccc tac  ccc cat atc gat ccc  ttc gac ctc tct        4078
Arg  Gly Ala Pro Pro Tyr  Pro His Ile Asp Pro  Phe Asp Leu Ser
1260                 1265                 1270

cac  ttc ctg gct cag ggc  cgc cgc ctg cct cag  cct gag tac tgt        4123
His  Phe Leu Ala Gln Gly  Arg Arg Leu Pro Gln  Pro Glu Tyr Cys
1275                 1280                 1285

cct  gat tca ctg tat cac  gtg atg ctt cga tgc  tgg gag gct gac        4168
Pro  Asp Ser Leu Tyr His  Val Met Leu Arg Cys  Trp Glu Ala Asp
1290                 1295                 1300

cca  gcg gca cga ccc acc  ttc aga gcc cta gtg  ctg gaa gta aag        4213
Pro  Ala Ala Arg Pro Thr  Phe Arg Ala Leu Val  Leu Glu Val Lys
1305                 1310                 1315

cag  gta gtg gcc tca ctg  ctt ggg gac cac tat  gtg cag ctg aca        4258
Gln  Val Val Ala Ser Leu  Leu Gly Asp His Tyr  Val Gln Leu Thr
1320                 1325                 1330

gca  gct tat gtg aac gta  ggc ccc aga gcg gtg  gat gat ggg agt        4303
Ala  Ala Tyr Val Asn Val  Gly Pro Arg Ala Val  Asp Asp Gly Ser
1335                 1340                 1345

gtg  cct ccg gag cag gta  cag ccc tcg cct cag  cat tgc agg agc        4348
Val  Pro Pro Glu Gln Val  Gln Pro Ser Pro Gln  His Cys Arg Ser
1350                 1355                 1360

acg  tca aag ccc cgg cct  ctc tca gag cca ccc  ctg ccc act tga        4393
Thr  Ser Lys Pro Arg Pro  Leu Ser Glu Pro Pro  Leu Pro Thr
1365                 1370                 1375
```

ccaaagccct gagtaggcca caggcactag atctgctaag tggccttgag caaattacaa 4453

gctgcctctg ggcctaggac aagcctcagc atggaaaacc tccactcttt agctttctgg 4513

ggccactgaa ggtgggaaac cgggcccatt tgagcccctc gttccagcat gagccagtga 4573

cattttgta gcatgtattt atgtaatgtc tgttttgtac ctgtttcgga atacagagga 4633

tccagcagtg atcacagaga tactacagta taaaataata taaataaata aatgaatgaa 4693

tattcgagca caaaaaaaaa aaaaaaa 4720

<210> 47
<211> 1378
<212> PRT
<213> Mus musculus

<400> 47

Met Gly Leu Pro Leu Pro Leu Leu Gln Ser Ser Leu Leu Leu Met Leu
1 5 10 15

Leu Leu Arg Leu Ser Ala Ala Ser Thr Asn Leu Asn Trp Gln Cys Pro
20 25 30

Arg Ile Pro Tyr Ala Ala Ser Arg Asp Phe Ser Val Lys Tyr Val Val
35 40 45

Pro Ser Phe Ser Ala Gly Gly Arg Val Gln Ala Thr Ala Ala Tyr Glu
50 55 60

Asp Ser Thr Asn Ser Ala Val Phe Val Ala Thr Arg Asn His Leu His
65 70 75 80

Val Leu Gly Pro Asp Leu Gln Phe Ile Glu Asn Leu Thr Thr Gly Pro
85 90 95

Ile Gly Asn Pro Gly Cys Gln Thr Cys Ala Ser Cys Gly Pro Gly Pro
100 105 110

His Gly Pro Pro Lys Asp Thr Asp Thr Leu Val Leu Val Met Glu Pro
115 120 125

Gly Leu Pro Ala Leu Val Ser Cys Gly Ser Thr Leu Gln Gly Arg Cys
130 135 140

Phe Leu His Glu Leu Glu Pro Arg Gly Lys Ala Leu His Leu Ala Ala
145 150 155 160

Pro Ala Cys Leu Phe Ser Ala Asn Asn Asn Lys Pro Glu Ala Cys Thr
165 170 175

Asp Cys Val Ala Ser Pro Leu Gly Thr Arg Val Thr Val Val Glu Gln
180 185 190

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

Ala Ala Ser Phe Ser Pro Arg Ser Val Ser Ile Arg Arg Leu Lys Ser
    210                 215                 220

Asp Thr Ser Gly Phe Gln Pro Gly Phe Pro Ser Leu Ser Val Leu Pro
225                 230                 235                 240

Lys Tyr Leu Ala Ser Tyr Leu Ile Lys Tyr Val Tyr Ser Phe His Ser
                245                 250                 255

Gly Asp Phe Val Tyr Phe Leu Thr Val Gln Pro Ile Ser Val Thr Ser
            260                 265                 270

Pro Pro Ser Ala Leu His Thr Arg Leu Val Arg Leu Asn Ala Val Glu
        275                 280                 285

Pro Glu Ile Gly Asp Tyr Arg Glu Leu Val Leu Asp Cys His Phe Ala
    290                 295                 300

Pro Lys Arg Arg Arg Arg Gly Ala Pro Glu Gly Thr Gln Pro Tyr Pro
305                 310                 315                 320

Val Leu Gln Ala Ala His Ser Ala Pro Val Asp Ala Lys Leu Ala Val
                325                 330                 335

Glu Leu Ser Ile Ser Glu Gly Gln Glu Val Leu Phe Gly Val Phe Val
            340                 345                 350

Thr Val Lys Asp Gly Gly Ser Gly Met Gly Pro Asn Ser Val Val Cys
        355                 360                 365

Ala Phe Pro Ile Tyr His Leu Asn Ile Leu Ile Glu Glu Gly Val Glu
    370                 375                 380

Tyr Cys Cys His Ser Ser Asn Ser Ser Ser Leu Leu Ser Arg Gly Leu
385                 390                 395                 400

Asp Phe Phe Gln Thr Pro Ser Phe Cys Pro Asn Pro Pro Gly Gly Glu
                405                 410                 415

Ala Ser Gly Pro Ser Ser Arg Cys His Tyr Phe Pro Leu Met Val His
            420                 425                 430

Ala Ser Phe Thr Arg Val Asp Leu Phe Asn Gly Leu Leu Gly Ser Val
        435                 440                 445

Lys Val Thr Ala Leu His Val Thr Arg Leu Gly Asn Val Thr Val Ala
    450                 455                 460
```

```
His Met Gly Thr Val Asp Gly Arg Val Leu Gln Val Glu Ile Ala Arg
465                 470                 475                 480

Ser Leu Asn Tyr Leu Leu Tyr Val Ser Asn Phe Ser Leu Gly Ser Ser
                485                 490                 495

Gly Gln Pro Val His Arg Asp Val Ser Arg Leu Gly Asn Asp Leu Leu
            500                 505                 510

Phe Ala Ser Gly Asp Gln Val Phe Lys Val Pro Ile Gln Gly Pro Gly
        515                 520                 525

Cys Arg His Phe Leu Thr Cys Trp Arg Cys Leu Arg Ala Gln Arg Phe
    530                 535                 540

Met Gly Cys Gly Trp Cys Gly Asp Arg Cys Asp Arg Gln Lys Glu Cys
545                 550                 555                 560

Pro Gly Ser Trp Gln Gln Asp His Cys Pro Pro Glu Ile Ser Glu Phe
                565                 570                 575

Tyr Pro His Ser Gly Pro Leu Arg Gly Thr Thr Arg Leu Thr Leu Cys
            580                 585                 590

Gly Ser Asn Phe Tyr Leu Arg Pro Asp Asp Val Val Pro Glu Gly Thr
        595                 600                 605

His Gln Ile Thr Val Gly Gln Ser Pro Cys Arg Leu Leu Pro Lys Asp
    610                 615                 620

Ser Ser Ser Pro Arg Pro Gly Ser Leu Lys Glu Phe Ile Gln Glu Leu
625                 630                 635                 640

Glu Cys Glu Leu Glu Pro Leu Val Thr Gln Ala Val Gly Thr Thr Asn
                645                 650                 655

Ile Ser Leu Val Ile Thr Asn Met Pro Ala Gly Lys His Phe Arg Val
            660                 665                 670

Glu Gly Ile Ser Val Gln Glu Gly Phe Ser Phe Val Glu Pro Val Leu
        675                 680                 685

Thr Ser Ile Lys Pro Asp Phe Gly Pro Arg Ala Gly Gly Thr Tyr Leu
    690                 695                 700

Thr Leu Glu Gly Gln Ser Leu Ser Ile Ala Thr Ser Arg Ala Ala Leu
705                 710                 715                 720

Val Asn Gly Thr Gln Cys Arg Leu Glu Gln Val Asn Glu Glu Gln Ile
                725                 730                 735
```

```
Leu Cys Val Thr Pro Pro Gly Ala Gly Thr Ala Arg Val Pro Leu His
            740                 745                 750

Leu Gln Ile Gly Gly Ala Glu Val Pro Gly Ser Trp Thr Phe His Tyr
        755                 760                 765

Lys Glu Asp Pro Ile Val Leu Asp Ile Ser Pro Lys Cys Gly Tyr Ser
    770                 775                 780

Gly Ser His Ile Met Ile His Gly Gln His Leu Thr Ser Ala Trp His
785                 790                 795                 800

Phe Thr Leu Ser Phe His Asp Gly Gln Ser Thr Val Glu Ser Arg Cys
                805                 810                 815

Ala Gly Gln Phe Val Glu Gln Gln Gln Arg Arg Cys Arg Leu Pro Glu
            820                 825                 830

Tyr Val Val Arg Asn Pro Gln Gly Trp Ala Thr Gly Asn Leu Ser Val
        835                 840                 845

Trp Gly Asp Gly Ala Ala Gly Phe Thr Leu Pro Gly Phe Arg Phe Leu
    850                 855                 860

Pro Pro Pro Ser Pro Leu Arg Ala Gly Leu Val Glu Leu Lys Pro Glu
865                 870                 875                 880

Glu His Ser Val Lys Val Glu Tyr Val Gly Leu Gly Ala Val Ala Asp
                885                 890                 895

Cys Val Thr Val Asn Met Thr Val Gly Gly Glu Val Cys Gln His Glu
            900                 905                 910

Leu Arg Gly Asp Val Val Ile Cys Pro Leu Pro Pro Ser Leu Gln Leu
        915                 920                 925

Gly Lys Asp Gly Val Pro Leu Gln Val Cys Val Asp Gly Gly Cys His
    930                 935                 940

Ile Leu Ser Gln Val Val Arg Ser Ser Pro Gly Arg Ala Ser Gln Arg
945                 950                 955                 960

Ile Leu Leu Ile Ala Leu Leu Val Leu Ile Leu Leu Val Ala Val Leu
                965                 970                 975

Ala Val Ala Leu Ile Phe Asn Ser Arg Arg Arg Lys Lys Gln Leu Gly
            980                 985                 990

Ala His Ser Leu Ser Pro Thr Thr  Leu Ser Asp Ile Asn  Asp Thr Ala
        995                 1000                1005
```

```
Ser Gly  Ala Pro Asn His Glu  Glu Ser Ser Glu Ser  Arg Asp Gly
    1010                 1015                 1020

Thr Ser  Val Pro Leu Leu Arg  Thr Glu Ser Ile Arg  Leu Gln Asp
    1025                 1030                 1035

Leu Asp  Arg Met Leu Leu Ala  Glu Val Lys Asp Val  Leu Ile Pro
    1040                 1045                 1050

His Glu  Gln Val Val Ile His  Thr Asp Gln Val Ile  Gly Lys Gly
    1055                 1060                 1065

His Phe  Gly Val Val Tyr His  Gly Glu Tyr Thr Asp  Gly Ala Gln
    1070                 1075                 1080

Asn Gln  Thr His Cys Ala Ile  Lys Ser Leu Ser Arg  Ile Thr Glu
    1085                 1090                 1095

Val Gln  Glu Val Glu Ala Phe  Leu Arg Glu Gly Leu  Leu Met Arg
    1100                 1105                 1110

Gly Leu  His His Pro Asn Ile  Leu Ala Leu Ile Gly  Ile Met Leu
    1115                 1120                 1125

Pro Pro  Glu Gly Leu Pro Arg  Val Leu Leu Pro Tyr  Met Arg His
    1130                 1135                 1140

Gly Asp  Leu Leu Arg Phe Ile  Arg Ser Pro Gln Arg  Asn Pro Thr
    1145                 1150                 1155

Val Lys  Asp Leu Val Ser Phe  Gly Leu Gln Val Ala  Cys Gly Met
    1160                 1165                 1170

Glu Tyr  Leu Ala Glu Gln Lys  Phe Val His Arg Asp  Leu Ala Ala
    1175                 1180                 1185

Arg Asn  Cys Met Leu Asp Glu  Ser Phe Thr Val Lys  Val Ala Asp
    1190                 1195                 1200

Phe Gly  Leu Ala Arg Gly Val  Leu Asp Lys Glu Tyr  Tyr Ser Val
    1205                 1210                 1215

Arg Gln  His Arg His Ala Arg  Leu Pro Val Lys Trp  Met Ala Leu
    1220                 1225                 1230

Glu Ser  Leu Gln Thr Tyr Arg  Phe Thr Thr Lys Ser  Asp Val Trp
    1235                 1240                 1245

Ser Phe  Gly Val Leu Leu Trp  Glu Leu Leu Thr Arg  Gly Ala Pro
    1250                 1255                 1260
```

```
Pro Tyr  Pro His Ile Asp Pro  Phe Asp Leu Ser His  Phe Leu Ala
    1265                1270                1275

Gln Gly  Arg Arg Leu Pro Gln  Pro Glu Tyr Cys Pro  Asp Ser Leu
    1280                1285                1290

Tyr His  Val Met Leu Arg Cys  Trp Glu Ala Asp Pro  Ala Ala Arg
    1295                1300                1305

Pro Thr  Phe Arg Ala Leu Val  Leu Glu Val Lys Gln  Val Val Ala
    1310                1315                1320

Ser Leu  Leu Gly Asp His Tyr  Val Gln Leu Thr Ala  Ala Tyr Val
    1325                1330                1335

Asn Val  Gly Pro Arg Ala Val  Asp Asp Gly Ser Val  Pro Pro Glu
    1340                1345                1350

Gln Val  Gln Pro Ser Pro Gln  His Cys Arg Ser Thr  Ser Lys Pro
    1355                1360                1365

Arg Pro  Leu Ser Glu Pro Pro  Leu Pro Thr
    1370                1375
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<210> 48
<211> 1413
<212> DNA
<213> Artificial Sequence

<220>
<223> MOR07919 heavy chain

<220>
<221> CDS
<222> (1)..(1413)

<400> 48

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atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg          48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

gtc ctg tcc cag gtg caa ttg gtt cag agc ggc gcg gaa gtg aaa aaa          96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

ccg ggc gaa agc ctg aaa att agc tgc aaa ggt tcc gga tat tcc ttt         144
Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe
        35                  40                  45

act aat tat tgg att tct tgg gtg cgc cag atg cct ggg aag ggt ctc         192
Thr Asn Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu
    50                  55                  60

gag tgg atg ggc ttt atc tat ccg gat gat agc tat acc cgt tat tct         240
Glu Trp Met Gly Phe Ile Tyr Pro Asp Asp Ser Tyr Thr Arg Tyr Ser
65                  70                  75                  80

ccg agc ttt cag ggc cag gtg acc att agc gcg gat aaa agc att agc         288
```

```
Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser
                85                  90                  95

acc gcg tat ctt caa tgg agc agc ctg aaa gcg agc gat acg gcc atg  336
Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met
            100                 105                 110

tat tat tgc gcg cgt ttt tct tat cgt cat tat ctt gat atg gat gat  384
Tyr Tyr Cys Ala Arg Phe Ser Tyr Arg His Tyr Leu Asp Met Asp Asp
        115                 120                 125

cat tgg ggc caa ggc acc ctg gtg acg gtt agc tca gcc tcc acc aag  432
His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
    130                 135                 140

ggt cca tcg gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg  480
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145                 150                 155                 160

ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg  528
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
                165                 170                 175

gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc  576
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
            180                 185                 190

ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg  624
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
        195                 200                 205

gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac  672
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220

gtg aat cac aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc  720
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro
225                 230                 235                 240

aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa  768
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255

ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac  816
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270

acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac  864
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285

gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc  912
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
    290                 295                 300

gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac  960
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320

agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg 1008
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                325                 330                 335

ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca 1056
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
            340                 345                 350

gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa 1104
```

```
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
        355                 360                 365

cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac       1152
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
    370                 375                 380

cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc       1200
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385                 390                 395                 400

gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc       1248
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415

acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag       1296
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
            420                 425                 430

ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc       1344
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445

tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc       1392
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
    450                 455                 460

tcc ctg tct ccg ggt aaa tga                                          1413
Ser Leu Ser Pro Gly Lys
465                 470
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<210> 49
<211> 470
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 49

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe
        35                  40                  45

Thr Asn Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu
    50                  55                  60

Glu Trp Met Gly Phe Ile Tyr Pro Asp Asp Ser Tyr Thr Arg Tyr Ser
65                  70                  75                  80

Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser
                85                  90                  95

Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met
            100                 105                 110
```

```
Tyr Tyr Cys Ala Arg Phe Ser Tyr Arg His Tyr Leu Asp Met Asp Asp
        115                 120                 125

His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
    130                 135                 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145                 150                 155                 160

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
                165                 170                 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
            180                 185                 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
        195                 200                 205

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro
225                 230                 235                 240

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
    290                 295                 300

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                325                 330                 335

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
            340                 345                 350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
        355                 360                 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
    370                 375                 380
```

```
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385                 390                 395                 400

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
            420                 425                 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
    450                 455                 460

Ser Leu Ser Pro Gly Lys
465                 470


<210>  50
<211>  1401
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  MOR07692, MOR07923, MOR07924, MOR07925 and MOR07926 heavy chain


<220>
<221>  CDS
<222>  (1)..(1401)

<400>  50
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg          48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

gtc ctg tcc cag gtg caa ttg gtg gaa agc ggc ggc ggc ctg gtg caa          96
Val Leu Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
            20                  25                  30

ccg ggc ggc agc ctg cgt ctg agc tgc gcg gcc tcc gga ttt acc ttt         144
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
        35                  40                  45

aat tct tat tct atg tct tgg gtg cgc caa gcc cct ggg aag ggt ctc         192
Asn Ser Tyr Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60

gag tgg gtg agc tat atc tct tct cgt tct agc act acc tat tat gcg         240
Glu Trp Val Ser Tyr Ile Ser Ser Arg Ser Ser Thr Thr Tyr Tyr Ala
65                  70                  75                  80

gat agc gtg aaa ggc cgt ttt acc att tca cgt gat aat tcg aaa aac         288
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
                85                  90                  95

acc ctg tat ctg caa atg aac agc ctg cgt gcg gaa gat acg gcc gtg         336
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
            100                 105                 110
```

```
tat tat tgc gcg cgt ggt tat ttt cat ggt atg gat tat tgg ggc caa          384
Tyr Tyr Cys Ala Arg Gly Tyr Phe His Gly Met Asp Tyr Trp Gly Gln
        115                 120                 125

ggc acc ctg gtg acg gtt agc tca gcc tcc acc aag ggt cca tcg gtc          432
Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
    130                 135                 140

ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc          480
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
145                 150                 155                 160

ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg          528
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
                165                 170                 175

tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc          576
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
            180                 185                 190

cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc          624
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
        195                 200                 205

tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag          672
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
    210                 215                 220

ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt gac          720
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
225                 230                 235                 240

aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga          768
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
                245                 250                 255

ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc          816
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
            260                 265                 270

tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa          864
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
        275                 280                 285

gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat          912
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
    290                 295                 300

aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac cgg          960
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
305                 310                 315                 320

gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag         1008
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
                325                 330                 335

gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag         1056
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
            340                 345                 350

aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac         1104
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
        355                 360                 365

acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc ctg         1152
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
    370                 375                 380
```

```
acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg       1200
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
385                 390                 395                 400

gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg       1248
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
                405                 410                 415

ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac       1296
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
            420                 425                 430

aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat       1344
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
        435                 440                 445

gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg       1392
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
    450                 455                 460

ggt aaa tga                                                          1401
Gly Lys
465
```

<210> 51
<211> 466
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 51

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

Val Leu Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
            20                  25                  30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
        35                  40                  45

Asn Ser Tyr Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60

Glu Trp Val Ser Tyr Ile Ser Ser Arg Ser Ser Thr Thr Tyr Tyr Ala
65                  70                  75                  80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
                85                  90                  95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Arg Gly Tyr Phe His Gly Met Asp Tyr Trp Gly Gln
        115                 120                 125

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
```

130 135 140

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
145 150 155 160

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
165 170 175

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
180 185 190

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
195 200 205

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
210 215 220

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
225 230 235 240

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
245 250 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
260 265 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
275 280 285

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
290 295 300

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
305 310 315 320

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
325 330 335

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
340 345 350

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
355 360 365

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
370 375 380

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
385 390 395 400

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val

405 410 415

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
420 425 430

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
435 440 445

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
450 455 460

Gly Lys
465

<210> 52
<211> 702
<212> DNA
<213> Artificial Sequence

<220>
<223> MOR07919 light chain

<220>
<221> CDS
<222> (1)..(702)

<400> 52

```
atg gcc tgg gct ctg ctg ctc ctc acc ctc ctc act cag ggc aca gga          48
Met Ala Trp Ala Leu Leu Leu Leu Thr Leu Leu Thr Gln Gly Thr Gly
1               5                  10                  15

tcc tgg gct gat atc gaa ctg acc cag ccg cct tca gtg agc gtt gca          96
Ser Trp Ala Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala
            20                  25                  30

cca ggt cag acc gcg cgt atc tcg tgt agc ggc gat tct ctt ggt tct         144
Pro Gly Gln Thr Ala Arg Ile Ser Cys Ser Gly Asp Ser Leu Gly Ser
        35                  40                  45

aag tat gtt cat tgg tac cag cag aaa ccc ggg cag gcg cca gtt ctt         192
Lys Tyr Val His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu
    50                  55                  60

gtg att tat cgt gat aat aag cgt ccc tca ggc atc ccg gaa cgc ttt         240
Val Ile Tyr Arg Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe
65                  70                  75                  80

agc gga tcc aac agc ggc aac acc gcg acc ctg acc att agc ggc act         288
Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr
                85                  90                  95

cag gcg gaa gac gaa gcg gat tat tat tgc cag tct tat gat gct act         336
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ala Thr
            100                 105                 110

gag ttt act tat gtg ttt ggc ggc ggc acg aag tta acc gtc cta ggt         384
Glu Phe Thr Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
        115                 120                 125

cag ccc aag gct gcc ccc tcg gtc act ctg ttc ccg ccc tcc tct gag         432
Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
    130                 135                 140
```

```
gag ctt caa gcc aac aag gcc aca ctg gtg tgt ctc ata agt gac ttc        480
Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
145                 150                 155                 160

tac ccg gga gcc gtg aca gtg gcc tgg aag gca gat agc agc ccc gtc        528
Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
                165                 170                 175

aag gcg gga gtg gag acc acc aca ccc tcc aaa caa agc aac aac aag        576
Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
            180                 185                 190

tac gcg gcc agc agc tat ctg agc ctg acg cct gag cag tgg aag tcc        624
Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
        195                 200                 205

cac aga agc tac agc tgc cag gtc acg cat gaa ggg agc acc gtg gag        672
His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
    210                 215                 220

aag aca gtg gcc cct aca gaa tgt tca tag                               702
Lys Thr Val Ala Pro Thr Glu Cys Ser
225                 230
```

<210> 53
<211> 233
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 53

```
Met Ala Trp Ala Leu Leu Leu Leu Thr Leu Leu Thr Gln Gly Thr Gly
1               5                   10                  15

Ser Trp Ala Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala
            20                  25                  30

Pro Gly Gln Thr Ala Arg Ile Ser Cys Ser Gly Asp Ser Leu Gly Ser
        35                  40                  45

Lys Tyr Val His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu
    50                  55                  60

Val Ile Tyr Arg Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe
65                  70                  75                  80

Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr
                85                  90                  95

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ala Thr
            100                 105                 110

Glu Phe Thr Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
        115                 120                 125
```

```
Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
    130                 135                 140

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
145                 150                 155                 160

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
                165                 170                 175

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
            180                 185                 190

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
        195                 200                 205

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
    210                 215                 220

Lys Thr Val Ala Pro Thr Glu Cys Ser
225                 230
```

<210> 54
<211> 708
<212> DNA
<213> Artificial Sequence

<220>
<223> MOR07692 light chain

<220>
<221> CDS
<222> (1)..(708)

<400> 54

```
atg gtg ttg cag acc cag gtc ttc att tct ctg ttg ctc tgg atc tct          48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1               5                   10                  15

ggt gcc tac ggg gat atc gtg ctg acc cag agc ccg gcg acc ctg agc          96
Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
            20                  25                  30

ctg tct ccg ggc gaa cgt gcg acc ctg agc tgc aga gcg agc cag tct         144
Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
        35                  40                  45

gtt tct ttt gat tat ctg ggt tgg tac cag cag aaa cca ggt caa gca         192
Val Ser Phe Asp Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala
    50                  55                  60

ccg cgt cta tta att tat ggt gct tct aat cgt gca act ggg gtc ccg         240
Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro
65                  70                  75                  80

gcg cgt ttt agc ggc tct gga tcc ggc acg gat ttt acc ctg acc att         288
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
                85                  90                  95

agc agc ctg gaa cct gaa gac ttt gcg act tat tat tgc cag cag tat         336
Ser Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr
```

```
          100                 105                 110

tat aat atg cct tat acc ttt ggc cag ggt acg aaa gtt gaa att aaa        384
Tyr Asn Met Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
        115                 120                 125

cgt acg gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag        432
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
    130                 135                 140

cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc        480
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145                 150                 155                 160

tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa        528
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
                165                 170                 175

tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc        576
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
            180                 185                 190

acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag        624
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
        195                 200                 205

aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg        672
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
    210                 215                 220

ccc gtc aca aag agc ttc aac agg gga gag tgt tag                       708
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235


<210>  55
<211>  235
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  55

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1               5                   10                  15


Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
            20                  25                  30


Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
        35                  40                  45


Val Ser Phe Asp Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala
    50                  55                  60


Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro
65                  70                  75                  80


Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
                85                  90                  95
```

Ser Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr
100 105 110

Tyr Asn Met Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 56
<211> 708
<212> DNA
<213> Artificial Sequence

<220>
<223> MOR07923 light chain

<220>
<221> CDS
<222> (1)..(708)

<400> 56
atg gtg ttg cag acc cag gtc ttc att tct ctg ttg ctc tgg atc tct 48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

ggt gcc tac ggg gat atc gtg ctg acc cag agc ccg gcg acc ctg agc 96
Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

ctg tct ccg ggc gaa cgt gcg acc ctg agc tgc aga gcg agc cag tct 144
Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

gtt tct ttt gat tat ctg ggt tgg tac cag cag aaa cca ggt caa gca 192
Val Ser Phe Asp Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

ccg cgt cta tta att tat ggt gct tct aat cgt gca act ggg gtc ccg 240

```
Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro
65                  70                  75                  80

gcg cgt ttt agc ggc tct gga tcc ggc acg gat ttt acc ctg acc att  288
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
                85                  90                  95

agc agc ctg gaa cct gaa gac ttt gcg acc tat tat tgc ttt cag tat  336
Ser Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Tyr
            100                 105                 110

ctt att gtt cct ttt acc ttt ggc cag ggt acg aaa gtt gaa att aaa  384
Leu Ile Val Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
        115                 120                 125

cgt acg gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag  432
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
    130                 135                 140

cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc  480
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145                 150                 155                 160

tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa  528
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
                165                 170                 175

tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc  576
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
            180                 185                 190

acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag  624
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
        195                 200                 205

aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg  672
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
    210                 215                 220

ccc gtc aca aag agc ttc aac agg gga gag tgt tag                  708
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235


<210>  57
<211>  235
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  57

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1               5                   10                  15


Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
            20                  25                  30


Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
        35                  40                  45


Val Ser Phe Asp Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala
    50                  55                  60
```

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

Ser Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Tyr
100 105 110

Leu Ile Val Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 58
<211> 708
<212> DNA
<213> Artificial Sequence

<220>
<223> MOR07924 light chain

<220>
<221> CDS
<222> (1)..(708)

<400> 58
atg gtg ttg cag acc cag gtc ttc att tct ctg ttg ctc tgg atc tct 48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

ggt gcc tac ggg gat atc gtg ctg acc cag agc ccg gcg acc ctg agc 96
Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

```
ctg tct ccg ggc gaa cgt gcg acc ctg agc tgc aga gcg agc cag tct        144
Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
        35                  40                  45

gtt tct ttt gat tat ctg ggt tgg tac cag cag aaa cca ggt caa gca        192
Val Ser Phe Asp Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala
    50                  55                  60

ccg cgt cta tta att tat ggt gct tct aat cgt gca act ggg gtc ccg        240
Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro
65                  70                  75                  80

gcg cgt ttt agc ggc tct gga tcc ggc acg gat ttt acc ctg acc att        288
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
                85                  90                  95

agc agc ctg gaa cct gaa gac ttt gcg acc tat tat tgc cag cag tat        336
Ser Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr
            100                 105                 110

aat att aat cct ttt acc ttt ggc cag ggt acg aaa gtt gaa att aaa        384
Asn Ile Asn Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
        115                 120                 125

cgt acg gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag        432
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
    130                 135                 140

cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc        480
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145                 150                 155                 160

tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa        528
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
                165                 170                 175

tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc        576
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
            180                 185                 190

acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag        624
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
        195                 200                 205

aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg        672
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
    210                 215                 220

ccc gtc aca aag agc ttc aac agg gga gag tgt tag                       708
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
```

<210> 59
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 59

```
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1               5                   10                  15

Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
```

20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

Val Ser Phe Asp Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

Ser Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr
100 105 110

Asn Ile Asn Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 60
<211> 708
<212> DNA
<213> Artificial Sequence

<220>
<223> MOR07925 light chain

<220>
<221> CDS
<222> (1)..(708)

<400> 60

```
atg gtg ttg cag acc cag gtc ttc att tct ctg ttg ctc tgg atc tct        48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1               5                  10                  15

ggt gcc tac ggg gat atc gtg ctg acc cag agc ccg gcg acc ctg agc        96
Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
            20                  25                  30

ctg tct ccg ggc gaa cgt gcg acc ctg agc tgc aga gcg agc cag tct       144
Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
        35                  40                  45

gtt tct ttt gat tat ctg ggt tgg tac cag cag aaa cca ggt caa gca       192
Val Ser Phe Asp Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala
    50                  55                  60

ccg cgt cta tta att tat ggt gct tct aat cgt gca act ggg gtc ccg       240
Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro
65                  70                  75                  80

gcg cgt ttt agc ggc tct gga tcc ggc acg gat ttt acc ctg acc att       288
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
                85                  90                  95

agc agc ctg gaa cct gaa gac ttt gcg acc tat tat tgc ctt cag tat       336
Ser Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Tyr
            100                 105                 110

ttt aat cct cct cat acc ttt ggc cag ggt acg aaa gtt gaa att aaa       384
Phe Asn Pro Pro His Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
        115                 120                 125

cgt acg gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag       432
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
    130                 135                 140

cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc       480
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145                 150                 155                 160

tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa       528
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
                165                 170                 175

tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc       576
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
            180                 185                 190

acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag       624
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
        195                 200                 205

aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg       672
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
    210                 215                 220

ccc gtc aca aag agc ttc aac agg gga gag tgt tag                       708
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
```

<210> 61
<211> 235
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 61

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Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1               5                  10                  15

Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
            20                  25                  30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
        35                  40                  45

Val Ser Phe Asp Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala
    50                  55                  60

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro
65                  70                  75                  80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
                85                  90                  95

Ser Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Tyr
            100                 105                 110

Phe Asn Pro Pro His Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
        115                 120                 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
    130                 135                 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145                 150                 155                 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
                165                 170                 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
            180                 185                 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
        195                 200                 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
    210                 215                 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
```

<210> 62
<211> 708
<212> DNA
<213> Artificial Sequence

<220>
<223> MOR07926 light chain

<220>
<221> CDS
<222> (1)..(708)

<400> 62

```
atg gtg ttg cag acc cag gtc ttc att tct ctg ttg ctc tgg atc tct          48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1               5                   10                  15

ggt gcc tac ggg gat atc gtg ctg acc cag agc ccg gcg acc ctg agc          96
Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
            20                  25                  30

ctg tct ccg ggc gaa cgt gcg acc ctg agc tgc aga gcg agc cag tct         144
Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
        35                  40                  45

gtt tct ttt gat tat ctg ggt tgg tac cag cag aaa cca ggt caa gca         192
Val Ser Phe Asp Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala
    50                  55                  60

ccg cgt cta tta att tat ggt gct tct aat cgt gca act ggg gtc ccg         240
Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro
65                  70                  75                  80

gcg cgt ttt agc ggc tct gga tcc ggc acg gat ttt acc ctg acc att         288
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
                85                  90                  95

agc agc ctg gaa cct gaa gac ttt gcg acc tat tat tgc ttt cag gct         336
Ser Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Ala
            100                 105                 110

ctt att atg cct ttt acc ttt ggc cag ggt acg aaa gtt gaa att aaa         384
Leu Ile Met Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
        115                 120                 125

cgt acg gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag         432
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
    130                 135                 140

cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc         480
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145                 150                 155                 160

tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa         528
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
                165                 170                 175

tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc         576
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
            180                 185                 190

acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag         624
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
        195                 200                 205

aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg         672
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
    210                 215                 220

ccc gtc aca aag agc ttc aac agg gga gag tgt tag                         708
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
```

225 230 235

<210> 63
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 63

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

Val Ser Phe Asp Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

Ser Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Ala
100 105 110

Leu Ile Met Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 64
<211> 1551
<212> DNA
<213> Artificial Sequence

<220>
<223> MOR7919 heavy chain

<220>
<221> CDS
<222> (45)..(1457)

<400> 64
taatacgact cactataggg agacccaagc tggctagcgc cacc atg aaa cac ctg 56
Met Lys His Leu
1

tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg gtc ctg tcc cag 104
Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln
5 10 15 20

gtg caa ttg gtt cag agc ggc gcg gaa gtg aaa aaa ccg ggc gaa agc 152
Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser
25 30 35

ctg aaa att agc tgc aaa ggt tcc gga tat tcc ttt act aat tat tgg 200
Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Asn Tyr Trp
40 45 50

att tct tgg gtg cgc cag atg cct ggg aag ggt ctc gag tgg atg ggc 248
Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
55 60 65

ttt atc tat ccg gat gat agc tat acc cgt tat tct ccg agc ttt cag 296
Phe Ile Tyr Pro Asp Asp Ser Tyr Thr Arg Tyr Ser Pro Ser Phe Gln
70 75 80

ggc cag gtg acc att agc gcg gat aaa agc att agc acc gcg tat ctt 344
Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
85 90 95 100

caa tgg agc agc ctg aaa gcg agc gat acg gcc atg tat tat tgc gcg 392
Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
105 110 115

cgt ttt tct tat cgt cat tat ctt gat atg gat gat cat tgg ggc caa 440
Arg Phe Ser Tyr Arg His Tyr Leu Asp Met Asp Asp His Trp Gly Gln
120 125 130

ggc acc ctg gtg acg gtt agc tca gcc tcc acc aag ggt cca tcg gtc 488
Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
135 140 145

ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc 536
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
150 155 160

ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg 584
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
165 170 175 180

tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc 632

```
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                185                 190                 195

cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc      680
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            200                 205                 210

tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag      728
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        215                 220                 225

ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt gac      776
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
    230                 235                 240

aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga      824
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
245                 250                 255                 260

ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc      872
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                265                 270                 275

tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa      920
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            280                 285                 290

gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat      968
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        295                 300                 305

aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac cgg     1016
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    310                 315                 320

gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag     1064
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
325                 330                 335                 340

gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag     1112
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                345                 350                 355

aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac     1160
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            360                 365                 370

acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc ctg     1208
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
        375                 380                 385

acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg     1256
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    390                 395                 400

gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg     1304
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
405                 410                 415                 420

ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac     1352
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                425                 430                 435

aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat     1400
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            440                 445                 450

gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg     1448
```

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
455 460 465

ggt aaa tga gggcccgttt aaacgggtgg catccctgtg acccctcccc 1497
Gly Lys
470

agtgcctctc ctggccctgg aagttgccac tccagtgccc accagccttg tcct 1551

<210> 65
<211> 470
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 65

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe
35 40 45

Thr Asn Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu
50 55 60

Glu Trp Met Gly Phe Ile Tyr Pro Asp Asp Ser Tyr Thr Arg Tyr Ser
65 70 75 80

Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser
85 90 95

Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met
100 105 110

Tyr Tyr Cys Ala Arg Phe Ser Tyr Arg His Tyr Leu Asp Met Asp Asp
115 120 125

His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
130 135 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145 150 155 160

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
165 170 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
180 185 190

```
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
        195                 200                 205

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro
225                 230                 235                 240

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
    290                 295                 300

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                325                 330                 335

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
            340                 345                 350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
        355                 360                 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
    370                 375                 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385                 390                 395                 400

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
            420                 425                 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
    450                 455                 460
```

Ser Leu Ser Pro Gly Lys
465 470

<210> 66
<211> 1539
<212> DNA
<213> Artificial Sequence

<220>
<223> MOR7692, MOR7923, MOR7924, MOR7925 and MOR7926 heavy chain

<220>
<221> CDS
<222> (45)..(1445)

<400> 66
taatacgact cactataggg agacccaagc tggctagcgc cacc atg aaa cac ctg 56
Met Lys His Leu
1

tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg gtc ctg tcc cag 104
Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln
5 10 15 20

gtg caa ttg gtg gaa agc ggc ggc ggc ctg gtg caa ccg ggc ggc agc 152
Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
25 30 35

ctg cgt ctg agc tgc gcg gcc tcc gga ttt acc ttt aat tct tat tct 200
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Ser Tyr Ser
40 45 50

atg tct tgg gtg cgc caa gcc cct ggg aag ggt ctc gag tgg gtg agc 248
Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
55 60 65

tat atc tct tct cgt tct agc act acc tat tat gcg gat agc gtg aaa 296
Tyr Ile Ser Ser Arg Ser Ser Thr Thr Tyr Tyr Ala Asp Ser Val Lys
70 75 80

ggc cgt ttt acc att tca cgt gat aat tcg aaa aac acc ctg tat ctg 344
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
85 90 95 100

caa atg aac agc ctg cgt gcg gaa gat acg gcc gtg tat tat tgc gcg 392
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
105 110 115

cgt ggt tat ttt cat ggt atg gat tat tgg ggc caa ggc acc ctg gtg 440
Arg Gly Tyr Phe His Gly Met Asp Tyr Trp Gly Gln Gly Thr Leu Val
120 125 130

acg gtt agc tca gcc tcc acc aag ggt cca tcg gtc ttc ccc ctg gca 488
Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
135 140 145

ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg 536
Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
150 155 160

gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc 584
Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
165 170 175 180

gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca 632
Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser

185 190 195

gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg 680
Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
200 205 210

ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac acc 728
Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
215 220 225

aag gtg gac aag aga gtt gag ccc aaa tct tgt gac aaa act cac aca 776
Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
230 235 240

tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc 824
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
245 250 255 260

ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct 872
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
265 270 275

gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc 920
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
280 285 290

aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca 968
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
295 300 305

aag ccg cgg gag gag cag tac aac agc acg tac cgg gtg gtc agc gtc 1016
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
310 315 320

ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc 1064
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
325 330 335 340

aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc 1112
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
345 350 355

aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca 1160
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
360 365 370

tcc cgg gag gag atg acc aag aac cag gtc agc ctg acc tgc ctg gtc 1208
Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
375 380 385

aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg 1256
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
390 395 400

cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac 1304
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
405 410 415 420

ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg 1352
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
425 430 435

cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac 1400
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
440 445 450

aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tga 1445
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

455 460 465

gggcccgttt aaacgggtgg catccctgtg acccctcccc agtgcctctc ctggccctgg 1505

aagttgccac tccagtgccc accagccttg tcct 1539

<210> 67
<211> 466
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 67

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Asn Ser Tyr Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ser Tyr Ile Ser Ser Arg Ser Ser Thr Thr Tyr Tyr Ala
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
85 90 95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Gly Tyr Phe His Gly Met Asp Tyr Trp Gly Gln
115 120 125

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
130 135 140

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
145 150 155 160

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
165 170 175

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
180 185 190

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
195 200 205

```
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
    210                 215                 220

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
225                 230                 235                 240

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
                245                 250                 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
            260                 265                 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
        275                 280                 285

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
    290                 295                 300

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
305                 310                 315                 320

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
                325                 330                 335

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
            340                 345                 350

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
        355                 360                 365

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
    370                 375                 380

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
385                 390                 395                 400

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
                405                 410                 415

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
            420                 425                 430

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
        435                 440                 445

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
    450                 455                 460

Gly Lys
465
```

<210> 68
<211> 840
<212> DNA
<213> Artificial Sequence

<220>
<223> MOR07919 lambda light chain

<220>
<221> CDS
<222> (45)..(746)

<400> 68
taatacgact cactataggg agacccaagc tggctagcgc cacc atg gcc tgg gct 56
Met Ala Trp Ala
1

ctg ctg ctc ctc acc ctc ctc act cag ggc aca gga tcc tgg gct gat 104
Leu Leu Leu Leu Thr Leu Leu Thr Gln Gly Thr Gly Ser Trp Ala Asp
5 10 15 20

atc gaa ctg acc cag ccg cct tca gtg agc gtt gca cca ggt cag acc 152
Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln Thr
25 30 35

gcg cgt atc tcg tgt agc ggc gat tct ctt ggt tct aag tat gtt cat 200
Ala Arg Ile Ser Cys Ser Gly Asp Ser Leu Gly Ser Lys Tyr Val His
40 45 50

tgg tac cag cag aaa ccc ggg cag gcg cca gtt ctt gtg att tat cgt 248
Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Arg
55 60 65

gat aat aag cgt ccc tca ggc atc ccg gaa cgc ttt agc gga tcc aac 296
Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn
70 75 80

agc ggc aac acc gcg acc ctg acc att agc ggc act cag gcg gaa gac 344
Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu Asp
85 90 95 100

gaa gcg gat tat tat tgc cag tct tat gat gct act gag ttt act tat 392
Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ala Thr Glu Phe Thr Tyr
105 110 115

gtg ttt ggc ggc ggc acg aag tta acc gtc cta ggt cag ccc aag gct 440
Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala
120 125 130

gcc ccc tcg gtc act ctg ttc ccg ccc tcc tct gag gag ctt caa gcc 488
Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala
135 140 145

aac aag gcc aca ctg gtg tgt ctc ata agt gac ttc tac ccg gga gcc 536
Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala
150 155 160

gtg aca gtg gcc tgg aag gca gat agc agc ccc gtc aag gcg gga gtg 584
Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val
165 170 175 180

gag acc acc aca ccc tcc aaa caa agc aac aac aag tac gcg gcc agc 632
Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser
185 190 195

agc tat ctg agc ctg acg cct gag cag tgg aag tcc cac aga agc tac 680

Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
200 205 210

agc tgc cag gtc acg cat gaa ggg agc acc gtg gag aag aca gtg gcc 728
Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala
215 220 225

cct aca gaa tgt tca tag gggcccgttt aaacgggtgg catccctgtg 776
Pro Thr Glu Cys Ser
230

acccctcccc agtgcctctc ctggccctgg aagttgccac tccagtgccc accagccttg 836

tcct 840

<210> 69
<211> 233
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 69

Met Ala Trp Ala Leu Leu Leu Leu Thr Leu Leu Thr Gln Gly Thr Gly
1 5 10 15

Ser Trp Ala Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala
20 25 30

Pro Gly Gln Thr Ala Arg Ile Ser Cys Ser Gly Asp Ser Leu Gly Ser
35 40 45

Lys Tyr Val His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu
50 55 60

Val Ile Tyr Arg Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe
65 70 75 80

Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr
85 90 95

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ala Thr
100 105 110

Glu Phe Thr Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
115 120 125

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
130 135 140

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
145 150 155 160

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
165 170 175

```
Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
            180                 185                 190

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
        195                 200                 205

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
    210                 215                 220

Lys Thr Val Ala Pro Thr Glu Cys Ser
225                 230
```

<210> 70
<211> 846
<212> DNA
<213> Artificial Sequence

<220>
<223> MOR07692 kappa light chain

<220>
<221> CDS
<222> (45)..(752)

<400> 70

```
taatacgact cactataggg agacccaagc tggctagcgc cacc atg gtg ttg cag          56
                                                 Met Val Leu Gln
                                                 1

acc cag gtc ttc att tct ctg ttg ctc tgg atc tct ggt gcc tac ggg          104
Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly
5                   10                  15                  20

gat atc gtg ctg acc cag agc ccg gcg acc ctg agc ctg tct ccg ggc          152
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
                25                  30                  35

gaa cgt gcg acc ctg agc tgc aga gcg agc cag tct gtt tct ttt gat          200
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Phe Asp
            40                  45                  50

tat ctg ggt tgg tac cag cag aaa cca ggt caa gca ccg cgt cta tta          248
Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        55                  60                  65

att tat ggt gct tct aat cgt gca act ggg gtc ccg gcg cgt ttt agc          296
Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
    70                  75                  80

ggc tct gga tcc ggc acg gat ttt acc ctg acc att agc agc ctg gaa          344
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
85                  90                  95                  100

cct gaa gac ttt gcg act tat tat tgc cag cag tat tat aat atg cct          392
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Asn Met Pro
                105                 110                 115

tat acc ttt ggc cag ggt acg aaa gtt gaa att aaa cgt acg gtg gct          440
Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
            120                 125                 130
```

```
gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct        488
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        135                 140                 145

gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag        536
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    150                 155                 160

gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc        584
Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
165                 170                 175                 180

cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc        632
Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                185                 190                 195

agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc        680
Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            200                 205                 210

tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag        728
Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
        215                 220                 225

agc ttc aac agg gga gag tgt tag gggcccgttt aaacgggtgg catccctgtg        782
Ser Phe Asn Arg Gly Glu Cys
    230                 235

acccctcccc agtgcctctc ctggccctgg aagttgccac tccagtgccc accagccttg       842

tcct                                                                   846
```

<210> 71
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 71

```
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1               5                   10                  15

Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
            20                  25                  30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
        35                  40                  45

Val Ser Phe Asp Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala
    50                  55                  60

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro
65                  70                  75                  80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
                85                  90                  95

Ser Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr
```

100 105 110

Tyr Asn Met Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 72
<211> 846
<212> DNA
<213> Artificial Sequence

<220>
<223> MOR07923 kappa light chain

<220>
<221> CDS
<222> (45)..(752)

<400> 72
taatacgact cactataggg agacccaagc tggctagcgc cacc atg gtg ttg cag 56
Met Val Leu Gln
1

acc cag gtc ttc att tct ctg ttg ctc tgg atc tct ggt gcc tac ggg 104
Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly
5 10 15 20

gat atc gtg ctg acc cag agc ccg gcg acc ctg agc ctg tct ccg ggc 152
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
25 30 35

gaa cgt gcg acc ctg agc tgc aga gcg agc cag tct gtt tct ttt gat 200
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Phe Asp
40 45 50

tat ctg ggt tgg tac cag cag aaa cca ggt caa gca ccg cgt cta tta 248
Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
55 60 65

```
att tat ggt gct tct aat cgt gca act ggg gtc ccg gcg cgt ttt agc        296
Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
    70                  75                  80

ggc tct gga tcc ggc acg gat ttt acc ctg acc att agc agc ctg gaa        344
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
85                  90                  95                  100

cct gaa gac ttt gcg acc tat tat tgc ttt cag tat ctt att gtt cct        392
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Tyr Leu Ile Val Pro
                105                 110                 115

ttt acc ttt ggc cag ggt acg aaa gtt gaa att aaa cgt acg gtg gct        440
Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
            120                 125                 130

gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct        488
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        135                 140                 145

gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag        536
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    150                 155                 160

gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc        584
Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
165                 170                 175                 180

cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc        632
Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                185                 190                 195

agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc        680
Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            200                 205                 210

tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag        728
Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
        215                 220                 225

agc ttc aac agg gga gag tgt tag gggcccgttt aaacgggtgg catccctgtg        782
Ser Phe Asn Arg Gly Glu Cys
    230                 235

acccctcccc agtgcctctc ctggccctgg aagttgccac tccagtgccc accagccttg       842

tcct                                                                   846
```

<210> 73
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 73

```
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1               5                   10                  15

Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
            20                  25                  30
```

```
Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
        35                  40                  45

Val Ser Phe Asp Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala
    50                  55                  60

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro
65                  70                  75                  80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
                85                  90                  95

Ser Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Tyr
            100                 105                 110

Leu Ile Val Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
        115                 120                 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
    130                 135                 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145                 150                 155                 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
                165                 170                 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
            180                 185                 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
        195                 200                 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
    210                 215                 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235


<210>  74
<211>  846
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  MOR07924 kappa light chain


<220>
<221>  CDS
<222>  (45)..(752)

<400>  74
taatacgact cactataggg agacccaagc tggctagcgc cacc atg gtg ttg cag        56
                                                Met Val Leu Gln
```

```
acc cag gtc ttc att tct ctg ttg ctc tgg atc tct ggt gcc tac ggg        104
Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly
5                   10                  15                  20

gat atc gtg ctg acc cag agc ccg gcg acc ctg agc ctg tct ccg ggc        152
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
                25                  30                  35

gaa cgt gcg acc ctg agc tgc aga gcg agc cag tct gtt tct ttt gat        200
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Phe Asp
            40                  45                  50

tat ctg ggt tgg tac cag cag aaa cca ggt caa gca ccg cgt cta tta        248
Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        55                  60                  65

att tat ggt gct tct aat cgt gca act ggg gtc ccg gcg cgt ttt agc        296
Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
    70                  75                  80

ggc tct gga tcc ggc acg gat ttt acc ctg acc att agc agc ctg gaa        344
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
85                  90                  95                  100

cct gaa gac ttt gcg acc tat tat tgc cag cag tat aat att aat cct        392
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Asn Pro
                105                 110                 115

ttt acc ttt ggc cag ggt acg aaa gtt gaa att aaa cgt acg gtg gct        440
Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
            120                 125                 130

gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct        488
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        135                 140                 145

gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag        536
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    150                 155                 160

gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc        584
Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
165                 170                 175                 180

cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc        632
Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                185                 190                 195

agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc        680
Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            200                 205                 210

tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag        728
Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
        215                 220                 225

agc ttc aac agg gga gag tgt tag gggcccgttt aaacgggtgg catccctgtg        782
Ser Phe Asn Arg Gly Glu Cys
    230                 235

acccctcccc agtgcctctc ctggccctgg aagttgccac tccagtgccc accagccttg        842

tcct                                                                    846
```

<210> 75

<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 75

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

Val Ser Phe Asp Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

Ser Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr
100 105 110

Asn Ile Asn Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 76
<211> 846
<212> DNA
<213> Artificial Sequence

<220>
<223> MOR07925 kappa light chain

<220>
<221> CDS
<222> (45)..(752)

<400> 76
taatacgact cactataggg agacccaagc tggctagcgc cacc atg gtg ttg cag 56
Met Val Leu Gln
1

acc cag gtc ttc att tct ctg ttg ctc tgg atc tct ggt gcc tac ggg 104
Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly
5 10 15 20

gat atc gtg ctg acc cag agc ccg gcg acc ctg agc ctg tct ccg ggc 152
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
25 30 35

gaa cgt gcg acc ctg agc tgc aga gcg agc cag tct gtt tct ttt gat 200
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Phe Asp
40 45 50

tat ctg ggt tgg tac cag cag aaa cca ggt caa gca ccg cgt cta tta 248
Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
55 60 65

att tat ggt gct tct aat cgt gca act ggg gtc ccg gcg cgt ttt agc 296
Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
70 75 80

ggc tct gga tcc ggc acg gat ttt acc ctg acc att agc agc ctg gaa 344
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
85 90 95 100

cct gaa gac ttt gcg acc tat tat tgc ctt cag tat ttt aat cct cct 392
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Tyr Phe Asn Pro Pro
105 110 115

cat acc ttt ggc cag ggt acg aaa gtt gaa att aaa cgt acg gtg gct 440
His Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
120 125 130

gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct 488
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
135 140 145

gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag 536
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
150 155 160

gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc 584
Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
165 170 175 180

cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc 632
Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
185 190 195

agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc 680

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
200 205 210

tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag 728
Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
215 220 225

agc ttc aac agg gga gag tgt tag gggcccgttt aaacgggtgg catccctgtg 782
Ser Phe Asn Arg Gly Glu Cys
230 235

acccctcccc agtgcctctc ctggccctgg aagttgccac tccagtgccc accagccttg 842

tcct 846

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<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 77

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
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Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

Val Ser Phe Asp Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

Ser Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Tyr
100 105 110

Phe Asn Pro Pro His Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

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Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
            180                 185                 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
        195                 200                 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
    210                 215                 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235


<210>  78
<211>  846
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  MOR07926 kappa light chain


<220>
<221>  CDS
<222>  (45)..(752)

<400>  78
taatacgact cactataggg agacccaagc tggctagcgc cacc atg gtg ttg cag          56
                                                Met Val Leu Gln
                                                1

acc cag gtc ttc att tct ctg ttg ctc tgg atc tct ggt gcc tac ggg          104
Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly
5                   10                  15                  20

gat atc gtg ctg acc cag agc ccg gcg acc ctg agc ctg tct ccg ggc          152
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
                25                  30                  35

gaa cgt gcg acc ctg agc tgc aga gcg agc cag tct gtt tct ttt gat          200
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Phe Asp
            40                  45                  50

tat ctg ggt tgg tac cag cag aaa cca ggt caa gca ccg cgt cta tta          248
Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        55                  60                  65

att tat ggt gct tct aat cgt gca act ggg gtc ccg gcg cgt ttt agc          296
Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
    70                  75                  80

ggc tct gga tcc ggc acg gat ttt acc ctg acc att agc agc ctg gaa          344
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
85                  90                  95                  100

cct gaa gac ttt gcg acc tat tat tgc ttt cag gct ctt att atg cct          392
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Ala Leu Ile Met Pro
                105                 110                 115

ttt acc ttt ggc cag ggt acg aaa gtt gaa att aaa cgt acg gtg gct          440
Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
            120                 125                 130
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gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct        488
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        135                 140                 145

gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag        536
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    150                 155                 160

gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc        584
Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
165                 170                 175                 180

cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc        632
Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                185                 190                 195

agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc        680
Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            200                 205                 210

tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag        728
Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
        215                 220                 225

agc ttc aac agg gga gag tgt tag gggcccgttt aaacgggtgg catccctgtg        782
Ser Phe Asn Arg Gly Glu Cys
    230                 235

acccctcccc agtgcctctc ctggccctgg aagttgccac tccagtgccc accagccttg       842

tcct                                                                   846
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<210> 79
<211> 235
<212> PRT
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<220>
<223> Synthetic Construct

<400> 79

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Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1               5                   10                  15

Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
            20                  25                  30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
        35                  40                  45

Val Ser Phe Asp Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala
    50                  55                  60

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Val Pro
65                  70                  75                  80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
                85                  90                  95

Ser Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Ala
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100 105 110

Leu Ile Met Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 80
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<212> PRT
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<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (99)..(116)
<223> Xaa can be any naturally occurring amino acid

<400> 80

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60

Xaa Xaa Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100 105 110

Xaa Xaa Xaa Xaa Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 81
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable heavy chain 5

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<220>
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<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (99)..(116)
<223> Xaa can be any naturally occurring amino acid

<400> 81

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60

Xaa Xaa Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr

65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100 105 110

Xaa Xaa Xaa Xaa Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 82
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<212> PRT
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<220>
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<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (86)..(86)
<223> T

<220>
<221> misc_feature
<222> (90)..(98)
<223> Xaa can be any naturally occurring amino acid

<400> 82

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95

Xaa Xaa Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 83
<211> 110
<212> PRT
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<223> Xaa can be any naturally occurring amino acid

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<222> (48)..(55)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (88)..(98)
<223> Xaa can be any naturally occurring amino acid

<400> 83

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

Thr Ala Arg Ile Ser Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Xaa Val Ile Xaa
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95

Xaa Xaa Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
100 105 110